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                    GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on:   October 8, 2002, 22:59:14 ; Search time 866 Seconds
                                        (without alignments)
                                        18626.341 Million cell updates/sec

Title:           US-09-828-498-1
Perfect score:   9395
Sequence:        1 tgacgtggggggttgatcc.........cccaaaggccgggttctact 9395

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        173436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters:      3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_032802:*
   1: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/NA1980.DAT:*
   2: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/NA1981.DAT:*
   3: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/NA1982.DAT:*
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   5: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/NA1984.DAT:*
   6: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/NA1985.DAT:*
   7: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/NA1986.DAT:*
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  22: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/NA2001A.DAT:*
  23: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/NA2001B.DAT:*
  24: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/NA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8100.6	86.2	9395	19	AAT76930	GT110 gene cDNA se
2	7979	84.9	9392	19	AAV66102	HGV-PNF2161 varian
3	7979	84.9	9392	19	AAV56058	HGV isolate PNF 21
4	7979	84.9	9392	20	AAX16351	Polynucleotide seq
5	7979	84.9	9392	20	AAX02334	US5856134 Seq ID 1
6	7979	84.9	9392	20	AAV82093	Hepatitis G virus
7	7977.4	84.9	9392	17	AAT08812	Hepatitis G virus
8	7971.8	84.9	9391	17	AAT15656	HGV-PNF 2161 polyp
9	7971.8	84.9	9391	18	AAT94168	Hepatitis G virus
10	7885.6	83.9	9327	19	AAV66279	Recombinant HGV se
11	7885.6	83.9	9327	19	AAV56242	HGV isolate 32HGV-
12	7885.6	83.9	9327	20	AAX16505	Polynucleotide seq
13	7885.6	83.9	9327	20	AAX02517	US5856134 Seq ID 2
14	7885.6	83.9	9327	20	AAV82248	Hepatitis G virus
15	7884	83.9	9327	17	AAT08958	Hepatitis G virus
16	7760.6	82.6	9103	17	AAT15657	HGV-JC variant pol
17	7760.6	82.6	9103	17	AAT08856	Hepatitis G virus
18	7760.6	82.6	9103	19	AAV66229	Hepatitis G virus
19	7760.6	82.6	9103	19	AAV56192	HGV variant JC cDN
20	7760.6	82.6	9103	20	AAX16395	Consensus sequence
21	7760.6	82.6	9103	20	AAX02467	US5856134 Seq ID 1
22	7760.6	82.6	9103	20	AAV82137	Hepatitis G virus
23	7548.2	80.3	9390	19	AAT76929	GT230 genomic RNA
24	7548.2	80.3	9390	19	AAT76931	GT230 gene cDNA se
25	7469.6	79.5	9390	19	AAV23078	Fragment HGJ1789 o
26	7418.4	79.0	9391	19	AAV23083	Fragment K3732(2Y)
27	7414.4	78.9	9391	19	AAV23076	Fragment HGJ1737 o
28	7373.8	78.5	9391	19	AAV23081	Fragment HGJ1668 o
29	7373	78.5	9014	18	AAT45836	Hepatitis GB virus
30	7369.6	78.4	9391	19	AAV23077	Fragment HGJ1741 o
31	7311.6	77.8	9331	19	AAV23079	Fragment HGJ1916 o
32	7288.2	77.6	9256	19	AAV23075	Fragment HGJ606 of
33	7243.6	77.1	9333	19	AAV23084	Fragment F1029 of
34	7200.8	76.6	9271	19	AAV23080	Fragment HGJ2141 o
35	7141.6	76.0	9126	19	AAV39074	Hepatitis GB virus
36	7141.2	76.0	9126	18	AAT96447	Fragment of HGBV N
37	7141.2	76.0	9126	18	AAT45828	Hepatitis GB virus
38	7106.6	75.6	9122	17	AAT42920	GB-C viral genomic
39	7034.6	74.9	9034	21	AAA55380	Hepatitis GB virus
40	7033	74.9	9034	16	AAT04247	Hepatitis GB virus
41	6711.8	71.4	8630	19	AAV23082	Fragment HGJ1775 o
42	3861.8	41.1	5091	22	AAA55442	Hepatitis GB virus
43	2143.4	22.8	2561	18	AAT94159	Hepatitis G virus
44	2141.8	22.8	2561	18	AAT94162	Hepatitis G virus
45	2141.8	22.8	2561	18	AAT94160	Hepatitis G virus

ALIGNMENTS

```
RESULT 1
AAT76930
ID   AAT76930 standard; cDNA; 9395 BP.
XX
AC   AAT76930;
XX
DT   11-SEP-1998  (first entry)
XX
DE   GT110 gene cDNA sequence for detection of GBV-C/HGV gene.
XX
KW   Hepatitis virus; GT110 gene; GT230 gene; GBV-C/HGV; detection; ss.
XX
OS   Hepatitis virus.
XX
PN   JP09276000-A.
XX
PD   28-OCT-1997.
XX
PF   18-APR-1996;  96JP-0134117.
XX
PR   18-APR-1996;  96JP-0134117.
XX
PA   (NIAK-) NIAKKU YG.
XX
DR   WPI; 1998-022168/03.
XX
PT   NonA nonB non C hepatitis virus gene - used for the detection of
PT   GBV-C/HGV in a sample
XX
PS   Claim 5; Pages 29-34; 42pp; Japanese.
XX
CC   This represents the cDNA sequence of the GT110 gene. Sequences shown in
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CC   AAT76929 to AAT76931 can be used for the detection of GBV-C/HGV gene.
CC   An oligonucleotide consisting of at least 20 nucleotides which belong to
CC   3'- or 5' untranslated region of GBV-C/HGV and is high in storage
CC   ability among the above polynucleotide sequences can also be used for
XX   the detection of the GBV-C/HGV genetic-type specific gene.
SQ   Sequence 9395 BP; 1692 A; 2554 C; 2995 G; 2154 T; 0 other;

Query Match             86.2%;  Score 8100.6;  DB 19;  Length 9395;
Best Local Similarity   91.4%;  Pred. No. 0;
Matches 8586;  Conservative   0;  Mismatches 809;  Indels   0;  Gaps     0;

Qy          1 TGACGTGGGGGGGTTGATCCCCCCCCCGCACTGGGTCAAGCCCATAAACCGACGC 60
              ||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Db          1 TGACGTGGGGGGGTTGATCCCCCCCCCGGCACTGGGTCAAGCCCCAGAAACCGACGC 60

Qy         61 CTATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCGACCGGCCAAAAGGTGGTGGAT 120
              ||||||||||||||||||||||||||||||| |||||| || |||||||||||||||||
Db         61 CTATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCGACCGGCCAAAAGGTGGTGGAT 120

Qy        121 GGGTGGTGACAGGGTTGGTAGTGCGTAAATCCCGTCATCCTGGTAGCCACTATAGGTGG 180
              ||||| |||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Db        121 GGGTGATGACAGGGTTGGTAGTGCGTAAATCCCGTCATCCTGGTAGCCACTATAGGTGG 180

Qy        181 GTCTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTGCGGCCAGACCGCGCACGGTCCACAG 240
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        181 GTCTTAAGAGAAGGTCAAGATTCCTCTTACGCCTGCGGCCAGACCGCGCACGGTCCACAG 240

Qy        241 GTGCTGGCCTACCGGTGTGAATAAGGGCCCGACGTCGTCAGGCTCGTAAACCGAGCCC 300
              ||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||
Db        241 GTGTTGGCCTACCGGTGTGAATAAGGGCCCGACATCAGGCAAATCAGGCTCGTAAACCGAGCCC 300

Qy        301 GTCACCCACTGGGCAAACAGCACGCCCACGTACGGTCCACGTCGCCCTTCAATGTCTCTCT 360
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTACCCGCCTGGGCAAACAGCACGCCCACGTACGGTCCACGTCGCCCTTCAATGTCTCTCT 360

Qy        361 TGACCAATAGGTTTATCCGGCAGTTGACAAGGACCAGTGGGGCCCAGGGGTTATGGGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGACCAATAGGTTTATCCGGCAGTTGGCAAGGACCAGTGGGGCCCGGGGGGTTATGGGGA 420

Qy        421 AGGACCCCAAACCCTGCCCTTCCCGGTGGGCGGGGAAATGCATGGGGCCACCAGCTCCG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGACCCCAAGCCCTGCCCATCCCGGCCGGGAAATGCATGGGGCCACCCAGCTCCG 480

Qy        481 CGGCGCCTCAGCCGCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGGCATTTCTC 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGGCGCCTCAGCCGCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGGCATTTTCT 540

Qy        541 TTTTCTATACCATCATGGCCACTGTATCAGGCGGGGTTGGCTGTGCGGCCCGGCCATTC 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTTACCATCATGGCCACTGTATCAGGCGGGGTTGGCTGTGCGGCCCGGCCAGT 600

Qy        601 TGGCCCCGGCCAGCTGTGGGGAGCAACCACGCGTTGCTGAGCGCAATATTTCCTCACAAATGCTGTG 660
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        601 TGGCCCCGGCCAGCTGTGTGGGAGCAACTGGGGAAATGGCAATATTTCCTCACAAATTGTTGCGC 660

Qy        661 CCCCGGAAGACATCGGGTTCTGCCGTCTCGGAAGGCGGATGGCTTGGTGCCCTGGGGTGCACGG 720
              |||| |||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCAGGAAGACACATTGGGTTCTGCCTTGAAGGTGAGGGCGTTGGGCCTGGGGTGCACAG 720

Qy        721 TTTGCACCGACCGGTTGCTGGCCACTGTATCAGGCGGGGTTTGGCTGTGCGGCCCGGCAAGT 780
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        721 TTTTGTACTGACGATCGTGATCAGGCGGGGTTTGGCCTTGAGCGTGTGCGGCCCGGCAAGT 780

Qy        781 CGGCGGCCCAGCTCGGGGGAGCGCGTACGGGACCCTTGTCGGGCCTTTGTTACGGGTCTCGGCTT 840
              ||||| ||| | ||||| |||||||||||||||||||||||||||||||||||||||||||
Db        781 CCGCAGCTCAGCTGTGGGAGCAACTGGGGAGCCCTTATCCGGTCCTCGCGGTATGGGTCTCGGCCT 840

Qy        841 ACGTAGCCGGGATCCTGGGTCTGGCGGAGGTTTACTCCGGGTTTACTCACGAGTTGGTGTTG 900
              ||||| || |||| ||||| |||| ||||||| |  | |  |  |||||||||||||||||
Db        841 ACGTGGCCGGGATCTTGGGCCTGGAGCGTGTCTTAAACAGTTGGTTCAGTTGGTGTTG 900

Qy        901 CGTTGAGGGCGCCGGGCTACACCTGATGCCCAACCTGAAGTGTGCAGTAGAAATGTGACGTTA 960
              |||| || ||| ||||| | |||| |   |||||||||||||||||||||||| |||   |||
Db        901 CGTTGACGCGCCGGCGGGCTACCCCGATGCCCAACCTCACGTGTGCAGTAGAGAGTGCAGTCGTTA 960

Qy        961 AGTGGGAAGTGAGTTTGGAGATGGACTGAGCAGTTGGCCTCCAATTACTGGATTTTGG 1020
              ||||| ||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||
Db        961 AGTGGGAAAGTGAGTTTGGAGATGGACTGAGCGGTGGCCTCCAATTACTGGATTCTGG 1020

Qy       1021 AATACCTTTGGAAAGTCCCATTTGAATTTTGGAGACGGAGTGATGAGCCTGACCCCCTCTGT 1080
              ||||| ||| || ||||||||||||||||||||||||||||||||||||||||||||||| |
Db       1021 AATATCTCTGGAAGGTCCCGTTTGACTTCTCGGAGGGGGTGTGATGAGCTTGACCCCCTGC 1080

Qy       1081 TGGTTTGGGTGGCCCATTGCTTTTGCTGGAGCAACGGATTGTCATGGTTTTCCTGCTGG 1140
              ||||||||||||| |||||||||||||||||||||||||||||||||||||||| |||||
Db       1081 TGGTTTGCGTGGCCCGTTTGCTTTTCTACTGTGGAGCAACGGATTGTCATGGTCCTGCTGG 1140

Qy       1141 TGACGATGGCCGGGGATGTTGCAAGGCGCCCGGTCCCGTTTGGGGTGTCCCGCCCCTTTG 1200
              |||||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||
Db       1141 TGACGATGGGGCCGGGATGTGGGGACCGGTGGGAACGTGGGCCTCCCGCCCCTTTG 1200

Qy       1201 ACTACGGGTTGAAGTGGCAGTCATGCTCCTGCAGGGCTAACGGGTCGGTATTCCCACTG 1260
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ACTACGGGTTGACATGGCAGTCCTGCTGCAGGGCGAATGGGTCGCGTATCCCTACTG 1260

Qy       1261 GGGAGAGGGTGTGGGATCGGAGGGAATGTCGGTGGGAACGTGGGGCGGCTAACGGGTCCCCT 1320
              |||||||| || ||||||||||| | ||||||||||||||||||||||||||||||||| ||
Db       1261 GGGAGAAGGGTGTGGGACCGGTGGGAACGTGGGAACGTGGGGCGGCTCACGGTCCACGGCCGGTCCGT 1320

Qy       1321 GGGTTTGGGTCCGGCCCTTTGTCGGCGGTTGGTGGGGCGCACCCCATCACCCATTGGA 1380
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Qy       1381 GCCACGGACAAAACAGTGGCCCCTATCATGCCCCAATATGTCTATGGGTCTGTGTCCG 1440
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Qy       1441 TAACGTCGTGTGGGGTTCCGTGCCTGGTTTGCCTCGACCGCGGTCGTGATTCGAAGA 1500
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Db       1441 TCACATCGTGTGGGGTCCGTGCCTGGTTTGCCTCGACCGGCGGATTCGAAAA 1500

Qy       1501 TCGATGTGTGGAGTTGGTGCCGGTGGATCGCCAGCTGCAGCTGCACCATAGCCGCTCTAGGGT 1560
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Db       1501 TCGACGTGTGGAGTTGGTTGTTCCAGTTGGTCGCGGCGGCACCGGCGCACCATAGCTGCTCCACTCGGTT 1560

Qy       1561 CATCGGATCCGACACGGTGGTTGAGCTCTCCGCTGGGGAGTGGGGAGTCCGTGCGTAACGTGTA 1620
              ||  | || || || |||||||||||||||||||| |||||||||||||||||||| |||||||
Db       1561 CTTCGGACCGGCGATACGGTGGTTGCGAGCTCGTCGCAGCTCTGAGTGGGGTCCCGTGCCGTAACGTGTA 1620

Qy       1621 TTCTGGACCGTCGGCCTGCTTCATGTGCACCGGCTGTGTGGGACTGCTGGGCCCGAAACCG 1680
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Qy       1681 GGTCGGTTAGATTCCTTTCCATCGGTGCGCGACAGCGGCCTCGGCGTGACAAAGGACTTGG 1740
              |||||||| || ||||| |||||||||||||||||||||||||| || |||||||||| ||
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Qy       1741 AAGCTGTGCCCCTTCGTCAACAGGACAACTCCCTTCACCATGAGGGCGCCCTGGGCAACC 1800
              ||| |||| ||| |||||||||||||||||||||||| ||||  |||||||||||||||||
Db       1741 AAGCTGTGCCCCTTCGTCAACAGGACAACTCCCTTCACCATAAGGGTCCCCTGGGCAACC 1800

Qy       1801 AGGGGAGGGCAACCCGGTGCGCCCGGTTTTGGGTTTTGGGTCCTACCATGACCAAGA 1860
              ||||| |||| |||||| |||| |||| || |||||| ||| | ||| |||||| |||
Db       1801 AGGGGAGGGTAACCCGGTGCGGCCTTACCACCATGACCAAAA 1860

Qy       1861 TCCGGGATTCCCTGCCATTGGTGAAATGTCCCACACCACCAGCCTTCCGACTGGAA 1920
              |||| |||| ||| |||||||||||| ||||||||||||||||||| ||| ||||||
Db       1861 TCCGGGACTCCCTGCCATTGGTGAAATGTCCCACACCACCAGCCTTCCCACTGGGA 1920

Qy       1921 CGTTCGGGTCTTCCCCGGAGTCCTCGGCGAGTTTACTCACCGAGTTGGTGTTG 1980
              |||| |||| |||| ||||| |||||| ||||| ||| |||| ||||||||||
Db       1921 CGTTCGGGTTTTTCCCCGGAGTCCTCGGCGGCCCCCTCAACAACTGTCTTAACAGTTGGTTTG 1980

Qy       1981 TGTCTGAGGCATTGGGCGGAGCTGGGCGGGGTTCTACGGCCTTCTCACGGCCTCTGGTTGTG 2040
              |||| || || ||||| |  ||| ||   |||||||| ||||| ||||| || |||| |  ||
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Db 1981 TGTCCGAAGCATTAGGTGGGCTGGCCTTACGGGGGATTCTATGAACCCTTGGTGCGCA 2040

Qy 2041 GGTGTTCGGAGCTGATGGGACGCGCGAAATCCGGTTGCCCGGGTACCCATGGCTGTCCT 2100
          |||||||||||||||||| ||||||| |||||| |||||||| |||||||||||||||
Db 2041 GGTGTTCGGAGCTGATGGGACGCGCGAAATCCGGTTGCCCGGGTATGGCATGGCTGTCCT 2100

Qy 2101 CTGGTAGACCTGACGGGTTCATCACGTTCAGGGGCACCTGACGGGTGGATCGGGGCA 2160
          | ||| |||||| ||||| |||| |||||||||| |||||| |||||| |||| ||||
Db 2101 CGGGTCGGCCTGATGGGTTTATACATGTTCAGGGACACTTGCAGGGATGATGCAGGCA 2160

Qy 2161 ACTTCATCCTCCTCCACGCTGGTTGCTCCTGGATTTTGTATTTGTCCTGCTCTATCTGA 2220
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Db 2161 ACTTCATCCCCCTCCACGCTGGTTGCTCCTGGACTTTGTATTTGTCCTATTATACCTGA 2220

Qy 2221 TGAAGCTGCTGAGGCACGTTGGTCCCGTGATCTTGCTTCTGCTGTGTGTGGTGGGTGA 2280
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db 2221 TGAAGCTGCTGAGGCACGTTGGTCCCGTGATCTTGCTTCTGCTGTGTGTGGTGGGTCA 2280

Qy 2281 ACCAGTTGGCGGTTCTAGGACTGCCGGCTGTCCGGTGGACGCTGGCGGGTGAAGTTTTG 2340
          |||||||||| ||||||| | ||| |||| | |||| |||||| |||| ||||||||||
Db 2281 ACCAGTTGGCGGTTCCTTGGGCGGTCCAGCGTGTGCACGCGCCGTGGCGGGCTGAAGTTTTG 2340

Qy 2341 CGGGCCCTTGCCTTCTGTCATGGTGTTTGGGCCTTCCACTGTCAGTATGATACTAGGTCTAG 2400
          ||||| ||| |||||||| | ||| ||| ||||||| | ||||| |||||| ||||||
Db 2341 TGGGCCCCGCTGTCGTGTGCTTAGGCTCCCCACTGTTAGCACTGTTAGCATGACTCGGTCTGG 2400

Qy 2401 CAAACCTGGTGTTGTTGTACTTTCGGTGATGGCCCTCAGCGCCTTCAGTGTTCCTCGTGTTGT 2460
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Db 2401 CAAACCTGTGTTGTTGTACTTTCGGTGATGGCCCTCAGCGCCTTCAGTGTTCCTCGTGTTGT 2460

Qy 2461 GGAAGCTCCTCGGGGAGCTTTCCCGCCTGCACTTTGATGGGGATTTCGGCGACCCGCG 2520
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Db 2461 GGAAGCGCGGAGGGGGTGGAGCCACAAGCCTGGCTCGATGGGATCTCGATGGGGTCGCGACCCGCG 2520

Qy 2521 GGGCCACTTCGTGTCCGGGGCCCCAGAGTTCTGCTTCGATGCTTCGATGTCACATTCGAGGTGACACTT 2580
          |||| ||| ||| | ||||| || || |||| || ||| |||| ||||| |||||| |||
Db 2521 GGGCCACTTCGTGTCCGGGGCCCCAGAGTTCTGCTTCGATGCTTCGATGTCACATTCGAGGTGACACGT 2580

Qy 2581 CGGTGTTGGGCTGGTGGTGGCCCAGCGTGCGTGGTGGCCCATAGCCTTGGGCTCCTGAGCTCAA 2640
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Db 2581 CGGTGTTGGGCTGGTGGTGGGCTGGTGTGGCCCAGCGTGGTAGCCCTGGGCCATTTGGTCGCTGGCTCGA 2640

Qy 2641 TGAGCGCAGGGGGTGGAAGCACAAGGCCGTGGTCTATAGGACGTGGTAAAGGGTACC 2700
          |||||| ||| ||||| ||| ||||| | |||| |||||||| ||||||||||||||
Db 2641 TGAGCGCGGGGAGGTGGAGGCACAGAACCGTGATCTTCAGTGGCTTGACCGTGGGTAAAGGGTACC 2700

Qy 2701 AGGCTGTGCGCCAGAGGGTGGTCGCGGACGGGCGGCGTCCTACCAAGCTTC 2760
          |||| ||||| |||| ||||||| | ||||||| |||| |||||||| |||
Db 2701 AGGCTATTCGCCAAAGGTGGTGAGGTCGGCGCGGTTGCGCGTTGTGCGTGTGTCCTACTACCAAAACCCC 2760

Qy 2761 TGACGTTCGCCTGGTGCTTGGTCCCATCACGTATTCCACTTACCATATGTCTCATAGATGTGGTGGTGG 2820
          |||| |||| || ||||||| ||||||||||||| |||||| ||||| || ||||||||||||||||
Db 2761 TGACGTTTGCCTGGTGCTTGGTCCCATCACGTATTCCACTTACCATATGTCCGTGATGTGGTGGTGG 2820

Qy 2821 TGGCCTTGGTGTCCTCCTCGTGGGGACGGCACTGGACTGGGACTGGGACGCTCC 2880
          | |||| ||||||| ||| ||||||||||||||| |||||||||||||||||||
Db 2821 TTGCCTTGGTGTCCTCCTCGTGGGGACGGCACTGGACTGGGACTGGGACGCTCT 2880

Qy 2881 TGGTCTCCCGGCCCTCGTTACGGCGACTGGCACGGGTGGTGTTGAGTGTCGTGATTGGCGG 2940
          | |||||||||||| || |||| |||| ||||||||||||| | ||| |||||||||| ||
Db 2881 TGGTTTCCCGGCCCTCGTTACGGCGACTGGCACGGGTGTTGAATGGCGTGTTGAATGGCGG 2940

Qy 2941 GCGAGAAGGCCACCACCGACTCGGTCTCCAAGATGTGCGCAAGAGGGGCCTACCTGT 3000
          ||||| ||||||| ||||||||| |||||||||||||||||||||| | |||||||||
Db 2941 GTGAGAAGGCCACACCGACTCGTCTTCTACCATGGAGTTCTGCGCCCAACCCTAGGAGTTGGACGCGG 3000

Qy 3001 TTGACCACATGGGCTCTTTCTCCGCGGCCGTGTTGGAATGGACGCGG 3060
          | ||||| ||||||||||||||||| | |||||||||| ||||||||
Db 3001 TCGACCATATGGGCTCTTTCTCCGCGGCCGTGTTGGAATGGACGCGG 3060

Qy 3061 CTTTGGACGCCCTTGTCATTCACTGCAAGCTGACGGACTGCGCATCATCCGACATCACTAGGACGGAGA 3120
          ||||||| |||| ||| |||||| ||| | || |||| |||| ||||||||| |||||| ||||| ||
Db 3061 CTTTGGAACCACTGTCATTCACTGAGCTGACGGACTGCGCATCATAAGAGATGCCGCATCATCAAGAGA 3120

Qy 3121 CCCTGTCCTGCGGACAGTGCGTCATGGGTTTACCCGTGGTAGCACGGCCGCGCGCGGTGATGAGGG 3180
          |||||||||||||||||||| ||||||||||||| ||||||||| ||||||||| |||||||||||
Db 3121 CCCTGTCCTGCGGACAGTGCGTCATGGGTCTACCCGTGGTAGCCCGCGCGCGGTGATGAGGG 3180

Qy 3181 TTCTCATCGGCTGTCTTTCAGGATGTGAATACATTTGCC 3240
          | |||||||||| || ||||||||| | |||||||||| |||||| ||||||||||||
Db 3181 TGCTCATCGGCTGTCTTTCAGGATGTGAATCATTGCCTGCGGGTTCGCCTCCCGGGTCGTCCGGACCGCGGC 3240

Qy 3241 CAGTTGTCATCCGGTGGCGGGAAAGGGCTTCACGGGGGTCACGAGGCAGCCTTGACAG 3300
          | |||||||||| ||||||||||||| ||||||||| ||||||| ||||| ||||||||
Db 3241 CCGTTGTCATCCGGCGGGGAAGGGGTTCCTGGGGTCACTAAGGCTCAAGGCTGCCTTGACAG 3300

Qy 3301 GTAGGGATCCTGACTTACATCCAGGAACGTCATGGGTGTTGGGGACGGCTCACGTCACGAA 3360
          |||||||||| ||||| |||||| ||||| |||||||||| ||||||||| |||||||||||
Db 3301 GTCGGGATCCTCGACTTGCATCCAGGAACGTCATGGGTGTTGGGGACTGCGACGTGCGCGAA 3360

Qy 3361 GCATGGCACATGTCTGAATGCCGTCGTGTTCACAACTTCATCCCGAA 3420
          |||||||||||||| | || ||||| ||||||||||| ||||||||||
Db 3361 GCATGGGAACGTGTTTGAACGGCTTGCTCTTCACAACTTTCATCCCGAA 3420

Qy 3421 CCATCGCCACGCCGTGGGGGCCTTAATCCCAGGTGGTGTCAGCCAGTGATGACGTCA 3480
          |||| | ||||||||||| || |||| ||||||||| || |||||||||||| |||
Db 3421 CCATCGCTACACCTGTGGGGCCCTAAATCCCAGGTGGTGTCGGCAAGTGGTGATGATGTCA 3480

Qy 3481 CGGTGTACCCGCTTCCAGATGGGGCAACTTCGTTGACGCGCCCTGCACTTGCCAGGCGGAGT 3540
          |||||||||| | ||| |||||| |||| |||| |||| |||||||||| ||||||||| |
Db 3481 CGGTGTACCCGCTTCCCCGGATGGGCAACCGCTTAACACCCGTCGCCACTTGCCAGGCTGAGT 3540

Qy 3541 CCTGTGTTGGTTATTAGATCCGGAGGAGATTTCGGCGACCCGCG 3600
          ||| ||| |||| ||||| || |||||||| |||||| |||||||
Db 3541 CCTGTTGGGTCATCCGATCAGACGGGGCGCTTTATGCCATGGCTTGAGCCAAGTTGAGCAAAG 3600

Qy 3601 TTGAGCTGGATGTGGCCATGGGCCGGCAAAAGGAGTTTCAAGGAGGCCCCGTCC 3660
          |||||||||||||||||||||| ||||| |||| |||||||||||||| ||||||
Db 3601 TAGAGCTGGATGTGGCCATGGGCCGGCAAAAGGAGTTTCAAAGAGGCCCCGTTCACCTGTCT 3660

Qy 3661 TTTGGCACAAGGGGCACGCAGTAAGAATGCTCGTCGTGTCAGTCAAGCTCAGGGG 3720
          ||||| || ||||| ||||| |||| ||| || |||||| ||||||||| ||| |||
Db 3661 TGTGTGACGAGGGACACAGAGCAGTAGGAATGCTCCGTGTCAGTGTCGTCGGG 3720

Qy 3721 TTACTTCGGCGGCCGATTCACTTAGGCCTGGAGTCAAGATGCCAACAGATGCCAAGAGACTACCA 3780
          |||| | |||| ||| |||||| || ||| || |||| || ||| | |||| |||||| |||||
Db 3721 TCACGCCGCGGTGCATTTCACTGTGACCCGTGAGAGTCGTGGACCCCCAAGTTCCAACAGTTACACCA 3780

Qy 3781 CAGAACCCCTTCGGTGCGGCGAAAAGGAGTTTCAAGGAGGCCCCGTCCTA 3840
          | ||| | || |||| ||||| ||||||||||||||||| || |||||||
Db 3781 CTGAACCCCTTCGGATGCGGCCAAAGGAGTTTCAAAGAGGCCCCGTTTATGCCTA 3840

Qy 3841 CGGGGCGGGAAAGAGCACCCGCGTCAACATGGGCCAACATGGGCCACAAGGCT 3900
          ||| ||||| ||||| |||||||| ||||||||| ||||||||| ||||||||||
Db 3841 CGGGGCGCGGGAAAGAGCACGCGCCCGTCCGTTGGAGTACGGGCAACATGGGCACAAGGCT 3900

Qy 3901 TGATCTTGAACCCGTCGGTAGCTCCCTCCAGTGGACTGGGCCCATACATGAGCGGCTGG 3960
          |||| ||||| ||| ||| ||||| | ||||| |||||| ||||||||| ||||||||||
Db 3901 TAATCCTAAACCCCTCAGTTGTGACAGTGTGACGAGTGCTGTGAGAGCCATGTTACGTGCTGG 3960

Qy 3961 CGGGAAACACCCCAGTATTTACTGTGCCATGACACCACTACTCTTCCAAGGATCACTG 4020
          ||| | | ||||||||| ||||| |||||||||||||||| ||||||||| ||||
Db 3961 CGGGCAAACATTCCAAGCATACTGTGCCATGACACCACCACTGCTTTCCGACGATTACTG 4020

Qy 4021 ACTCGCCCCTTACGTATTCCAACCTTAGGCAGATGCTGA 4080
          |||| | || |||| || |||||| ||| ||| ||||| |
Db 4021 ACTCCCCCCTGACGTATTCTACCTATGGAGTTCTCGGCCAACCCTAGGCAGATGCTCC 4080

Qy 4081 GGGGTCGTCGGTGGTGCTGCATTGTGACCAGTCATCAGTGTGTTTGG 4140
          ||| | | | ||||| || |||| ||||| |||| ||||||||||||
Db 4081 GGGGGTTTCGGTGGTGCATCGTGACGAGTGCCACGAGCCATGTGTGTTTACTGG 4140

Qy 4141 GCATTGGGCGTGTCAGGGAGCTGGCGCGGACGATGTGGAGTGCAATTGGTGCTCTACGGCCA 4200
          |||| |||| | || || ||||| ||||| |||||| |||||| ||| ||||| |||||||||
Db 4141 GCATCGGCGGAGTACGGAGCTGGCGCGGACGATGCCGGAGTGCAGCTTGTGCTCTACCGCGAGA 4200

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Qy  4201 CTGCCACCCCTCCCGGATCCCCGATGACCCAGCACCCATCAATCATTGAGACAAAACTGG 4260
              ||||||| ||| || ||||||||||||||||||||||| ||||| |||||||||
Db  4201 CTGCCACACCTCCCGGCATCCCCTATGGGCCACCCATCAATTATTGAGACCAAAACTGG 4260

Qy  4261 ACGTGGGAGAGATCCCCTTCTATGGGCCATATGGCATACCTCTTGAGCGGATGCGGACCGGAA 4320
              | |||||||||||| ||||| |||||||||||| || ||||||||||||||| |||||
Db  4261 ATGTGGGAGAGATCCCCTTCTATGGGCCATATGGCATACCCTCCGAGCGGATGCGGTCGGGG 4320

Qy  4321 GGCATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGCGCCTGGCGGCCAGTTTTCGG 4380
              |||||||||||| ||||||||||||||| | ||| |||||| || |  |||||||||
Db  4321 GGCATCTTGTATTCTGCCATTCCAAGCGGAGTGTGAGCGGCTTGCCGGCCAGTTTTCCG 4380

Qy  4381 CTAGGGGGTAAATGCCATCGCCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATG 4440
              | ||||| || || ||| |||||||||| || |||||||||| |||||||||| ||
Db  4381 CGAGGGGGTCAACGCCATCGCCTATTATAGGGGAAAAGGACAGTTCTATCATCAAGGACG 4440

Qy  4441 GAGACCTGGTGGTGTGTGCCACAGACGCACTATCCACTGGGTACACTTGGGAACTTCGATT 4500
              | ||||||||||||||||||| |||||| |||| | |||||| ||||||||||| ||||
Db  4441 GTGACCTGGTGGTGTGTGCCACAGACGCACTATCCACTGGGTACACTTGGGAACTTCGATT 4500

Qy  4501 CTGTCACCGATTGTGGTTAGTGTGGGTGAGGAGTCGTCTGCGAGGTGACCCTTGATCCCCACCA 4560
              |||||||||||| |||| ||||||||||||||||| |||| ||| |||||||||||||||
Db  4501 CTGTCACTGATTGTGGTGCGTCTTGGGTGAGGAGTCGTTCAGGTGACCCTTGAGTCCCACCA 4560

Qy  4561 TTACCATCTCCCTGCCACGCGTGCCGCGCTCGGCTGCGACTGTCAGCGGCCAGGGAC 4620
              ||||||||||| ||||| | |||||| ||||| |||||||| ||| | |||||||||||
Db  4561 TTACCATCTCCCTGCCACAGCTGCCATCGCGGTCGCGACTGTCGCGGCCAGGGAC 4620

Qy  4621 GCACGGGTAGGGGCAGGCAGTCTGGGCGTACTACTACCGGCAAGGCCCCTGCTG 4680
              |||||||||||| ||||||||||||| ||||||||||||| |||||||||  ||
Db  4621 GCACGGGTAGAGGCAGGCAGTCTGGACGTCTGGGGTCGGCAAGGCGTGGGCAAAGCCCCTGCGG 4680

Qy  4681 GTGTGGTGCGCTCAGGTCCTGCTGGGCGGCCGGTGTGACCTGGTACGGAA 4740
              |||||||||||| ||||| |||||||| |||||||||||||||||||||||
Db  4681 GTGTGGTGCGCTCAGGTCCTGCTGGGCGAAGCCGGAGTTGACCTGGTACGGAA 4740

Qy  4741 TGGAACCTGACACGACAAACTGACGAGTTTTACGACAACTGCCCTCCAG 4800
              | ||||||| |||| |||||| ||||||||||||||||||||||||| |||
Db  4741 TGGAACCTGACACTGACACAAACCTTACGACGACTGCCCTTACACCGAG 4800

Qy  4801 CCGTCCAGCTGACATTGGGAAGCCGCGGTGTTCTTTCGGGGGCTTGCCCCGTTGAGGA 4860
              ||||||||| || |||||||| |||||||||||||||| ||| ||||||| ||||||||
Db  4801 CCGTCGGGGCGACATCGGGCACGGGGCCCGGGGCGAGGGGTGTTTCTCCGGGTTGAGGA 4860

Qy  4861 TGCATCCGATGTAGCTGGGCAAAAGTTCGCGCGGGTCAACTGGCCCCTCCTGGTGGGTG 4920
              || |||||||||||||||||||||||| ||||||| ||||||||| ||||||||||||||
Db  4861 TGCACCCGATGTTAGCTGGGCAAAAGTTGCGCGGTCCGGTCAATTGGCCCCTCTTGGTGGGTG 4920

Qy  4921 TTCAGCGGACCCATGGCCGGGGAAAACTGTCTCCCGGCCATCGGATGACCCCAGTGGG 4980
              |||||||| ||||| ||||| |||||||| |||||||||| |||| |||||||| ||||
Db  4921 TTCAGCGGACTTGACAGCAAAACCTTCGTAGCCTTGCATTCGATGTGCGACGACCCCAATGGG 4980

Qy  4981 CAGGTCTGAAGGCCCGAATCCTGTCCCACTCCTGCTGAGGTGGGCAATGATTTACCAT 5040
              ||||||||||||||  || ||||||||| ||||| |||||||||||||||||||| ||||
Db  4981 CAGGTCTGAAGGCCCAAATCCTGTCCCACTACCTGCTGAGGTGGGCAATGATTTACCAT 5040

Qy  5041 CTAAAGTGGCCGGCCATCACATCGTGACGACCTGGTCCGTAGGCTCGGTGGGCCGAGG 5100
              ||||||||| |||||| ||| ||| || |||||| |||| ||||||||| ||||||||
Db  5041 CTAAGGTGGCAGCCGGCCACCACATTGTTGACGACCTGGTTCGTAGGCTCGGTGGGCGAGG 5100

Qy  5101 GTTACGTCCGTCTGGCCATGATGCGGGGACCCATCTTCGATGTGGCGGGGCCA 5160
              |||||||||||| ||||| || | |||||||||||| ||| |||||||||||||
Db  5101 GTTACGTCCGTCTGGCTGCGCACGTGCGGGGATGGGCCATCTTTGATGTGGCCATGGGGGCA 5160

Qy  5161 TGATCTATGGCGTCATACACCGGTCTCTGTGGTTACAGACTGGGATGGCAACTCAACAAAG 5220
              || |||||||||||| ||||||| ||| ||||||||| |||| |||||||||| ||||||
Db  5161 TGATCTACGGCGTCTTCACACCGGTGTCTCGTTGTCGTGACACTGGGATGGCCATGGTCATGGG 5220

Qy  5221 GTGGCAGCCCGGTGCTGCAGTCGGCATGGGAGAGACCACGCCCCAGCCGTTGCAGTTGG 5280
              |||||||||| |||||||||||||||||||||||| |||||||||||||||||||||||
Db  5221 GTGGCAGCCGGTGCTGCAGTCGGCATGGGAGAGACCACGCCCCAGCCGTTGCAGTTCC 5280

Qy  5281 CCCCGGTAGAGACCATCGCGGGGGAGAGTCTGCGCCATCGGATGCGCCATCGTCGACAG 5340
              ||||||| || | |||| ||||||||||||||||||||||| |||||||||||||| |||
Db  5281 CCCCGGTAGACCATCGGCCGGGGGGGGAATCGGCCATCGGATGCCGATCGTCGATGACAG 5340
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Db   6361  AACCAGTTACTTCTACCAAGCTGTGCAGGCACTATTGGATGGGGACCGTTCCTGTGAACA  6420

Qy   6421  TGCTGGGCTATGGCGGAGACGTCGCGCTTTGCTGCCTCGCCTCAGACACCCCGAAGGTGGTACCAT  6480
           |||||  ||| || ||  |||  ||| || ||||  ||||| ||||| |||||||||| ||  ||
Db   6421  TGCTGGGGTTACGGCGGAAACATCCCCGTCCCTCGCCTGGCTTCCGACACTCCAAAGGTGGTTCCTT  6480

Qy   6481  TCGGGACGTCTGGGTCGTGGTGACCCCTACCCCACGTTGTGTGATCAGGCGAA  6540
           | |||||||| ||  ||| |||||| || |||||||||||| ||||| ||  |
Db   6481  TTGGGACGTCGGGCTGGTGGTGACCCCTACCCCACGTTGTGATCGGATCAGGAGGA  6540

Qy   6541  CATCCCGCCTACAAACTGCTGCGCCAGCAAATCCTGTCGCGCTGCTGTTGCTGAGCCCTATT  6600
           |||| ||| || |||||||||||||| |||||||||| || || || || ||| |||||||
Db   6541  CCTCTTCCTACAAGTTGCTGCGCCAGCAAATCCTATCAGCTGTTGCTGAGCCCTATT  6600

Qy   6601  ACGTCGACGACGGCCATACCACCGGTCTCATGGGACCGCGAGCGCGAGCCGCCATGGCTCTATG  6660
           || |  ||||  ||  ||||||||| || | |||  || || |||||| ||  ||  || ||
Db   6601  ATGTTGATGGCATACCACCGGTCTCATGGGGACGCGAGCGCGAGCCGCTATGGTTTATG  6660

Qy   6661  GCCCTGGGCAAAGTGTCACCATTGACGGGGAACGCTACACCCTTCCGCATCAACTGCGGC  6720
           |||||||||||||||  ||||||||||||  ||  ||| | ||| ||||  || ||||
Db   6661  GCCCTGGGCAAAGTGTTACCATTGACGGGGACGCGCTACACCCGTGCCGCCACCAGTTGCGGC  6720

Qy   6721  TTAGGAATGTGCGCCCCTCTGAGGTGTCATCCGAGGTGTCATTGACATTGGGACCGGAGA  6780
           |||||||||| |||| ||||||||  |  ||||  | |  ||  | |||  ||  ||||||
Db   6721  TTAGGAATGTTGCGCCCCTCTGAGGTTTCATCCGAGGTGTCCATAGACATTGGGACCGGAGA  6780

Qy   6781  CTGAAGACTCAGAACTGACTGAGGACCTGCCCGGCGGCCCCTTCAGGCTA  6840
           ||||||||||||||||| || ||| |||| |||  ||||  ||||| | |
Db   6781  CTGAAGACTCAGAACTGACTGAGGCCGACCTGCTGCCACCAGCTGCTGCCAAGCGA  6840

Qy   6841  TCGGAGAATGCTGCGAGATTCTTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTA  6900
           | |||||||| |||||| ||||||||| | || |  || ||||||  |||||  ||||| |
Db   6841  TCCGAGAATGCTGCGAGATTCTTGAACCGCACCGCATGTCATCATGGAAGACTGCAGTA  6900

Qy   6901  CACCCTCTCTTTGTGGTAGCCGAGAGATGCCTGTGTGGGGAGAAGACATACCCCGCA  6960
           ||||||||||| ||||| ||||||||||| ||||| |||  || ||||||||||||||
Db   6901  CACCCTCTCTTTGTGGTAGCCGAGAGATGCCTGTGTGGGGAGAAGACGTCCCCGCA  6960

Qy   6961  CTCCACGCCGCAGCACTTATCTCGGTACTGAGAGCGCCAGAGTGAAGAGACCCGTCGG  7020
           ||||| |||||||||||||||||| ||||||||| ||||||||||||||||||||||||
Db   6961  CTCCATGCCGCAGCACTTATCTCGGTACTGAGAGCAGCTCAGATGAAGAGACCCGTCGG  7020

Qy   7021  TGTCTTCCTCGGAGGATACCCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCG  7080
           |||  ||| ||| |||| ||||||||||  |  ||||| | |||||| ||||||||||
Db   7021  TGTCCCTTCGGAGGATACCCCGTCTTCCTCCTCAGACTTCATCCAAGAGTCCG  7080

Qy   7081  AGACAGCCGAAGGGGAGGGAAAGCGTCTTCAACGTCTTTCGTACTAAAAGCCTTGT  7140
           |||||||| ||| || ||||||| |||||||| | || || |||| |||||||| |
Db   7081  AGACAGCTGAAGGGGAGGGAAAGCGTCTTCAACGTCTTTCGTATTAAAAGCCTTGT  7140

Qy   7141  TTCCCAGAGCCGGCATGCCACAGAAAACTTACCGTTAAGATGTCATCGTGTGTGAGAAGA  7200
           ||  |||||||| |||| |||||  || ||||| ||||||| || |||| | | |||||||
Db   7141  TTCCACAGAGCCGGATGCTACCAGAAAGCTTACCGTTAAGATGTCTTGTGTCTGAGAAGA  7200

Qy   7201  GGCTAACACGCTCTTTTCATTGGATTGACGGCGCTCGGCAAGCCGCAGGGCACTCCGA  7260
           |||  ||||||||| || || ||  ||| ||||| ||| ||||| ||| | |||| |||
Db   7201  GCTGTCACACGCTTCTTCCTACACGGTTGACGGCCTGGCAAGCCGTAGCCTGTCTGTGAAA  7260

Qy   7261  TGGAAATCCAGAAACCATACAGCCTATTGTGACAAGTTGCGCACTTGCAGGGAATTGCAGG  7320
           |||||||||||| || |||||||||| | || |||||| ||||| || |||| |||||||
Db   7261  TGGAAATCCAGAACCATACAGCCTATTGTGACAAGTTGACAAGCTGCGACGG  7320

Qy   7321  TTGGGTGTTGGGGGGCAATGAACTTACCTTTGAAATGACAAGTGTGAGGCTAGGCAAG  7380
           || || | ||||||| ||||| || |||||| |||||||| | || |||||||| |||
Db   7321  TTGGGTGCTTGGGGCAATGAACTTACCTTTGAATTGACAAGTGAGGCGCAGGCCAGCCAAG  7380

Qy   7381  AGACCTTGGCTTCTTCTCCTACATCGGTTCGGGTGGCCACTCCGG  7440
           | || ||| ||| ||||||  | | || | || |||||| |||||
Db   7381  AGACCAGATGGGAAGGGACGCGCCATTGACTCGGGGCCACTCCGG  7440

Qy   7441  CCAAGCCCCTGTGGTGTGAGGCCGGTAGGCCGCAGGACCACCAAGGTGT  7500
           || |  |  ||||| | ||||||| ||| || || |||| | || ||||
Db   7441  CTAAACCACCTGGTGTGAGGGCCGGTTAGTGGCTGACAACTACTAAAGTGT  7500
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Qy   7501  ATGTCACCAACCCGACAATGTTGGGAAGAGAGTTGACAAGGTTACCTTCTGGCGTGCCC  7560
           ||||   ||| || ||||||||| |||||| |||||||||| || ||||||||||  |
Db   7501  ATGTTACCAACCAGACAATGTGGGGAGGAGGGTAGACAAGGTGACCTTCTGCGGCGCCTC  7560

Qy   7561  CTAGGGTTCATGACAAATTCCTCTGGACTCCATAGAGGCGCTAAGAGGGCAGCTCAAG  7620
           |||||||||||||||||||||||||||| | || | || ||||||||||| ||||||
Db   7561  CTAGGGTTCATGACAAATTCCTCGATTCGATCGAGGGCCTAAGAGGGCCGCTCAAG  7620

Qy   7621  CCTGCCTAAGCATGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTG  7680
           |||||||||||||||||||||||||||||| || ||||||||| |||||| ||||||||
Db   7621  CCTGCCTAAGCATGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTG  7680

Qy   7681  CCATGGGCTGGGATCTAAGGTGTCGGTCAAGGACCTCGGGGGGAAGATGG  7740
           |||||||  ||||||||||||||||||  |||| || || |||||| |||
Db   7681  CCATGGGCTGGGATCGTCGGTCAAGGTGTCGGTCAAGGACTTGGCCACCCCGGGGAAGAATG  7740

Qy   7741  CTGTCCATGACCGGCTCCAGGAGATACTTGAAGGGACGCGACTCCCTTTACTCTTACTG  7800
           || ||||   | |||| |||||  ||||| |||  || ||| |||| |||||||||||||
Db   7741  CGGTTCACGACCGGCTTCAGGAGATACTTGAAAGCCGCGCCAGTCCCTTTACTCTTACTG  7800

Qy   7801  TGAAAAGGAAGTGTTCTTCAAAGACCGAAAGGAAAGGAGAGAGGCCCCCGCCATTGTGT  7860
           |||||||||  | | |||||||  |  | ||||  | ||| ||||||||||  || ||||
Db   7801  TGAAAAGGAGGTGTTCTTCAAAGACCGTAAGGAGAGGGAGAGGAGGCCCCGCCATTGTGT  7860

Qy   7861  TCCCCCCCTGGACTTCCGGATAGCTGACGTCTGGACCCTGGACCGGGGTAG  7920
           ||||||||||||||| ||||||| ||||| || ||||  || |||| |||||
Db   7861  TCCCCCCCTGGACTTCCGGATAGCTGAGCGTTGGGGACATCCAGGGGTGG  7920

Qy   7921  CCAAGGCCGTGTTGGGGGGGCCTTCACGCGTTGGGGGATTGTAGATCCTTGACCA  7980
           |||||||||||| ||||||||||  || | || ||||| ||||||  ||| ||||||
Db   7921  CCAAGGCCGTGTTGGGGGGCCTTCACGCGTTATGCCTTCCAGGGGTCTTGACCA  7980

Qy   7981  AGATGCTCAAACTGTGGGATCAAAGAAGCACCATGGCCACAT  8040
           |||||||||||||||||||||||| |||  ||||||||| ||
Db   7981  AGATGCTCAAACTGTGGGATCAAAGAAAACACCTGGATGCCACGT  8040

Qy   8041  GCTTCGCACAGTAGCATAACTGAGAGGACGGTGGCGCTGGAGCGTTATGCCCCTGG  8100
           |||||||||||||| |||||||||||||||||| ||| ||||| ||||| ||||||||
Db   8041  GCTTCGCACAGTAGTATTACTGAAGAGGACGGTGGCATTGGAGCTGTATGCTCTGG  8100

Qy   8101  CTTCAGACCATCCAGAATGGTGCGCCTCGGGGAAATACTATCGCTGGCCACAATGG  8160
           ||||||||||||||||||| ||||||  ||||||||||||||| |||| |||||||
Db   8101  CTTCCGCCATCCAGAGTTGGTGCGCCTGCCAGGGGAAATACTATCATTCGCAGCCACCATGG  8160

Qy   8161  TAACCCCGAGGGGGTGCCAGTGGGTGAGAGGTATTGTAGATCCTTGACCA  8220
           | ||||||||||||||||||| |||||||||| |||||||||| ||||||
Db   8161  TCACCCCGAGGGGGTGCCAGTGGGTGAGAGGTAGTATCCTTGACCA  8220

Qy   8221  CCAGTGCGAGCAACTGCTTGACTGCTTATCGCGCGCCGCCTGGAGGGGTGG  8280
           ||||||| |||||||||||||||||| ||||  ||| ||||| ||| |||
Db   8221  CTAGTGCGAGCAACTGCTTGACTGCTACAACGTGGAGAGGGGTGG  8280

Qy   8281  GGCTGAAAAATGTCTCGCTCCTCCATCGCTGGGCAATATGCGAACGGC  8340
           |||||| ||||| | || | ||  |||| ||| ||| ||| |||||||||
Db   8281  GGCTGAAGACGTCTCACTCCTCCATAGCCGGCGGCAATACTGCGAACATGG  8340

Qy   8341  CTGTGTGCGATCCTAGCGACGCTTGGGCGAGCCTTGGGCTACGGCATGCG  8400
           ||||||||||||||  ||||||||||| | || |||||||||||| |||||
Db   8341  CGATGTGTGCGAGTGATCCTAGTGACGCTTGGGTAGGTACGGGGTTACGGCGTGCCG  8400

Qy   8401  AGCCTTCGTATCATGCATCACTGACATCACTGGCTAGCTGAGT  8460
           |||||||| |||||||||| ||  | |||| ||||||||||||
Db   8401  AGCCTTCGTATCATGCATCATTGACACCGACACTGGCTTGCTTGCCGAGT  8460

Qy   8461  GCAATGCAGATGGGAAACGCCATTCGGTTCGGAGGGGCCACTCCGG  8520
           |||||||||||  || || || || |||| |||||| ||| |||||
Db   8461  GCAATGCAGATGGGAAGCGCGCCATTCGGTTCGGAGGCCGCTCGCTC  8520

Qy   8521  GCATGTCGAGCGAGTACAGTGACCCCACCAAGGTGT  8580
           |||||||||||||||||| ||||||  ||  | |||
Db   8521  GCATGTCGAGCGAGTACAGTGACCCCATGGTTACATCCTCCTATATC  8580
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Qy  8581  CTTGGCATCCTATCACACGGTGGTCATCATCCCTCACGTGCTCACCTGCGCGTTTAGGG  8640
          | ||||| || |||||||||||| |||||||||||||| || | |||| ||||||||||
Db  8581  CCTGGCACCCATCACACGGTGGGTCATCATCCCTCACTTGCGCCTTTTAGGG          8640

Qy  8641  GTGGTGGCACACCGTCTGATCCGTCAGTGTGTGCCAGTACATGGTAATTACTACAAGTTTC  8700
          ||||||||||||||||||||||||||||| ||| ||||| ||||||||||||||||||||
Db  8641  GTGGTGGCACACCGTCTGATCCGTCAGTGCATGGTGCCAGTGTAATTACTACAAGTTTC    8700

Qy  8701  CACTGACAAACTGCCTAACATCATCGTGCCCTCCACGACCAGCGTTGAGGGTTA         8760
          |||||||||||||||||| |||||||||||||||||||||||| | |||||||| |
Db  8701  CACTGACAAACTGCCTAATATCATCGTGCCCTCCACGACCAGCAGCGTTGAGGGTCA      8760

Qy  8761  CCGCAGACACAACTAAGACAAAAAATGGAGGCTGCCAAGTGCTGGCCAAGTGCTGGCGACCTCAAGCTCC  8820
          |||||||| || | ||||||||||||| ||||| || ||||||||| ||||||||||||||
Db  8761  CCGCAGACACAACCAACAAAACAAAAAATGGAAGCCCGGTAAGCCGGTCTGCGACCTCAAGCTCC        8820

Qy  8821  CTGGCCTAGCAGTCCACCGGAAGAAGCCCGGGCATTGCGAACGCGTATGCTCCCGGTCGC   8880
          ||||||| ||| ||||||||| ||||| ||||||||||| |||||| |||||||||||||
Db  8821  CTGGCCTGGCGGTCCACCGGCGTCCAGGCGTGGGGCATTGCGAACACGCATGCTCCCGGTCGC  8880

Qy  8881  GCGGTTGGGCTGAGTTGGCTAGGGGGCGTGTTGTGGCGCCTCCAGGCCTGCGGCTTCCCCCTC  8940
          |||||||| |||||| || ||| |||||||||| ||||| |||||||||||| |||||||||
Db  8881  GCGGTTGGGCTGAGCTGGCTGGCTAGGGGCGTGTTGTGCCATCCCAGGCCTGCCTCCCGGCTCCCCCCTC  8940

Qy  8941  CGGAGATTGCTGGTATCCCCGGGGGTTCCCCCTTTCCCCCCTTTCCCCCCCTATATGGGGTGGTTC  9000
          | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8941  CCGAGATGCTGGTATCCCCGGGGGTTCCCCCTTTCCCCCCTTTCCCCCCCTATATGGGGTGGTTC    9000

Qy  9001  ATCAATTGGATTTCACAAGCCAGAGGAGTCGCTGCGGTTGGTTCTTAGCCCTGC        9060
          ||||||||||||||||||||||||||||||||||||||||| ||||| |||||||||
Db  9001  ATCAATTGGATTTCACAAGCCAGAGGAGTCGCTGCGGTTGGGTCGTCGTTAGCCCTGC      9060

Qy  9061  TCATCGTAGCCCTCTCGGGTGAACTAAATTCATCTGTTGCGGCGCAAGGTCCGGTGACTGA  9120
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  9061  TCATCGTGGCTCTCTCGGGTGAACTAAATTCATCTGTTGCGGCGCAAGGTCCGGTGACTGA  9120

Qy  9121  TCATCACTGGAGGAGGTTCCCGCCCCCAGGGGTCTCCCCGCGTCCCCGCCTAAAAAG       9180
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  9121  TCATCACTGGAGGAGGTTCCCGCCCCTCCCCGCCTCCCGCCCCCCAGGGGTCTGGGTAAAAAG 9180

Qy  9181  GGCCCGGCCTTGGGAGGCATGGTGGTTACTAAACCCCCTGGCAGGGTCAAAGCCTGATGGT  9240
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  9181  GGCCCGGCCTTGGGAGGCATGGTGGTTACTAAACCCCCTGGCAGGGTCAAAGCCTGATGGT  9240

Qy  9241  GCTAATGCACTGCCACTTCGGTGGCGGGGTCGCTACCTTATAGCGTAATCCGTGACTACGG  9300
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  9241  GCTAATGCACTGCCACTACGGTGGCGGGGTCGCTACCTTATAGCGTAATCCGTGACTACGG  9300

Qy  9301  GCTGCCTCGCAGAGCCCTCCCGGCGATGGGGCCACAGTGGGGTGCACC                9360
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  9301  GCTGCCTCGCAGAGCCCTCCCGGCGATGGGGCCACAGTGCGGGGGTGCACC             9360

Qy  9361  CCGGTAAGAGCTCGGCCCAAAGGCCGGGTTCTACT                             9395
          |||||||||||||||||||||||||||||||||||
Db  9361  CCGGTAAGAGCTCGGCCCAAAGGCCGGGTTCTACT                             9395
```

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Query Match             84.9%;  Score 7979;  DB 19;  Length 9392;
Best Local Similarity   90.7%;  Pred. No. 0;
Matches 8515;  Conservative    1;  Mismatches  876;  Indels    1;  Gaps    1;

Qy    3  ACGTGGGGGGTTGATCCCCCCCCCGGCACTGGGTGCAAGCCCCATAAACGACGCCT        62
         | |||||||| |||||||||||||||||||||||||||||||||| |||||||||||
Db    1  ACGTGGGGGGAGTTGATCCCCCCCCCGGCACTGGGTGCAAGCCCCAGAAAACGACCCCT      60

Qy   63  ATCTAAGTAGACGCAATGACTCGGCGGCCGACTCGGCGGCCGACCGGCCAAAAGGTGGTGGATGG   122
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  ATCTAAGTAGACGCAATGACTCGGCGGCCGACTCGGCGGCCGACCGGCCAAAAGGTGGTGGATGG   120

Qy  123  GTGGTGACAGGGTTGGTAGGTCGTAAATCCCGGCGTCCCGGCGTCCGGCGACCGGCGTCCACAGGT   182
         ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GTGATGACAGGGTTGGTAGGTCGTAAATCCCGGCGTCCCGGCGTCCGGCGACCGGCGTCCACAGGT   180

Qy  183  CTTAAGAGAAGGTCAAGACTCCTCGTTGTGCCCTGGGAGACCGGTCCCAGGGT           242
         ||||||||||||| |||| |||||| ||||||||||||||||||||||||||||
Db  181  CTTAAGAGAAGGTTAAGATTCCTCTGTGCCCTGGGAGACCGGTCCCAGGGT              240

Qy  243  GCTGCCTCGCAGAGCCCTCCCGGCGATGGGGCCACAGTGGGGTGCACC                 302
         |  || |||| |||||||||||||||||||||||||||||||| ||||
Db  241  GTTGGCCCTACCGGTGGAATAAGGGCCCGACGTCGGCTGCGTCGTTAAACCGACCCGT       300

Qy  303  CACCCACCTGGGCAAACGACGCCCCACCTACGGGCCGTCCACGTCTTCAATGTCTCCTTG      362
         |||||||||||||||||||||| |||||||||||| |||||||||||||||||||||||||
Db  301  TACCCACCTGGGCAAACGACGACCCCACCTACGGTCCACGTCCACGTCGCCCTTCAATGTCTCCTTG  360

Qy  363  ACCAATAGGTTTATCCCGCAGTTGACAAGGACCAGTGGGGGGCCGGGAAG               422
         ||||||||  |  |||||||||| | |||||||||||||||| | ||| |
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RESULT 2
AAV66102

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Db   361 ACCAATAGGCGTAGCCGGCGAGTTGACAAGGACCAGTGGGGCGGCCGGGGGCT-TGGAGAGG  419

Qy   423 GACCCCAAAACCCTGCCCTTCCCGGTGGGCGGCCGGGGAAATGCATGGGGCCACCCCAGCTCCCGG  482
         ||| |||| ||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 GACTCCAAGTCCCGGCCCTTCCCGGTGGGCCGGCCGGGGAAATGCATGGGGCCACCCCAGCTCCGCG  479

Qy   483 GCGGCCTGCAGCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGGTGGCATTTCTCTT  542
         |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   480 GCGGGCCTGCAGCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGGTGGCATTTCCTTT  539

Qy   543 TTCTATACCATCATGGCAGTCCTTCTCTGCTCCTCCGCGGCCACTGTCTCGGCGGCCATTCTG  602
         |||||||||||||||||||||||||||  ||||||||  ||  ||||||||||||||||||
Db   540 TTCTATACCATCATGGCAGTCCTTCTCTGCTCCTCCGCGGCCACTGTCTCGGCGGGCCATTCTG  599

Qy   603 GCCCCGGCCGCCACCCACGCTTGTCGAGCGAATGGGCAATATTTCCTCACAAATTGCTGTGCC  662
         ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db   600 GCCCCGGCCGCCACCCACGCTTGTCGAGCGAATGGGCAATATTTCCTCACAAATTGTTGTGCC  659

Qy   663 CCGGAAGACATCGGGTTCTCGCCTGGAAGCGGATGCCTGGTGCCTGGGTGCACGGTT  722
         |||||||||||||||||||||||||||||||||||  ||||||||||||||||||  |
Db   660 CCGGAGGACATCGGGTTCTCGCCTGGGAGGGTGAGGTGCCTGGGTGCCCTGGGGTGCACGATT  719

Qy   723 TGCACCGACCGTTGCTGCCACTGTATCAGGCCGGGTTTGGCTGCGCGCCTGCCAAGTCC  782
         |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db   720 TGCACTGACCAATGCTGCCACTGTATCAGGGCGGGTTTGGCTGCGCGCCTGCCAAGTCC  779

Qy   783 GCGGCCCAGCTCGTTGGGGAACTGGGAGGAGCCGGCCTGTACGGGCTCTGTCGGCGCTTAC  842
         |||||||||||||||||||||||||||||  ||||  ||||||||| |||||||||||| |
Db   780 GCGGCCCAACTGTTGGGGAGCTGGGAGGTGCCTATACGGGCTCTGTCGGCGCTCGGCCTAT  839

Qy   843 GTAGCCGGGATCCTCGGGGTCTGGGCGGAGGTTACTCCGGGGTCCGACAGTTGGTGTGTTCGG  902
         ||  |||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db   840 GTGGCTGGGATCCTCGGGGTCTGGGCGGTGAGGTGTCCTAACGTGGGAGTCGGGAGTCGCCG  899

Qy   903 TTGAGGGCCGGGTCTACCTGGTCGCCCAACCTGAAGTGCAGTAGAATGTGACGTTAAG  962
         ||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db   900 TTGACGCCCGGGTCTACCTGGGTCCTGAGCAACTGTCAGTGCGCGTGTGAGCTAAAG  959

Qy   963 TGGGGAAGTGAGTTTGGAGATGGCAGCAGTTGCCTCCAATTACTGGATTTTGGAA  1022
         |||||||||||||||||||||||||| ||| |||||||||||||||||||||||
Db   960 TGGGAAAGTGAGTTTGGAGATGGCAGCAGTGGCCTCCAACTACTGGATTCTGGAA  1019

Qy  1023 TACCTTTGGAAAGTCCCATTGAATTTTGGAGAGGAGTGATGAGCCTGTGACCCCTCTGTTG  1082
         ||| ||||||| |||||||||||||||||||||||||||| |||||||||||||||||||
Db  1020 TACCTCTGGAAGTGTCCCATTTGATTTCTGGAGAGCCGTGATAAGCCTGACCCCCCTTGTTG  1079

Qy  1083 GTTTGGGTTGGCCCGGATCGCTTTGCTGAGCAACGGATTGTCATGGTTCATGGTGTCTGCTGTG  1142
         ||| ||||||||||||||||||| |||||||| |||||| ||||||||||||||||||||
Db  1080 GTTGCGTTGGCCCGGATCCCATTTGCTGAGCAACGGATTGTCATGGTTCATGGTGTCTGTTGGTG  1139

Qy  1143 ACGATGGCGGGAAGATGTTGCAAGCGGGATGGTTGCAGCCGTTGCCGTTTCCGGTCCCGTTTGAC  1202
         ||||||||||||| ||||||||||||||| |||||||||||||||||||||||||||||||||
Db  1140 ACGATGGCCGGGATGTTGGGACCGGACCGGTTACGCTTGCACGCGCCTCCGGTTTTTGAC  1199

Qy  1203 TACGGGTTGAGTGGCAGTCATGCTCCGAGGGCTAACGGGCTCGCGTATTCCCACTGGG  1262
         ||||||||||| ||||||||| |||||||||| ||| || ||| ||||||||||||
Db  1200 TACGGGTTGACTGGCAGTCATGCTCCGAGGGCCAACGGCCTCCCGTTTTTCGGACTGGG  1259

Qy  1263 GAGAGGGTGTGGATCGAGGGAATGTCACGCTTCAGGTTTGGGAGTTCCCAACGGCCCCTGG  1322
         |||||||||||||||||| ||||||||||| ||||||||||| ||||||||||||||||
Db  1260 GAGAAGGTGTGGGACCGTGGGAACGTTACGCTTACGGTTTGGGAGTTCCCGAACGGCCCCTGG  1319

Qy  1323 GTTTGAAGTGGCAGTGGCAGGCGGTTTGGGGTGGGCGGCGACCCCCATCAGCCATTGGAGC  1382
         |||| ||| ||||||||||||||||| || ||||| ||| |||||||||||||||||||||
Db  1320 GTGTGGTTGCCAGCCTTTTGCCAAGCAATCGGCTGGGGTGACCCATTATTGGAGC  1379

Qy  1383 CACGGACAAAACCAGTGCCCCATCATGCGCCCCAATAGTCTATGGGTCTGTCCGTA  1442
         |||||||||||| ||||||||||||||| ||| |||||||||||||||||||||||
Db  1380 CACGGGCAAAATCAGTGCGCCCCTTTCATGGCCCAGTAGTCTATGGGTCTGCTCGTC  1439

Qy  1443 ACGTGCGTGTGGGGTTCCGTCTTGTTCGCCTCGACCGCCGGGTCGTGATTCGAAGATC  1502
         || || |||||||||||||||||||||||| |||||||||||||||||||||||||
Db  1440 ACTTGCGTGTGGGGTTCCGTCTTCGGGGTTTGCTGCCACCAGTGCTGCCGACTCGAAGATA  1499
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Qy  1503 GATGTGTGAGTTTGGTGCCGGTTGGATCTGCCAGCTGCACCATAGCCGCTGCCTCTAGGGTCA  1562
         |||||||| ||||| |||||| ||| ||||||||| ||||||||||||||||||| || || ||
Db  1500 GATGTGTGGAGTTTAGTGCCAGTTGCCTCTGCCACCTGCCACCATAGCCGCTGCCACTTGGATCA  1559

Qy  1563 TCGGATCGGCACACGGTTGAGCTCTCCGAGTGGGAGTCCGTGCTGTAACGTGTATT  1622
         |||||||||||||||||| |||||||||||||||||| |||||||| ||||| |||
Db  1560 TCGGATCGGCACACGGTGCCTGGGCTCTCCGAGTGGGAATCCCGTGCCGTGCGACGTGTGTT  1619

Qy  1623 CTGGACCGTCGGCCTGCTTCGATGGCACCTGTGTCGCGGCACTGTCGGCCCGAAACCGGG  1682
         |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  1620 CTGGACCGTCGGCCTGCTTCGCGGCACCACCTGTGTGAGGGACTGCTGGCCCGAGACCGGG  1679

Qy  1683 TCGGTTAGATTCCCTTCCATCGGTGCGCGACACGGGGCCTCGGGCTGACAAAGGACTTGGAA  1742
         ||||||  ||| ||||||| |||||||||||||||||||||||||||||||||||||||||
Db  1680 TCGGTTAGGTTCCCCATTCCATCGGTGCGCGGCCTGGGGCCTCGGGCTGACAAAGGACTTGGAA  1739

Qy  1743 GCTGTGCCCTTCGTCAACGAGGACAACTCCCTTCACCATAAGGGGCCCCTGGGCAACCAG  1802
         ||| |||||||||||||||||||||||| ||| ||||||||| ||||||||||||||||
Db  1740 GCTGTGCCCTTCGTCAACGAGGACAACTCCCTTCACCATTAGGGGGCCCCTGGGCAACCAG  1799

Qy  1803 GGGAGAGGCAACCCGTGCGTGCGCCCCTGGGTTTTGGGTCCTCACACCATGACCAAGATC  1862
         ||  ||||||||||||||||||| |||||||| |||||||  ||||||||||||||| |
Db  1800 GGCCGAGGCAACCCGTGCGGCGGTCCCTGGGTTTTGGGTCCTCTACGCCATGACCAGGATC  1859

Qy  1863 CGGGAATTCCCTGCATTGGTGAAATGTCCACCAGCCATAGAGCCTCCGACTGGAACG  1922
         ||||||||||  ||||||||||||||| ||||||||||  ||||||||||||||||
Db  1860 CGAGATACCCTACATCTGGTGAGTGTCCCACCAGCCATTGAGCCTCCACCCGGGACG  1919

Qy  1923 TTCGGGTTCTTCCCCGGAGTCCTGACAGTTGGTGTCGG  1982
         ||||| |||||||||||| |||||||||||||| |||||
Db  1920 TTTGGGTTCTTCCCCGGACGCCGCCTCTTTGGGCACGGAAGTG  1979

Qy  1983 TCTGAGGCATTGGGCGGAGCTGGGTTCACGAGCCTCTGTTCCCAGG  2042
         || ||||||||||||||||| ||||||| ||||||||||||||||
Db  1980 TCCGAGGCACTTGGGCGGGGGGTTCGTTTCTTATGAACCCCTGTGCGCCAGG  2039

Qy  2043 TGTTCGGAGCTGATGGGACCGCGAAATCCGTTTGCCGGGTACGCGTGTCCTCT  2102
         ||||||||| ||||||||||| ||||||||||||||||||| |||||| || |
Db  2040 TGTTCGAAGCTGATGGGAAGCCGAAATCCGGTTTGTCATGGCCGTCTCTTCG  2099

Qy  2103 GGTAGCCTGCACGGGTTCATACACGTTCCAGGGCACTCGACGGAGGTGGATGCGGGCGAAC  2162
         ||  ||| |||||| ||||| |||||||||||||| |||| ||||||| ||||||||||||
Db  2100 GGCAGGCCTGATGGGTTTATACATGTCCAGGGTCACTTGCAGGAGTGGATGCAGGCGCAAC  2159

Qy  2163 TTCATCCCTCCTCCACGCTGGTTGCTTGGATTTTGTATTTGTCCTGCTATCTGATG  2222
         |||||| |||  ||||| ||||||||||||| |||||||| |||||||||||||||
Db  2160 TTCATCCCGCCCCCGCCGCTGGTTGCTTGGATTTGTATTTGTCCTGCTTGTATACCTGATG  2219

Qy  2223 AAGCTGGCTGAGGCACGCGGTTGGTCTGCCCGTTGAATCTTGCTCGTGGTGGTTGAAC  2282
         ||||||||||||||||||||||||| ||||||| ||||||||| |||||||||||||
Db  2220 AAGCTGGCTGAGGCACGGTTGGTCTGGTCTGATCTGTGCTGCTGCCTATGGTGGGGTTGAAC  2279

Qy  2283 CAGTTGGGGTTGTAGGACTTGGCCTGCTGCCTGTGCGGGGTGAGTTTTTGCG  2342
         || |||||| |||| |||  |||||||||||||| ||| |||||| |||||
Db  2280 CAGCTGGCAGTGTGTCTAGGGCGCTGGGCTGCGTTGCAGGTGGAAGTTCTTCGCG  2339

Qy  2343 GGCCCTGCCTGTCATGGTGTTTGGGGCCTTCCCAACTGTCAGTATGATGTCTAGCA  2402
         |||||||||||||  ||||| |||||||| ||||||| |||||||||||||| ||
Db  2340 GGCCCTGCCTGTGCTGGTGTCTGGGAGCTCCCCGGTCGTCAGTCAGTATGATATTGGGCA  2399

Qy  2403 AACCTGGTTGTGTACTTTCCGGTGAGTGGGATGGGCCCTCAGTGTTCCTGTGTGG  2462
         |||||||||  || ||||||||||||||||||||| |||||||||| |||| ||||
Db  2400 AACCTGGTTGCGTACTTTAGATGTGTGGGGGACCCCCACGCCGTGTGGATGTCCTGTGTGTG  2459

Qy  2463 AAGCTCGCTCGGGGAGCTTTCGGCGCCGGCCACCCGGG  2522
         ||||| |||||||||||| ||||||||  |||||||||||
Db  2460 AAGCTTGCTCGGGGAGCTTTCCCGCTGCCCTGGCGACCCGCGGG  2519

Qy  2523 CGCACCTCTGTCTCGGGGCCGAGTTCGTCGATGTCACATTCGAGGTGACACTTCG  2582
         ||||||||||||||| ||||||||||| |||||||||||| ||||||||||||||
Db  2520 CGCACCTCAGTGCTCGGGGCCGAGTTCGTCGATGCTACATTCGATGCTGCTACATTCGAGGTGGACACTTCG  2579
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Qy  2583  GTGGTTGGGCTGGGTGGGTGGCCAGCGTGGCTGGCTGGCCATAGCCTCCTGAGCTCAATG  2642
          ||||| |||||||||||||||||||| |||| |  ||||||||||||||||||| || ||
Db  2580  GTGGTTGGGCTGGGTGGGTGGCCAGTGTGGCTGGCCATTGCCGCTCCGTGAGCTCGATG  2639

Qy  2643  AGCGCAGGGGGTGAAGCACAAGGCCGTGATCATAGGACGTGGTGTAAAGGTACCAG  2702
          ||||| ||||||||| |||||||| |||||||||| |||||||||||||||||| ||
Db  2640  AGCGCAGGGGGTGGAGCACAAAGCCGTGATCATAGGACGTGGTGTAAGGGTACCAG  2699

Qy  2703  GCTGTGTCGCCAGAGGGTGGTGCGGAGCCGGGCGTCCTACCAAGCTTCTG  2762
          || ||| |||||||||||||||||| ||||||||| |||||||||||| |
Db  2700  GCAATCGTCAAAGGGTGGTGAGGAGCCCCGGGGAGGGGCGGCCGTGCCAAACCCCTG  2759

Qy  2763  ACGTTGCCTGGTGCTTGGCCTCATACATCTGGCCCGATGCTGTGATGATGTGGTGGTG  2822
          ||| ||||||||||| |||||||||||||||||||| | |||||||||||||||
Db  2760  ACCTTTGCCTGGTGCTTGGCCTCGTACATCTGGCCCAGATGCTGTGATGATGTGGTGGTT  2819

Qy  2823  GCCTTGGTCTCCTCCGCCTGTTCGACGCACTGGCACTGGGCCCTGGAGGAGCTCCTG  2882
          |||||||||| | |||||||| || || |  || ||||||||| ||| | ||| |  |
Db  2820  GCCTTGGTCTCCTCTTTGGCCTCGTTCGACGCGTTTGGCGGTGTTGAGTGCTGTGTGATGGCGGGGC  2879

Qy  2883  GTCTCCCCGGCCCTCGTTACGGCGACTGGCACGGGTGGTTGAGTGCTGTGTGATGGCCGGGC  2942
          | | |||||| |||||||| || || |||||| |
Db  2880  GTGTCCCGGCCCTCGTTGCGGCGTTTGGCTGCGGTTGGATTTGGGCCTTGGTGTGTGATGGCGGGGT  2939

Qy  2943  GAGAAGGCCACCACCATCCGACTCGTCTCCAAGATGTGCCAAGAGGGGCTACCTGTTT  3002
          |||||||||||||| |  ||||| |  |||||||||||||||||||| |||| |||
Db  2940  GAGAAGGCCACCAACCGTCCGGTCTCCGTGGTTGCCGAGAGGAGCTTATTTGTTC  2999

Qy  3003  GACCACATGGGCTCTTTCTCCGCCGTGTCAAGGAGCGTTGTTGGAATGGACGCGGCT  3062
          |  ||| |||| | || |  ||||| | ||||||| ||||||||||||||||||
Db  3000  GATCATATGGGCTCTTTTTCCGTGTGTCAAGGACGCGTTGGAATGGACGCGGCAGCT  3059

Qy  3063  TTGGAGCCCTTGTCATTCACTAGGACGGACTGTCCGCATCATCAGAGATGCCGCGAGGACC  3122
          |||||||  | || | || ||||||| ||||||||| |||| ||||||||||||||||||
Db  3060  CTTGAACCTCTGTCATTCACTAGGACGGACTGTCCGCATCATACGGGATCCCGCGAGGACT  3119

Qy  3123  CGTGTCCGGACAGTGCGTCATGGGTTACCCGTGGTAGCAGATGGGCGGCGGGCCTGGTGATGAGGTT  3182
          || ||||| || || ||||||||||||||||| ||| ||| ||||||||||| ||||||||||||
Db  3120  TTGTCCTGCGGGCAGTGCGTCATGGGTTACCCGTGGTTGCCAGATGGGCGGCGGGCCTGGTGATGAGGTT  3179

Qy  3183  CTCATCGGCGTCTTCAGGATGTGAATCATTTGCCTCCCGGGTTTGTTCCCGACTGCACCA  3242
          ||||| |||||||||||||||||| | ||||| |||| ||||||||||| ||||| ||
Db  3180  CTCATCGGCGTCTTCCAGGATGTGAATCATTTGCCTCCCGGGTTTGTTCCCGACCGCCT  3239

Qy  3243  GTTGTCATCCGGTGCGGAAAGGGCTTCCTGGGGTCACGAAGGCAGCCTTGACAGGT  3302
          ||||||||| ||||||| |||||||| ||||| |||||||||||||||||||||
Db  3240  GTTGTCATCCCACGGTGCCGAAAAGGGCTCTCTTGGGGCTCACCAAAGGCTGCCTTGACAGGT  3299

Qy  3303  AGGGATCCTGACTTACATCCCAGATGGGGCAACTTCGTTGACGCCCTTACGTGTGGGGACGGAAGC  3362
          ||||| | ||||| ||| |||||| ||||| |||||||||| | ||| ||||||||||||
Db  3300  CGGGATCCTGACTTACATCCCGGGACGGGGCGCTACTTGTTGGGTACTTGTTCCGTTAACACCTTGTACTTGCCCAGGCTGCAAGC  3359

Qy  3363  ATGGCACATGTCAGGATGTCCATGAATGGCCTGCTCCCAGGTCGTCAGCTGGTCTCACAACCG  3422
          ||||||||| | |||||||||||||||||||| |||||||||||||| ||||| ||| ||||
Db  3360  ATGGGAACATGCTGCGGGACCTGCTCCCAGGTCGTCACAACTGCTGGTCAGTGAATGCTGAT  3419

Qy  3423  ATCGCCACGCCCGTGGGGCTGGGGCCCTTAATCCCAGATGGTCACCCGTTGATGACTTCACG  3482
          ||||| ||||||||||||| |||||||||||| || ||||||| ||||||||||||||||
Db  3420  ATCGCCACACCCGTGGGGCTCTCCTTAATCCCAGATGGTCACCCGTTGATGACTTCACG  3479

Qy  3483  GTGTACCCGGTTCCAGATGGGGCAACTTCGTTGACGCCCTGCCAGGCGGTCC  3542
          |||||||| ||||||| ||||||||||| ||||| || ||||||||||| ||
Db  3480  GTGTATCCACCTCCCGATGGGGCCTACTTGTTCCGTTAACACCTTGTACTTGCCCAGGCTGCAGGGGGACAAGGTT  3539

Qy  3543  TGTTGGGTTATTAGATCCGACGGGCTTCTCGACTTCGTCTTGGTTCGTCTTCCTGCTTCACAACAAGCT  3602
          |||||| || | |||||| ||| || |||||||||||||| || ||
Db  3540  TGTTGGGTCATCAGAT CCCGACGGGCTTCGTCTTCGTCTTCCTGCTTCACAACAAGGT  3599

Qy  3603  GAGCTGCCTCGTCTCGACTTCGTCTTCCTGCTTCACCGTCCTT  3662
          |||| ||||||||||||||| |||| | |||||| ||||||||
Db  3600  GAGCTGCCTGATGTGGCCTCGTCTCGACTTCGTCTTGGCTCTCGGCTCTCCACCGTCCTA  3659

Qy  3663  TGCGACAAAGGGCACGCCAGTAAGAATGCTCGTCGTGTCGTCAGCGGCAGGGGTT  3722
          |||||| |  ||| || || ||  ||||||||| |||| ||||||
Db  3660  TGTGACGAAGGGCACCGCAGTAGGCTAGGAATGCTCGTCGTGTGTCACCAGCGTGTAGGGTC  3719

Qy  3723  ACTGCGCGCCGATTCACTGGACTCGTGACTCAAGTGCTGACCCCAAGTGCCAAAACCACTACT  3782
          || |||| ||| || |||||||||| | ||| |||| ||| ||| ||||||||| |
Db  3720  ACCGCGCCACGTTCACTAGCCTGGACTGCGTGACTCAAGTGCTGGACTGCCCAAGTGCCAACGATGCCAACGATCACTACT  3779

Qy  3783  GAACCCCTTCCGGTCCGGCAAAAGAGTTTTCAAGGAGGCCCGTTGTTTATGCCTACG  3842
          ||||||||||||||| || ||||| || | ||||||| ||| |||||||||||||
Db  3780  GAACCCCTCCGGTGCCGGCCAAAGAGTTTTCAAAGAGGTTTCAAAGAGGCCCGTGTTTTATGCCTACG  3839

Qy  3843  GGGGCGGGAAAGAGCACCCGCTACCGTTGGAGTACGACGGGCCACAAGGTCTTG  3902
          |||| ||||||||||| ||| ||| || || |||| ||||||| |  |||  |
Db  3840  GGAGCGGGAAAGAGCACTCGCCGCTCCGTTGGAGTACGACATAACATGGGCACAAGGTTCTTA  3899

Qy  3903  ATCTTGAACCCGTCGGTAGCTCGGTACCGTGAGGGCATGGCCCCATACAGTGACGGCTGGCGG  3962
          ||||||||||| ||| |||||||||||| | ||| ||||||| | |||| |||||||||||
Db  3900  ATCTTGAACCCCTCAGTGCGGCCGTCCGGCAGCTGGCCCATGGGCCATCGGGCCGTACATGGAGGCGGCTGGCG  3959

Qy  3963  GGGAAACACCCCAGTATTTACTGTGCCATGACACCACTGCTTTCACAAGGATCACTGAC  4022
          |||||| |||| || ||||||||| ||| |||| |||  | |||||||| |||||||||
Db  3960  GGTAAACATCCAAGTATATACTGTGGGCATGACAACTGCTTTCACAAGGATCACTGAC  4019

Qy  4023  TCGCCCCTTACGTACTGCCACTTACGGAAGGTTTTGGCCAACCCTAGGCAGCAGATGCCTGAGG  4082
          ||  |||| |||| || ||| |||| ||||| |||||||||||||||| || || ||| |||||
Db  4020  TCCCCCCTGCGGCTATTCAACCTATCGGAGGTTTTGGCCAACCCTAGGCAGCAGATGTCTACGG  4079

Qy  4083  GGTGTGCGGTGGTCATTGTGACGAGTGCCACAGTCAACTGTGTTGTTGGGC  4142
          | || |||||| |||| |||||||| || ||||| |||||| || | |||||
Db  4080  GGCGTTTCGGTGGTCATTGTGATGAGTGCCACAGTCATGTGCTGCTGTTAGGC  4139

Qy  4143  ATTGGCGTGTCAGGGAGCTGGCGCGAGGATGTGAGTGCGCAATTGGTGCTCTACGGCCACT  4202
          ||||||| || |||||| ||| ||||| |||||||| || |||||| |||| ||||||||
Db  4140  ATTGGGAGAGTCCGGGAGCTGCGCGAGGATGTGAGTGCGCAACTAGTGCTCTACGGCCACC  4199

Qy  4203  GCCACCCCTCCCCGGATCCCCGATGACCCCAGCACCATCAATCATTGAGACAAAAACTGGAC  4262
          ||| ||| | |  | ||| |||||  || ||||| ||| || |||| ||||||||| ||||
Db  4200  GCTACAACTCCCCGGATCCCCGATGACGCAGCACCCTTTCCATAATTGAGACAAAATTGGAC  4259

Qy  4263  GTGGGAGAGATCCCCTTCATGGGCATGGCATGGCGGATGCGGACGGGAAGG  4322
          | ||| |||||| || ||||||| || |||||| |||| |||||||||||
Db  4260  GTGGGCGAGATCCCCTTTTATGGGCATGGGAATACCCCTCGGGATGGCGATGCGGACGGGAAGG  4319

Qy  4323  CATCCGTATTCTGCCACTCCAAGGCTGAGTGCAAGGCGCGCCGCCAGTTTCGGCT  4382
          |||||||| ||||||| || ||| || | ||||| ||||| |||||||| ||||
Db  4320  CACCTCGTGTTCTGCCATTCTAAGGCTCTAAAGGCTGAGTGCGCGCCGCCAGTTCTCCCGCT  4379

Qy  4383  AGGGGGTAAATGCCATCGCCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATGGA  4442
          |||| ||||| ||||||| |||| ||||| |||||||||||| ||| || ||||||||
Db  4380  AGGGGGGTCAATGCCATTGCCTATTATAGGGGTAAAGACAGTTCTATCATCAAGGATGGG  4439

Qy  4443  GACCTGGTGGTGTGTGCTACAGACCGCCACTATCCCACTGGGTACACTCGGAACTTCGATTCT  4502
          | ||||||||||| ||||| ||| | |||| || || |||||| ||||||||||||  ||| |
Db  4440  GACCTGGTGGTGTCTGTGCTACAGACCGCTTTCCCACTGGGTACACTCGGAACTTCGAAATTTCGACTCC  4499

Qy  4503  GTCACCGATTGTGGGTTAGTGGTGGGAGGAGTCGTCGAGGTGACTTGCTTGATCCCACCATT  4562
          |||||||| ||| ||| ||||| |||||||||||||||||||| || |||||||| |||||
Db  4500  GTCACCGACTGTGGATTAGTGGTGGGAGGAGTCGTCGAGGTGACTTGCTTGATCCCACCATT  4559

Qy  4563  ACCATCTCCCTGCGCACGGTGTCGGCTCGGCTGCGAACTGTCGATGTCGGCGGAGACGCGC  4622
          ||||||||||| || ||||| ||||| || ||| ||||||| ||||| ||| |||||||
Db  4560  ACCATCTCCCTGCGGACAGTCTGGACGCTCGGCTGCATGTCGATGTCGATGTCGAAAGACGAGGACGC  4619

Qy  4623  ACGGGTAGGGCAGGTCAGGTCCTTGCGTCGGACGCTACTACGCGGGGTCGGCAAGGCCCCTGCTGGT  4682
          ||||||||| |||||||||||| || ||| ||| |||| || || ||||| ||||||| | |||
Db  4620  ACCATCTCCCTGCGGACAGTCTGGACGCTCGATGTCGATGTCGAAAGACGAGGACGC  4679

Qy  4683  GTGGTGCCTCCTGTCGGTCTCCGTGGTCGGCTGAGAAGCCGTGGTGTACGGAATG  4742
          | || |||||| |||| |  ||||| ||||| |||||||||| || |||||||
Db  4680  GTGGTGCCTCCAGGTCGCTGGTCTGGTCTGTCGTCGGCTGGAAGTGACGCTGGAAGTGACGCTGGAAATG  4739

Qy  4743  GAACCTGACCTGACAGCAACCTTACGACAACTGCCCTTCACCGCAGCC  4802
          |||||||| |||| ||||||||| ||| | |||||||||| ||||||
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Db 4740 GAACCTGACTTGACAGCTAACCTACTGAGACTTTACGACGACTGCCCTTACACCGCAGCC 4799

Qy 4803 GTCCAGCTGACATTGGGGAAGCCGCGGTGTCTTTGGGGCTTGCCCGTTGAGGATG      4862
        ||||| ||||| |||||||  ||||||||||||||||   ||| ||||||  ||||||||
Db 4800 GTCGCGGCTGATATCGGAGAAGCCGCGGTGTCTTCTCGGGCTGTTCTCGCCATTGAGGATG 4859

Qy 4863 CATCCCGATGTTAGCTGGGCAAAAGTTCGCGGCCTTCCGGCGTTCCGGTGGTGTT       4922
        || ||| |||||| |||||||||||||||||||||||||||| |||||||||||||
Db 4860 CACCCTGATGTCAGCTGGGCAAAAGTTCGCGGCCTTCCGGTGGTGTT                4919

Qy 4923 CAGCGGACCATGTGCCGGGAAACACTGTCTCCCGGCCCATCGGATGACCCCCAGTGGGCA  4982
        |||||||||||||||||||||||||||  ||| |||||||| ||||||| |||||||||||
Db 4920 CAGCGGACCATGTGCCGGGAAACACTGTCTCCCGGCCCATCGGATGACCCCCAGTGGGCA  4979

Qy 4983 GGTCTGAAGGGCCGAATCCTGCTCCTGCTCGAGTGTGGGCAATGATTACCATCT        5042
        ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db 4980 GGTCTGAAGGGCCCAAATCCTGTCCCACTCCTGCTGAGTGGTGGGCAATGATTATTACCATCT 5039

Qy 5043 AAAGTGGCCGGCCATCACATCGTGCGGGACGACCCATCTTGATGTGGCCGAGGGT        5102
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5040 AAAGTGGCCGGCCACCACATAGTCGGGACGACCCGGTGTGGGCGGAGGGT              5099

Qy 5103 TACGTCCCGCTGCGATGCGGGACCCATCTTGATGTGGCCTATTGCGGGGGCATG       5162
        ||||||||||||||||||||||||||||||||  |||||||| |||||||||||||
Db 5100 TACGTCCCGCTGCGACGCTGGGCCGATCGTCTAGCTAGCTTGATGATCCGCGGGGGAATG   5159

Qy 5163 ATCTATGGTCATACACCGGTCTCTCGTGGTTACGGACTGGGATGGAGGGGGT          5222
        |||| |||||||||||||||||||||  ||||||| ||||||||||| ||||||||||||
Db 5160 ATCTACGGTCATACACCGGTCTCGCTAGTGGTGTGACAGAGTGGGATGTGAAGGGGGT    5219

Qy 5223 GGCAGCCCCCTTTATCGGAGACCAGGCCACGCCCCAGCCGGTTGTGCAGGTCCCC       5282
        ||||||||||||||||||||||||| ||||||||||||||| |||||||||||||
Db 5220 GGCAGCCCCCTTTATCGGAGACCAGGCCACGCCCCAGCCGGTTGTGCAGGTTCCT       5279

Qy 5283 CCGGTAGACCATCGGCCCGGGGGGAGAGTCTGCCCGATCCGGATCCGGATGCCAACACAGTGACAGAT 5342
        ||||||||||||||||||||| |||||||||||||||||||| |||||||| |||| ||||||||||
Db 5280 CCGGTAGACCATCGGCCCGGGGGGGTGAATCAGACCACCATCCGATGCCAAGACAGTGACAGAT       5339

Qy 5343 GCGTGGCGGGCCATCCAGTTGGATTGCAGTTGCAGTCATGTCAGTCATGACCCTGCGATCGGGGAA    5402
        | |||||||||||||||||||||||||||| ||| ||| |||||||||||||||||| ||||||||||
Db 5340 GCGGTGGCAGCCATCCAGTTGGACTGCGATTGCGATTGCATCATGACTCTGTCGATCGGAGAA        5399

Qy 5403 GTGCGTGTCCTTGGGCCTCTAGGAGCGCGGACGCGGCGGCCTAACCAGTGCTTACGCAGCTACCACCAAGTGGCTT 5462
        ||| ||||| ||||||||||||||||||||| |||||||||||||||||||||| ||||  ||||||||| |||||
Db 5400 GTGTTGTCCTTGGGCTCTGGGGCGGGCCGAGGGGCCTAACCAGCAACCGCCACACCGCCAAGTTGGCTC        5459

Qy 5463 GCTTGGCTCTACACGGGGACGGGCCGGCCCGTCCCCACTCGTTTTCAATTGTTGACAAGCTCTTC      5522
        |||||||| ||||||||||||||||||||||||||||||||||||  ||||| |||||||||||||
Db 5460 GCTTGGCTGCTATACGGGGACGGGCCGGCCGTCTCCACTGTATCCATTGTTGACAAGCTCTTC        5519

Qy 5523 GCCGGGGGCTGGAGGCTTCTAGGGCCGTGGTAGGCCCATTGGCCACAGTGCCAGTGGCG      5582
        ||||||| ||||||||||| || |||||||||||||||||||||||||||||||||||||
Db 5520 GCCGGTTGGAGGCTTCTGGGGCCGTAGGCCATTGGCCACAGTGCTGCGGCTGTGCCGTATGGC 5579

Qy 5583 GCCTATGGGGCTTCTAGGAGCGCGGGACCCTCGGGTGCTGCTACCTCATGGGGTTG        5642
        ||||||| || ||||||||||| ||||||||| |||||||||||||||||||||||||
Db 5580 GCCTATGGGTTCTGGTCGTCAAGGTCTGCGGCCTTCCTACCTCATTGGGGGTTG        5639

Qy 5643 GGCCTCGGAGGGCAACGCGCGGGACCCCTAGCCTCCGCTCCTGCTCTCCTACTAGGGCCGCTGGG     5702
        |||||||||||||||||| | ||||||||||||||||| ||||||||||||||||||||||||||
Db 5640 GGCCTTGGCGGGCAACGCGCCAGGGCGCTCAGACGCGCTCCAGAGCTGCCCCTCCTGATGGGGTGA      5699

Qy 5703 ACCGCCCTCTGGGGCCACGCGTCGTGGGGTTAACCATGGGGCGGCCGTTCATGGGAAGTGCT        5762
        ||||||||||||||| |||||||| ||||| |||| |||||||||||||||| |||||||||
Db 5700 ACCGCCCTTGGGGCACTGGTCGTGGGTCGTTCAGGGCCGTTCATGGGGGGGCC           5759

Qy 5763 AGCCTTCTCCCCCCCTTGGTCACCATTTACTGGGGCCGTGGGGGCGTG               5822
        |||| |||||||||||||||||||||| |||  ||||||||| ||||||||||||||||
Db 5760 AGTGTCCTTGTCACCATTTATCACCATTTATTGGGCCGTCGAGGTTGGGAGGGTTG       5819

Qy 5823 GTGAATGCGGCTAGCCTTTATGCGGGGAAACTATCATCAGAAGATCTG               5882
        ||| |||||| |||| ||| |||| ||||| ||||||||||||||||||
Db 5820 GTCAACGCGGCGGCCGGCGCGGCCTTCATGCGGGGAAACTTCATCAGAAGATCTG        5879
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Qy 5883 TGGTATGCCATCGACTTGACCAGTGCTAACAACTGGCGGGGGCGGCCTTGCCCGGGATCGCCCTCGGG 5942
        |||||||||||| ||||||||||||||||||||| |||  |||| |||||| ||||| |||||||||||
Db 5880 TGGTATGCCATCCGATCCCGTACTGCTAACAACTGGCGGGGCGGCCTTGCCCGGGATCGCCCTCGGG   5939

Qy 5943 TTGGTGTTGTTACTCAGCTAACAACTGGCACTACCACTTGGTTGAACCGGTCGCTGCTGACT       6002
        ||||| |||||||||| |||||||||||| |||||||||||||||||||||||||| |||||||
Db 5940 TTGGTTTTGTTATTCAGCTAACAACTGGCACTACCACTTGGTTGAACCGGTCGCTGCTGACT      5999

Qy 6003 ACATTGCCAAGGTCCTCATGCGACATCCTGACAGTTACTTGCAGCCGCGATTACTGTGAC       6062
        || ||||||||| |||||||||| |||||||||||||||||||||||| || |||||||||
Db 6000 ACGTTACCAAGGTCTTCATGTATCCCGGACAGTTACTTGCAGCAAGTGACTATTGCCGAC       6059

Qy 6063 AAGGTCTCAGCTGTCTCCGACGCGTTTGAGCCTCACTCGCACCGTGTTGCCCTGGTTCAAC      6122
        |||||||||||||||||| |||||||||||||| ||||||||||||||||||||| ||||||
Db 6060 AAGGTCTCAGCTGTCTCCGACGCGTCCCGAGCCTCACCGCACAGTGGTGCCCTGGTTCAAC    6119

Qy 6123 AGGGAGCCTAAGGTGATGAGGTTCAGGTGGGTACGTCGGGGAGTTCTGGGGAGTGGATC      6182
        |||||||||||||||||||||||||||||| ||| ||| ||||||  |||||||||||||
Db 6120 AGGGAGCCTAAGGTGATGAGGTTACAGGTGGGTATGTCTGGGGTATGTCTGGGAGTGGATC  6179

Qy 6183 ATGCGTCAAGTGCGCATGGCCAGACTTCGGGGCCCTCGCCCGTGTGTCATTA            6242
        ||||||||||||||||||||||||| |||||||||||||||||||| |||||||||
Db 6180 ATGCGGCCAAGTGCGCGTGGCCAGAGCTCAGGGCCCGTGTCCCCGTTGTCGTCACTA       6239

Qy 6243 CCCTTATGGCACTGCGGGGAGGGGGTGTTCCGGAGAATGGTTGTTGACGGCCATGTTGAG    6302
        ||||| |||||  ||||||||||||| ||||| || ||||||||||| |||||||||||||
Db 6240 CCCTTGTGGGCATTGGCGGGGAGGGGGTTGTTCCGGGAATGGTTGCTTGACGGTCATGTTGAG   6299

Qy 6303 AGTCGTTGTCTTTGTTGGTTGGCAGCGTGATCACCGGTGATGTTTGAATGGCAACTCAAAGAT  6362
        ||||||||||| || ||||||||| |||||||||||||  |||||||||||||||||| |||||
Db 6300 AGTCGGCTGCTGCTTGGTTGGCGATGATCACCGGTGATCACTGGTGACGTTCTGAATGGCAACTCAAAGAA 6359

Qy 6363 CCAGTTACTCTACCAAGCTGTGCAGCTGTCTGCACCAGTGACAGATG                6422
        |||||| ||| ||||||||||| || |||||| |||||||||||||||||
Db 6360 CCAGTTACTCTACCAAGCTGTGCTGCCACTATTGGATGGGGACAGTGGAACATG         6419

Qy 6423 CTGGGCTATGGCAGACGCTGCGCCTTTGTGCCTCAGACACCCCGAAGGTGTACCAATTC    6482
        |||||| ||| |||||||| ||| |||||||||| ||||||||||||| |||| ||||| |
Db 6420 CTGGGTACGTGAAACGTCGCCTCTGGGGTTTGACCCCTCCGCCACACCCGGAAGGTGTCGCCCTTC  6479

Qy 6483 GGGAGTCGCTGGCTGGGCTGAGGTGGTGGTGAGGCCCTTGTTGTGATCAGGCGGCGAACA      6542
        |||||||||||||| |||||||||||||||||| |||||||||||||| ||||||| ||||
Db 6480 GGGACGTCTGCTGGGCTGAGGTGGTGGTGACCACTACCACGTGTAATCAGGAGGACC         6539

Qy 6543 TCCGGCTACAAACTGTCTGCGCCCACTGTTTCAATTGTTGACAGCTCTTC             6602
        ||| |||| |||||||||||||| |||| |||||||| |||||| ||||||| |||
Db 6540 TCCGGCTATAAAGTGTCTGCCCACTATCCATTGTTGACAGCTCTTCTAGCTGCGTGTGCTGTGTAGCTGCTACTAC 6599

Qy 6603 GTCGACGGCATACCCGTCATCGGCCGTCATGGGCCGCCATGGTCATGGC              6662
        |||||||||| |||||| ||| |||||||||||||||||||||| |||||||||||||||||
Db 6600 GTCGACGGCATTCCGTCATCGGCCGAGCGCGTCCGTCGCCCCATGTCTCATGTGGC       6659

Qy 6663 CCTGGGCAAAGTGTCACCCTTCCGGCTGCTCTCCAACTCGCGGCTT                 6722
        || |||||||||||||| |||||||||||||||| |||| ||||||||||||||||||||||
Db 6660 CCTGGGCAAAGTGTTACCTTCCTCCTCATCAACTGCTCCTCATCAACTGGGCTC          6719

Qy 6723 AGGAATGCTGGGCGCCCTGACTGAGGCGGAGACT                             6782
        |||||||| ||||||||||||||||||||||||||||||
Db 6720 AGGAATGCTCAGACTGACTCAGATCGAGGGCGGAGACT                         6779

Qy 6783 GAAGACTCAGAACTGCGGAGAATGCTCGAGGAAGATTGCAGTACA                  6842
        ||||||||||||||| |||||||| |||||||||||||| |||||||||||||||
Db 6780 GAAGACTCAGAACTCAGATCGAGGGGCGGCCGATCGAGGAAGATTGCAGTACA          6839

Qy 6843 GAGAATGCTCGCAGAATTCTTGAACCTCACATAGATGCAGTGCAGTACA              6902
        ||||||||||||| ||||| |||||||||||||||||| |||||||||||||||||||||||
Db 6840 GAGAATGCTGCGAGATTCTTGAACCGCCACATTGATGTCATCATGTCATCATGTGGGAGGTGCGTG 6899

Qy 6903 CCCTCTCTTGTGTGGAGTAGCCGAGAGATGCCGTGTGTGGGGGAAGACATACCCCCCACT   6962
        ||||| |||||||||||||||||||||||||| |||| ||||||| ||||||||||| ||||
Db 6900 CCCTCTTCTTTGTGGAGTAGCCGAGAGATGCCGTATGGGGGAGAAGACATCCCCGCTACT   6959
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Qy 6963 CCATCGCCAGCACTTATCTCGGTTACTGAGACGAGCCAGATGAGAGACCCGTCGGTG 7022
         |||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db 6960 CCATCGCCAGCACTTATCTCGGTTACTGAGACGAGCCAGATGAGAGACCCGTCGGTG 7019

Qy 7023 TCTTCCTCGCAGGAGGATACCCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCGAG 7082
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7020 TCCTCCTCGCAGGAGGATACCCCGTCTCTCGACTCATTCGAGGTCATCCAAGAGTCCGAG 7079

Qy 7083 ACAGCCGAAGGCGAAGGGGAGGAAAAGCGTCTTCAACGTGGCTCTTCCGTACTAAAAGCCTTGTTT 7142
         |||||||||||||||| |||||||||||||||||||||||||||||||||||||||| |||||
Db 7080 ACAGCCGAAGGCGAAGGGGAGGAAAAGTGTCTTCAACGTGGCTCTTTCCGTATTAAAAGCCTTATTT 7139

Qy 7143 CCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGATGTCATGCGTGTTGAGAAGAGC 7202
         ||||| |||| |||| ||||||| |||||||||||||| |||||| ||||
Db 7140 CCACAGAGCGACGCGGACCAGGAAAGCTTACCCGTCAAGATGTCGTCCTACGATGTAGGT... 7199

Qy 8040 TTCGACAGTAGCATAACTGAAGAGGACGTGGCCCTGGGAAATACTATGCCTCTGGCACAATGGTA 8099
         |||||||||||||||||||||||| ||| |||||||||||||||||||||||||||||||||
Db 8040 TTCGACAGTAGCATAACTGAAGAGGACGTGGCCCTGGGAAATACTATGCCTCTGGCACCATGGTC 8159

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CC   is a labelled monoclonal antibody or a labelled competing antigen. The
CC   HGV is characterised by producing elevated serum alanine aminotransferase
CC   levels in an infected primate, being serologically distinct from
CC   hepatitis A, B, C, D and E viruses and having a viral genome containing a
CC   nucleic acid region that is selectively hybridisable with a polypeptide
CC   having 203 base pairs as given in the specification.
XX
SQ   Sequence 9392 BP; 1694 A; 2551 C; 2998 G; 2148 T; 1 other;

Query Match             84.9%;  Score 7979;  DB 19;  Length 9392;
Best Local Similarity   90.7%;  Pred. No. 0;
Matches 8515;  Conservative  1;  Mismatches 876;  Indels  1;  Gaps 62;

Qy     3 ACGTGGGGGGTGATCCCCCCCCCCCGCACTGGTGCAAGCCCCATAAACCGACGCCT 62
         |||||||| ||||||||||||||||||||||||||||||||| |||||||||||||
Db     1 ACGTGGGGGGTTGATCCCCCCCCCCCGCACTGGTGCAAGCCCCAGAAACCGACGCCT 60

Qy    63 ATCTAAGTAGACGCAATGACTCGGCGCGCGACTCGGCGACCGGCCAAAAGGTGGTGGATGG 122
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ATCTAAGTAGACGCAATGACTCGGCGCGCGACTCGGCGACCGGCCAAAAGGTGGTGGATG 120

Qy   123 GTGGTGACAGGGTTGGTAGGTCGTAAATCCGGTCATCCGGTAGCCACTATAGGTGGGT 182
         ||| |||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   121 GTGATGACAGGGTTGGTAGGTCGTAAATCCGGTCACCTTGGTAGCCACTATAGGTGGGT 180

Qy   183 CTTAAGAGAAGGTCAAGACTCCTTCGTGCCTGCGGGCGAGACCGCGCACGGTCCACAGT 242
         |||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db   181 CTTAAGAGAAGGTTAAGATTCCTTCGTGCCTGCGGGCGAGACCGCGCACGGTCCACAGT 240

Qy   243 GCTGCGCCTACCGGTGTGAATAAGGGCCCAGCGGTCGTCGTTAAACCGGCCCGT 302
         | ||||||||||||| ||||||||||||| ||||||||||||||||||||||||
Db   241 GTTGCCCTACCGGTGGAATAAGGGCCCGACGTCGTCGTTAAACCGGCCCGT 300

Qy   303 CACCCACCTGGGCAAACGACGCCCAGTGACGGTCGCCCTTCAATGTCTCTCTTG 362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TACCCACCTGGGCAAACGACGCCCAGTGACGGTCGCCCTTCAATGTCTCTCTTG 360

Qy   363 ACCAATAGGTTTATTCCGGCGAGTTGACAAGGACCAGTGGGGCCGGGGTTATGGGGAAG 422
         ||||||||| ||  |||||||||||||||||||||||||||||||||||| ||||||||
Db   361 ACCAATAGGCGTAGCCGGCGAGTTGACAAGGACCAGTGGGGCCGGGGCT-TGAGAGAGG 419

Qy   423 GACCCCAAACCCTGCCCCTTCCCGTGGGCCGGGAAATGCATGGGGCCACCCAGCTCCCG 482
         ||| |||| | ||||||||||||| |||||||||||||||||||||||||||||||||
Db   420 GACTCCAAGTGCCCGCCCTTCCCGGGGTAGCCCAAGAATCCTTCGGGTGCATTTCTCTT 479

Qy   483 GCGGCCTGCAGCCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCCGGTGCATTTCTCTT 542
         |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   480 GCGGGCCTGCAGCCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCCGGTGCATTTCCTTT 539

Qy   543 TTCTATACCATCATGGCAGTCCTTCTGCTTCCTTCTCGTGGTTGAGGCCGGGGCCATTCTG 602
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540 TTCTATACCATCATGGCAGTCCTTCTGCTTCCTTCTCGTGGTTGAGGCCGGGGCCATTCTG 599

Qy   603 GCCCCGGCCACCCAGCCCACCACGCTTGTCGAGCGAATGGGCAATATTCCTCACAAATTGC 662
         |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   600 GCCCCGGCCACCCAGCCCACCACGCTTGTCGAGCGAATGGGCAATATTCCTCACAAATTGT 659

Qy   663 CCGGAAGACATCGGGTTCTGCCTGGAAGGCGATGCCTGGTGCCTGGGTGCACGGTT 722
         |||| ||||||||||||| |||||  |||||||||||||||||||||||||||| |
Db   660 CCGGAGGACATCGGGTTCTGCCTGGTGGATGGTGTGCCTGGTGCCTGGGTGCACGATT 719

Qy   723 TGCACCGACCGTTGCTGGCCACTGTATCAGGCGGTTTGCTGTTTGGCCTGCAAGTCC 782
         |||||||||||| |||||||||||  |||||||| |||||||||| ||||||||||
Db   720 TGCACTGACCAATCGGCCACTGCCACTCAGGCGGTTTGCGTGTTGCCTGCAAGTCC 779

Qy   783 GCGCCCAGCTCGTTGGGAGAACTGGGAGCCTGTACGGGCCCTTGTCTCGGCTTAC 842
         |||| ||||||||  ||||  ||||||||||| ||||||||||||||||||||| |
Db   780 GCGCCCAACTGGTTGGGGAGCTGGGAGCCTATACGGGCCCCTGTCTCGGCTTCGGCTTAT 839

Qy   843 GTAGCCGGGATCCTGGGCTGGGGCGGTGAGGTTACTCCGGGTCCTGACAGTGGTGTTGCG 902
         ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   840 GTTGCTGGGGATCCTGGGCTGGGGCGGTGAGGTTGACTCCGGGTCCTGACAGTGGTGTTGCG 899

Db  9120 ATCACCGGAGAGAGGTTCCGCGCCCTCCCGCGCCCAGGGGTCTCCCGCTGGGTAAAAAGGG 9179

Qy  9183 CCCGGCCTTGGGAGGCATGGTGTTACTAACCCCTGCCAGGGTCAAAGCCTGATGGTGC 9242
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9180 CCCGGCCTTGGGAGGCATGGTGTTACTAACCCCTGCCAGGGTCAAAGCCTGATGGTGC 9239

Qy  9243 TAATGCACTGCCACTTCGGTGGCGGTGCGCTACCTTATAGCGTAATCCGTGACTACGGGC 9302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9240 TAATGCACTGCCACTTCGGTGGCGGTGCGCTACCTTATAGCGTAATCCGTGACTACGGGC 9299

Qy  9303 TGCTCCGAGAGCCCTCCCCGGATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC 9362
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9300 TGCTCCGAGAGCCCTCCCCGGATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC 9359

Qy  9363 GGTAAGAGCTCGCCCAAAGGCCGGGTTCTACT 9395
          || |||||||||||  ||||||||||||||||
Db  9360 GGGAAGAGCTCGCCGCCCAAGGCCGGGGTTCTACT 9392


RESULT 3
AAV56058
ID   AAV56058 standard; cDNA; 9392 BP.
XX
AC   AAV56058;
XX
DT   06-NOV-1998 (first entry)
XX
DE   HGV isolate PNF 2161 variant cDNA.
XX
KW   Immunoreactive; detection; antibody; alanine aminotransferase;
KW   Non-A, Non-B, Non-C, Non-D, Non-E hepatitis virus; ds.
XX
OS   Hepatitis G virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             459..9080
FT                   /*tag= a
XX
PN   US5766840-A.
XX
PD   16-JUN-1998.
XX
PF   05-JUN-1995;   95US-0466033.
XX
PR   19-MAY-1995;   95US-0444733.
PR   20-MAY-1994;   94US-0246985.
PR   03-AUG-1994;   94US-0285543.
PR   03-AUG-1994;   94US-0285558.
PR   03-AUG-1994;   94US-0285561.
PR   26-OCT-1994;   94US-0329729.
PR   23-NOV-1994;   94US-0344271.
PR   16-DEC-1994;   94US-0357509.
PR   15-FEB-1995;   95US-0389886.
PR   05-JUN-1995;   95US-0466033.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fry KE, Kim JP, Linnen JM, Wages J, Young LM;
XX
DR   WPI; 1998-361677/31.
DR   P-PSDB; AAW76054.
XX
PT   Antibody to hepatitis G virus protein - useful for diagnosis of
PT   hepatitis G virus infection
XX
PS   Example 13; Column 99-120; 204pp; English.
XX
CC   This sequence is a used in a method which detects Non-A, Non-B, Non-C,
CC   Non-D, Non-E hepatitis G virus (HGV) in a biological fluid sample, e.g.
CC   from a test subject, especially using a kit comprising an anti-HGV
CC   antibody preparation and a reporter for detecting binding of an HGV
CC   polypeptide antigen to the antibody, preferably where the antibody is
CC   monoclonal and/or is attached to a solid support and where the reporter
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Qy   903 TTCAGGCCCCGGGTTCTACCTGATGCCCAACCTGAAGTGTGCAGTAGAATGTGACGTTAAG  962
         |||| ||| ||||| ||||||| |  ||||   || ||| ||| ||| ||  | |||| |||
Db   900 TTGACGCGCCGGTGCTACCCGGTGCGTCAACCTGACGTGCAGTGCGCCGGTGAGCTGTAAAG  959

Qy   963 TGGGGAAGTGAGTTTGGAGATGGACTGAGCAGTTGCCTCCAATTACTGGATTTTGGAA  1022
         ||||| ||||||||||||||| ||||||||| | ||  |||||||  || ||||||||
Db   960 TGGGAAAGTGAGTTTGGAGATCGACTGAACAGCTGGCCTCCAACTACTGGATTCTGGAA  1019

Qy  1023 TACCTTTGGAAAGTCCCATTGAATTTTGGAGAGGAGTGATGAGCCTGACCCCTCTGTTG  1082
         |||| ||||||| ||||||||| || |||||||| || || |||  | ||||||| |||
Db  1020 TACCTCTGGAAGTCCCATTTGATTTCTGGAGAGGCGTGATAAGCCTGATAAGCCCCTGTTG  1079

Qy  1083 GTTTGGGGTGGCCCGCATTGCTTTTGCTGGAGCAACGATTGTCATGGTTTCCTGCTGGTG  1142
         |||||||||||||||||||||||  | |||||||||| ||||||| | |||||||| |||
Db  1080 GTTTGCGTGGCCCGCATTGCTGCTCTGCAACGGATTGTCATGGTCTCCTGCTTCCTGTTGTG  1139

Qy  1143 ACGATGGCGGGGATGTTGCAAGGCGCCCCGCCCTTCGTTTGGGTCGCGTAACGGGTCGGG  1202
         || ||||| ||||| ||| ||||| ||||| |||| |||||  ||| |||| |||||||
Db  1140 ACGATGGCGGGGATGTCGCAAGGCGCCCCGCCCTGCCTCCTGTTTCCGTTTGTCACGACTGGG  1199

Qy  1203 TACGGGTTGAAGTGGCAGTCATGCGTCCTCTGCAGGGCTAACGGGTGCGGTATTCCCACTGGG  1262
         |||||||||| |  ||||||| |||| | || |||||||  || ||||| | ||||||||
Db  1200 TACGGGTTGACTTGGCACGACCTGCCTCCTCGCAGGGCAAGGGGTGCGGTTTTCGCGTTTGTCGACTGGG  1259

Qy  1263 GAGAGGGTGTGGGATCGAGGGAATGTCACGCTTGTGTGACTGCCCCAAGCGCCCCTGG  1322
         ||||| ||||||||| |  |||||||| ||| |||| || |||| || |||||| |||
Db  1260 GAGAAGGTGTGGGAACGTTACGCTTCAGTGTGACTGGACTGCCCCTAACGGCCCCTGG  1319

Qy  1323 GTTTGGGTCCCGGCCTTTTGCCAGGCGGTTGGGGCGACCCCATCACCACCATTGGAGC  1382
         || |||||||| || || ||||||| ||||||| ||  ||| |||||||||| |||||
Db  1320 GTGTGGGTCCCGGCCTTTTGCCAAGCAATCGGCTGGGGTGCCTGGGGTGACCCCATTATTGGAGC  1379

Qy  1383 CACCGACAAAACCAGTGGCCCCTATCATGCCCCAATATGTCTATGGGTCTGTGTCCGTA  1442
         | ||||| || |||||||||||| || |||||| || ||| ||||||||||||| |||
Db  1380 CACCGACAAAATCAGTGGCCCCTTTCATGCCCCAGTATGTCTATGGGTCTGTTGCTACAGTC  1439

Qy  1443 ACGTCGTGTGGGGTTCCGTGTCTTCCGCGCGGCCGGTCGTGATTCGAAGATC  1502
         |  ||||||||||||||||||| | || ||||| ||||||| |||||||
Db  1440 ACTTCGTGTGGGGTTCCGTGTCTTCCGCCCCACCAGTGTCGCGCGACTGCGAAGATA  1499

Qy  1503 GATGTGTGGAGTTTGGTGCCGGTTGGATCTGGAGTCCCGTGCCTGCCTAGGGTCA  1562
         ||||||||  |||||| ||||| | ||| |||||||||| |||| ||||||||||
Db  1500 GATGTGTGGAGTTTGGTGCCAGTTTAGTGCTGCCACTTGCCACCAGTGCCACCATAGCCGTCTAGGGTCA  1559

Qy  1563 TCGGATCGGCCACACGGTGTTGGTGAGCTGTCGGGAGTCCCGTGCCTAACCTGTATT  1622
         |||||||||| |||| | | ||  || ||||  |||||| ||| || || ||||| |
Db  1560 TCGGATCGGCCACACGGTGCTGCCGTCCCGTGTTGGGAATCCCGTGCCTGCCGTGGTGTT  1619

Qy  1623 CTGGACCGTCGGCCTGCTTCATGTGCACCTGTGTGCGGGACTGCTGGCCCGAAACCGGG  1682
         |||||||||||||||||||| ||| ||| ||||||||||||||||  || |||||||||
Db  1620 CTGGACCGTCGGCCTGCTTCAAAGGGTGGTGGTTGCGGGGACTGCTGGCCAAAGACCCCTG  1679

Qy  1683 TCGGTTAGATTCCCTTTCCATCGGTGCGGCCACGGTGCGCTCGGCTGACAAAGGACTTGGAA  1742
         |||||| ||||||  ||| |||||| |||| |||| |||| |||||| |||||||||||||
Db  1680 TCGGTTAGGTTCCATTTGCCATCGGTGCGGCCACGGTGCGCTCGGCTGACAAAGGACTTGGAA  1739

Qy  1743 GCTGTGCCCCTTGTCAACAGGACAACTCCCTTCACCATAAGGGCCCCTGGGCCAACCAG  1802
         | ||||||||||  ||||||| |||||| ||||||||| || ||||| ||||| |||||
Db  1740 GCTGTGCCCCTTGTCAACAGGACAACTCCCTTCACCATAAGGGCCCCTGGGCCAACCAG  1799

Qy  1803 GGGAGAGGCAACCCGTGCGTCGCCCGCCCATTAAACAACTGCATGCCGCTAGGCACCGGAAGATC  1862
         |||| |||||||||||| || | |||  ||| |||||| ||||| |  |||||||||||||
Db  1800 GGCCAGAGGCAACCCGTGCGTCGCCCGCCCATTGAACAACGCATGCCGCTCTTCGGGCACCGGAAGTG  1859

Qy  1863 CGGGATTCCCTGCATTTGGTGAAATGTCCCACCAGCCTCCGACTGGAACG  1922
         |||| |||||||||||| || | ||| |||||| |||||| || |||| |
Db  1860 CGAGATACCCGTCCGTCATCGGTGAGTGTCCCACCATTGACCAACGGGGACG  1919

Qy  1923 TTCGGGTTCTTCCCCGGAATGGCTCCCGCCGCTAGGCACCGGAAGTG  1982
         ||||||||||||||||| |||| ||||||  ||| ||||||| |||
Db  1920 TTTGGGTTCTTTCCCCGGCACGTCCGTGTCTTTGGGCACCGGAAGTG  1979

Qy  1983 TCTGAGGCATTGGGCGGAGCTGGGCTTACGCGGGGGTTCTACGAGCCCTCTGGTTCGCAGG  2042
         ||  |||||| |||||| |||||| |||   ||||||| ||||||||| ||||||||||||
Db  1980 TCCGAGGCACTTGGGGGGCTGGCCTCGCACGGGGGTTCTCATGAACCCCTGGTCGCGCAGG  2039
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Qy  2043 TGTTCGGAGCTGATGGACGCGCCGAAATCCGGTTCTCCGGGGTACGCATGGCTGTCCTCT  2102
         |||||||| |||| ||| ||| |||||||||||||| | ||||  | ||||||||| | |
Db  2040 TGTTCGAACTGATGGAGCCGAAATCCGGTTTGTCCGGGTTGCATGGCTCTCTTCG  2099

Qy  2103 GGTAGACCTGACGGTTCATCACGTGCTCTTCCTCGCAGGGCACCTGCGAGGTGGATGCGGGCAAC  2162
         || ||| |||| |||| |  ||| ||||||||||||||||| || |||||||||| |||| ||||
Db  2100 GGCAGGCCTGATGGGTTTATACATGTCAGGGGTGACTTGCAGGAGGTGGATGCGAGGCACAC  2159

Qy  2163 TTCATCCCCTCCACGTCGTTGCTTGTGCTCTTGGATTTGTATTTGTCCTGCTCTATCTGATG  2222
         || ||||| |||| |  | |||||||| ||||  | | |||||| ||  || |||| ||||
Db  2160 TTCATCCCGCCCGCGCTGGTTGCTTGTGCTCTTGGACTTGTATTTGTCCTGTTATACCTGATG  2219

Qy  2223 AAGCTGGCTGAGGCACGGTTGGTCCCGGTGCGCGGTCCCGGTGCGGTGAAGTTTTTGCG  2282
         |||||||| || ||||| |||||  |||| ||| |||| |||||| ||||  ||| |||
Db  2220 AAGCTGGCTGAGGCACGGTTGGTCCCGCGTGCTCTGCGCCGTGCGGTGAGGTGGTGAAGTTTTTGCG  2279

Qy  2283 CAGTTGGCCGGTTCTAGGAGCTGTGGCCTTCCCCACTGTCAGTATGGATACTAGGTCTAGCA  2342
         |||||||| | |||| ||||| ||| |||  |||| | |||||| || |||| |||||
Db  2280 CAGCTGGCAGTCCTAGGCTGCGTGTGTGCAAGCCGTGTGTGTGTCTCGGACTCGTCAGTATATTGGGTTTGGCA  2339

Qy  2343 GGCCCTGCCTTGTCATGGTGTTTGGGCCTTCCCACTGTCAGTATGATACTAGGTCTAGCA  2402
         ||||||||||||||| | ||||| || || ||| ||| |||| || |||||||
Db  2340 GGCCCTGCCTTGTCTCTGGGACTCGTCAGTATATTGGGTTTGGCA  2399

Qy  2403 AACCTGGTGTTGTACTTTCGGTGATGGGCCGACCCCACCATTGGAGC  2462
         |||||||| ||||||| | | |||| ||||| ||| |||||||||||
Db  2400 AACCTGGTCGTGTACTTTAGATGGTTGGGACCCCACCGCCTGATGGGATTTCCGTGTTGTGG  2459

Qy  2463 AAGCTCGCTCGGGGAGCTTTCCCGTGGCACTTTTGATGGGATTTCGCGAGGTGGACACTTCG  2522
         |||||||||||||||||| |||| ||| |||||||||||  || ||  || |||||||||||
Db  2460 AAGCTTGCTCGGGGAGCTTTCCCGCCGTGGCACTTTGATGGGATTTCGCGACTGGGACACTTCG  2519

Qy  2523 CGCACCTCTGTCTCGGGGTGGGTGGTGCCAGGTGGTGGCTTGGGCCATAGCCGTCTGAGTCAATG  2582
         ||||| || |||| |||| || ||||||||  |||||  || |||||||||| ||| || ||
Db  2520 CGCACCTCAGTGTCGGGGCGGGTGGTGCCAGGTGGTGGTTTGGGCCATTGCCAGTGTCTCCGTGTTCG  2579

Qy  2583 GTGTTGGGCTGGGTGGTGTGGAAGCACAAGGCCGTGATCATAGGACGTGGTGTAAAGGGTACCAG  2642
         |||||||| ||||| ||||| |||| |||| ||| |||| ||||||||||||||  |||||||||
Db  2580 GTGTTGGGCTGGGTGGTGTGGCAGTGGTAGCCGTGATCATAGGACGTGGTGTAAGGGGTACCAG  2639

Qy  2643 AGGCCAGGGGGGGTGAAGCACAAGCCGTGATCATCATAGGACGTGTTATT  2702
         ||||||||| ||||||||| |||  ||||||||  ||||| ||||| ||
Db  2640 AGGCCAGGGGGTGAGGGCACAAAGCCGTGATCATCATAGGACGTGTTACCAG  2699

Qy  2703 GCTGTGCGCCAGAGGTGGTGCGGAGCCCCTCGGGGAGGGCGTCCTACCAAGCTTCTG  2762
         | | ||| ||||||||| |  ||||| | |  ||||||| |  || ||||||||||
Db  2700 GCAATCCGTCAAAGGGGTGGTGGAGAGCCCCCCGGGGAGGGCGGCCCTGCCAAACCCCTG  2759

Qy  2763 ACGTTCGGCTGGTGCTTCTCATACATCTGGGCTCATACAATCTGGACGGATGCTGTGATGATTGGTGGTGTG  2822
         || |||||||||| |||| | ||  || ||||| | |||| |||||||||||||||||||||| |||
Db  2760 ACCTTTGCCTTGGTGCTTCTCGGTGTCGTCGTACATCTGGCCCAGATGTCTGTGATGTGGTGGTT  2819

Qy  2823 GCCTTGGTCCTCTTCTCCGGCCTCGTTCGACCGACTGGACTGCGTCCTGGACCCTGGAGAGCTCCTG  2882
         ||||||||||| | || | ||||| |||||||||| || || || |  ||||| |||||| | ||||
Db  2820 GCCTTGGTCCTCTTCTCTTTGGCCTTGTTCGACCGCGGTTGGATTGGCCTTGGAGGATCTTG  2879

Qy  2883 GTCTCCGGCCCACCACCATCCGACTGGGTCGTTTGTCGTGTGTCGCACGGGGCCTACCTGTTT  2942
         |  ||| ||||||||| |  ||||||| | |   | |   || || || ||  |||| ||||
Db  2880 GTGTCCCGGCCCACCAACCGTCCCGCGTTCCCGCGTTGGCGTGTGTCGTGTTGCGCCGGGGGCGGGT  2939

Qy  2943 GAGAAGGCCACCACCATCCGACTCGGTTTCTCTCGTTCTCTGCGCCGTGCAAGAGGGGCCTACCTGTTT  3002
         |||||||| | | ||||| ||   | | ||||  || | ||||| ||  |  | |||| ||| ||||
Db  2940 GAGAAGGCCACAAACGTCCCGCGTTCCCGCCTCTTTGCGGAGGAGCTTATTTGTTC  2999

Qy  3003 GACCACAGGTGGCTCTTTCTCCGCGGCGTCTTGTTCCTGCGGTCCGTCAAGGCACGGAAGTG  3062
         |||| | |||| |||   | |   | | | | | |||| ||| | | | |||| ||||| |
Db  3000 GATCATATGGGCTCTTTTCGGCGTGTCTTGTCAACAACTGCATGCTCTTGGCACGGAAGCT  3059

Qy  3063 TTGGAGCCCCTTGTCATTCACTGGACGGACGACTGTCGCATCATCAGAGATGCCCGAGGACC  3122
         |  ||  || || ||||||||||||||||||||||||||||||||||||||| | |||||||
Db  3060 TTTGGGTTCTTCCCCGGCACGTCCGTGTCTTTGGGCACCGGAAGTG
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Db 3060 CTTGAACCTTCGTCATTCACTAGGACGGACTGTCGCATCATACGGGATGCCGCGGAGGACT 3119

Qy 3123 CTGTCCTGCCGGACAGTGCGTCATGGGTT...GGTAGCACGGGCGGCGGCGTGATGAGGTT 3182
           |||||| ||| ||||||||||||||||||         ||||||| ||| || ||||||||||
Db 3120 TTGTCCTGCGGGCAGTGCGTCATGGGTT...GGTTGCGCCGCCTGGTGTGATGAGGTT 3179

Qy 3183 CTCATCGGCGGCTGTTTCAGGATGTGAATCATTTGCCTCCCGGGTTTGTCCGACTGCACCA 3242
Db 3180 CTCATCGGCGGCTGTTTCCAGGATGTGAATCATTTGCCTCCCGGGTTTGTCCGACCGCGCCT 3239

Qy 3243 GTTGTCATCCGTCGGTGCGGGAAAGGGCTTCCTGGGGTTCACGAAGGCAGCCCTTGACAGT 3302
Db 3240 GTTGTCATCCGACGGTGCGGGAAAGGGCTTCTAAGGCTGGGTCTGGCCCAGTTCTCCGCT 3299

Qy 3303 AGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTTGGGGACGGTACGTCACGGAAGC 3362
Db 3300 CGGGATCCTGACTTACATCCAGGAACGTCATGGTGTTGGGGACGGTACGTCGCGAAGC 3359

Qy 3363 ATGGGCACATGTCGAATGGCCTGCTTGTTGCCATGGCCTTCACAACTTTCCATCCCGAACC 3422
Db 3360 ATGGGAACATGTTGAACGGCCTGCTTGTTGCCATGGCCTTCACAACTTTCCATCCCGAACC 3419

Qy 3423 ATCGCCACGCCCGTGGGGGCCCTTAATCCACAGTTGGTGTCAGCCAGTGATGACGTCACG 3482
Db 3420 ATCGCCACACCCGTGGGGGCCCTTAATCCACAGTGGTGTCAGCCAGTGATGATGTCACG 3479

Qy 3483 GTGTACCCGCCTTCCAGATGGGGCAACTTCGTTGACGCCCTGCACTTGCCAGGCGGAGTCC 3542
Db 3480 GTGTATCCCCGGATGGGGCTACTTCGTTAACACCTTGTACTTGCCAGGCTGAGTCC 3539

Qy 3543 TGTTGGGTTATTAGATCCGACGGGGCTTTGTGCCATGGCTTGAGCAAGGGGACAAGGTT 3602
Db 3540 TGTTGGGTCATCAGATCCGACGGGGCCCTGACCGCTTGAGCAAGTGCCAAAACCACTACT 3599

Qy 3603 GAGCTGGATGTGGCCATGGAGTCTCTGACTTCCGTTCGTTCGTTCACCGGTCCTT 3662
Db 3600 GAGCTGGATGTGGCCATGGAGTCTCTGACTTCCGTTCGTTCGTTCACCGGTCCTA 3659

Qy 3663 TGGCACAAAGGCACGCAGTAAGAATGCTCGTGTCAGTGCTCCACCTCTGGCGCGGAGGGTT 3722
Db 3660 TGTGACGAAGGCACGCAGTAGGAATGCTCGTGTCGTTGCTTCACTCCGGTGGTAGGGTC 3719

Qy 3723 ACTGCGGCGCGATTCACTAGGCCGTGACTCAAGATGCCAAGACTACCACA 3782
Db 3720 ACCGGCACGGTTCACTACTAGGCCGTGACTCTGGAACCGCCAAAACCACTACT 3779

Qy 3783 GAACCCCGTCCGGTGCCGGCCAAAAAGGAGTTTCAAGGAGGCCCGTTGTTTATGCCTACG 3842
Db 3780 GAACCCCGTCCGGTGCCGGCCAAAAAGGAGTTTCAAAGAGGCCCGTTGTTTATGCCTACG 3839

Qy 3843 GGGGCGGGGAAAGAGCACCCGTACCCGTGGAGTACGGCGCAACATGGGGCACAAGGTCTTG 3902
Db 3840 GGAGCGGGGAAAGAGCACCCGTGTCCCGTGGAGTACGGCACAAGGGCACAAGGTCTTA 3899

Qy 3903 ATCTTGAACCGGTCGGTAGCTCATCGGTAGCTACCGTGAGGGGCCCATACATGGAGCGGC 3962
Db 3900 ATCTTGAACCCCTCACTGCGGCCACTGCGTAGGGGCCCGTACATGGAGCGGCTGCGG 3959

Qy 3963 GGGAAACACCCCCAGTATTACTGGCCACAGACCACCCCAGTTTCACAAGGATCACTGAC 4022
Db 3960 GGTAAACATCCAAGTATATACTGTGGCCATGATTACAACTGCTTTCACAAGGATCACTGAC 4019

Qy 4023 TCGCCCCTTACGTATTCCACTTACGGAAGGTTTTGGCCAACCTAGGCAGATGCTGAGG 4082
Db 4020 TCCCCCCTGACGTATTCAACCTATGGGAGGTTTTGGCCCAACCTAGGCAGATGCTACGG 4079

Qy 4083 GGTGTGTTCGGTGGTCATTTGTGATGAGTGCCACAGTGAGTGGCTCTCTACGCCCACT 4142
Db 4080 GGCGTTTCGGTGGTTCATTTGTGTGATGAGTCAACCGTGCTGCTTTAGGC 4139

Qy 4143 ATTGGGCGTCAGGGAGCTGGCCGCGAGGATGTGGGCTGGGGTGCGGGGTGCGCTCTCACGCCACT 4202
Db 4140 ATTGGGAGAGTCCCGGGAGCTGGCCGCGCTGGGGTGCGGGGTGCAACTAGTGCTCTCACGCCACC 4199
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Qy 4203 GCCACCCTCCGATCCCCGATGACCCAGCACCCATCAATCATTGAGACAAAACTGGAC 4262
Db 4200 GCTACACCTCCGGATCCCCGATGACCCCATGCAGCAGCACCCTTCCATAATTGAGACAAAATTGGAC 4259

Qy 4322 GTGGGAGAATCCCCCTTCATGGCGAGTCGATGGCGATGGCGACCGGAAGG 4322
Db 4263 GTGGGCGAGATTCCCTTTTATGGGGCATGGCGATGGCGAACCCCGAAGG 4319

Qy 4323 CATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGCGCCTGGCGCGCCCAGTTTCTGGCT 4382
Db 4320 CACCTCGTGTTCTGCCATTCTAAGGCTGAGTGCGAGCGCCTGGCGCGCCCAGTTCTCCGCT 4379

Qy 4383 AGGGGGTAAATGCCATCGCCTATTACAGGGGAAAGACAGTTCATCATCAAAGATGGA 4442
Db 4380 AGGGGGGTCAATGCCATTGCCTATTATAGGGGTAAAGACAGTTCATCATCAAGGATGGG 4439

Qy 4443 GACCTGGTGTGTGCTACAGACCGCCACTATCCACTGGGTACACTGGGACTTCGATTCT 4502
Db 4440 GACCTGGTGTGTCTGTGCTACAGACGCGCTTTCCCACTGGGTACACTGGAAATTTCGACTCC 4499

Qy 4503 GTCACCGATTGTGGGTTAGTGTGGTAGGAGGTCGTGAGGTCGTTGAGTGGTCGTGATCCCACCATT 4562
Db 4500 GTCACCGACTGTGGATTAGTGGTGGTAGGAGGTCGTGAGGTCGTTGAGTGGTCGTGATCCCACCATT 4559

Qy 4563 ACCATCTCCCTGCGCACGGTGCCCGCGTCTGCGATGCCAGCGGCGAGGACGACGC 4622
Db 4560 ACCATCTCCCTGCGGCACAGTGCCCTGCGTCGCTGCGATGCCGATGCGCAAAGACGAGGACGACGC 4619

Qy 4623 ACGGGTAGGGCAGGTCTGGGCGCGCTACTACTGTCGCGGGGGCCCCTGGT 4682
Db 4620 ACGGGTAGGGCAGGTCTGGGCGCGCTACTACTACGCGGGGGTGGGCAAAGCCCCTGCGGGT 4679

Qy 4683 GTGGTGCGCTCAGGTCCTGTCGGTTCGTTCGGCGGCGTGACCTGGCGCGGCTCAACTGGAATG 4742
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Qy 4743 GAACCTGACCTGACAGCAGCAAACTACTGAGACTTACGACAACTGCCCTTACCACCGGAGCC 4802
Db 4740 GAACCTGACTTGACAGCTAACTACTGAGACTTTACGACGACTGCCCTTACCACCGAGCC 4799

Qy 4803 GTCGCAGCTGACAATGGGAGGCCGGCGGTGTCTTTTCGGGGCTTGCCCCGTTGAGGATG 4862
Db 4800 GTCGCGCGCTGATATCGGAGAGCCCGGTTGTTCTTCTCTGGGCGCCCCCATTGAGGATG 4859

Qy 4863 CATCCCGATGTTAGCTCAGCAAAAGTTCGCGGCGTCAACTGGGCCCTTCCTGGTGGGTGTT 4922
Db 4860 CACCCCGATGTCAGCTCAGCAAAAGTTCGCGGCGTCAACTGGGCCCTTCCTGGTGGGTGTT 4919

Qy 4923 CAGGGGACCATGTGCCGGGAAACACTGTCTCCCGGCCATCGGATGACCCCAGTGGGCA 4982
Db 4920 CAGCGGACCATGTGCCGGGAAACACTGTCTCCCGGCCATCGGATGACCCCAATGGGCA 4979

Qy 4983 GGTCTGAAGGGCCCGAATCCTCGTCCCACTCCTGCTGAGGTTGGGCAATGATTTACCATCT 5042
Db 4980 GGTCTGAAGGGCCCAAATCCTCGTCCCACTCCTGCTGAGGTGGGGCAATGATTTACCATCT 5039

Qy 5102 AAAGTGGCCGGCCATCAACGTCACATCGTGGCGACGATCACTGAC 5102
Db 5043 AAAGTGGCCGGCCACCAGCGGTCCGGAGACTGGCTGTGGCGAGGGGT 5099

Qy 5103 TACGTCCGCGTCGGATGCGGGCCGATGGGCCTTCGCTGGTGGGGGCATG 5162
Db 5100 TACGTCCGCGTCGGACGCGTGGCCGATCTGGTCGGTCTAGCTATCGCGGGGGGAATG 5159

Qy 5163 ATCTATGGGCTCATACACCGGCTGTCTCTCATACACCGGCCACT 5222
Db 5160 ATCTACGCGTCATACACCGGGTCTCGGCTCAGATGTTGTGGGGGT 5219

Qy 5223 GGCAGCCCCTTATCGCATGGAGACCACCAGCCCACGCCCCGGTTGTGCAGTCCCC 5282
Db 5220 GGCGCCCCCTTATCGCATGGAGACCACCAGGCCACGCCCCGGTTGGTCAGTTCCT 5279
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Qy  5283 CCGGTAGACCATCGGCGGGGGAGTCTGCCCATCGGATCCAACACAGTGACAGAT 5342
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Db  5280 CCGGTAGACCATCGGCGGGGGAGTCTGCCCATCGGGGGTGAATCAGCACCAAGAAGACAGTGACAGAT 5339

Qy  5343 GCGGTGCCGGCCATCCAGGTGCGGGATTGCGATTGGCTAGTCAGTCATGACCCTGTCGATCGGGGAA 5402
         |||||| |||||||||||| |||||| |||||||||||||||||| ||||||||||||||||
Db  5340 GCGGTGCAGCCATCCAGGTGACTGCGATTGCGATTGGACTCTGTCGATCGGGAGAA 5399

Qy  5403 GTGCTGCTCCTTGGCCCAGGCTAAGACGGCCTAAGAGGGCCTACCACCAAGTGGCTT 5462
         |||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  5400 GTGTTGTCCTTGGCTCAGGCTAAGACGGCCTAAGAGCCCTACCACCAAGTGGCTC 5459

Qy  5463 GCTGGCTGCTCACACGGGGACGCGGGCCGTCCCCACTGTTTCAATTGTTGACAAGCTCTTC 5522
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Db  5460 GCTGGCTGCTATACGGGGACGCGGGCCGGGGCCGTTCCCACTGTATCCCACTGTATCCACTGTATCCCACTGACAAGCTCTTC 5519

Qy  5523 GCCGGGGCGTGGGCGCGGTGTAGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGGCG 5582
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Db  5520 GCCGGGGGTGGGCGGCGGTGTGTGGGCAGCCCGGCCGTTCCCACTGTATCCACTGGCGCGGTGCGGGCCG 5579

Qy  5583 GCCTATGGGGGCTTCTAGGAGCCCCTTGCTGCCGCTCTCCGCTCCTCTACCTACTGGGGTTG 5642
         |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||
Db  5580 GCCTACCGGGGCTTCAAGGAGCCCCCGCTGGCGCGGCCGCGCCTTCCTCTACCTGTGGGGTTG 5639

Qy  5643 GGGCTCGGAGGGAACGCGCAAAACCCGCTAGCCTCCGCTCTCCGCTCCTCGTGGG 5702
         ||||||||||||||| ||||||||||||||||||| |||| |||||||||||||
Db  5640 GGGCGGTTGGAGGCAACGCGTCAGACGCGCTCTCAGTCTGCCGCGCCTGCGTGGCTGCTGGA 5699

Qy  5703 ACCGGTCTGTCGTGTGGGGTTAACCATGGCGGGCGCCGTTCATGGGAAGTGCT 5762
         |||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  5700 ACCGCCTTGGGCGACTGGTCGCGGCTTGACCATGGCGCGTTGCGTTCATGGGGGGGGCC 5759

Qy  5763 AGCGGCTCTCCCCTCCTTGGTCACCATTTTACTGGGCGCCGTGGGGGCCGTG 5822
         || |||||||||||||||| ||||||||| ||||||||||||||||||||
Db  5760 AGTGTCTCTCCCCCTCCTTGGTCACCACTTTATTGGGGCCGGTTGGGGAGGGGTGTT 5819

Qy  5823 GTGAATGCGGCCTTGTCTTCGACTTTATGGCGGGGAAACTATCATCAGAAGATCTG 5882
         ||||||| |||||||||||||||||||| ||||||||||| |||||||||||||
Db  5820 GTCAACGCGGCGAGCCGGAGTCTTTGACTTGCGGGGAAACTTTCATCAGAAGATCTG 5879

Qy  5883 TGGTATGCCATCCAGTGCTAACCAGTCCGGGGGCCAGGACTTGCGCAGGATCGCCCTCCGGG 5942
         ||||| ||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  5880 TGGTATGCCATCCAGTGCTAACCAGTCCGGGGGCCAGGACTTACCGCAGGATCGCCCTCCGGG 5939

Qy  5943 TTGGTGTTGTTACTCAGCTAAACAACTCTGGCACTACCACTTGGTTGAACCGTTGCTGCGACT 6002
         |||||||| |||||||| ||||||| |||||||||||||||||||||||||||||||||||
Db  5940 TTTGGTTGTTTGTTATTCAGCTGAACAACTCTGGCACTACCACTTGGTTGAACCGTTGCTGCGACT 5999

Qy  6003 ACATTGCCAAGTGCCATGCGATCCATCCGGCCGATTACGTTACTGTGAC 6062
         ||| |||||||||||| |||| ||||||| |||| ||||||||||||||
Db  6000 ACGTTACCAAGTGCCATGCGATCCATCCGGACAGTTACTGTGTCAAGTGACTATTGCGAC 6059

Qy  6063 AAGGCTCAGCTGCTGCTCCGCGCGGGGAGGGGTGTCTCCGGGGATCCGCCTCGGG 6122
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  6060 AAGGCTCAGCTCATTCGCGCGGGGGTGTCTCCGGGAATGGTCGCGGTCCGCCTCAAC 6119

Qy  6123 AGGGAGCCTAAGGTGGATGAGGTTCAGGTGGGATTGCACTACGTTGTGACTGCGAT 6182
         ||||||||||||||||||||| ||||||| ||||||||||||||||||||||||||
Db  6120 AGGGAGCCTAAGGTGGATGAGGTGTACGAGGTCTGGGACTGTGGGGACTGTGGGAGTGGATC 6179

Qy  6183 ACATTGCCAAGTGCCATGCGATGGCGATAGCCATCACATCCGGTGTCATTA 6242
         ||||||||||||||||||||| ||||| || |||||||| |||| ||||||
Db  6180 ATGGCGCCAAGTGCCATGCGAT CCGGCCGACAGTTGACTTGCCCCGTGTCACTA 6239

Qy  6243 CCCTTATGGCGAGGAGGGGTGTCTCCGGGAGAATGGTTGTTGGACGGCCATGTTGAG 6302
         |||||| ||||||||||||| |||||||||||||| |||||||||||||||||||||
Db  6240 CCCTTGTGGGGAGGGGTGTCTCCGGGAATGGTTGCTTGCGGTCGTCATGTTGAG 6299

Qy  6303 AGTCGTTGTCTTTGTTGCCTCGTGGCTGCGGATCACCGGATCGTTTTTGAATGGCAACTCAAAGAT 6362
         ||||||||||| |||||| ||||||||||||||| |||||||| ||||||||||||||||||||||
Db  6300 AGTCGCCTCCTTCGTTGCCTCGTGGCTGCCGATGGATCACTGGAATGGGCAACTCAAAGAA 6359

Qy  6363 CCAGTTTACTCTACCAAGCTGCGCAGGCATTATTGGATGGGGAACAGTCCCTGTGAACATG 6422
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Right column:

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Db  6360 CCAGTTTACTCTACCAAGCTGCCCGGCCGCCACTATTGGGGACTGTCCCTGTCCGAACATG 6419

Qy  6423 CTGGGCTATGGCGAGACGTCGCGTTGCCGCCTTGCTCGCCGCCTCCGACACCCCGAAGGTGTACCATTC 6482
         ||||||| |||| || ||| ||||| |||||||||| | ||| ||||| ||||| ||||| |||||| |
Db  6420 CTGGGTTACGGTGAAACGTCGCGCCGCCTCCGGCCTCCGACACCCCGAAGGTGTGCCCCTTC 6479

Qy  6483 GGGACGTCTGGGTGGTGCTGAGGTGGTGTGACCCCTACCCACGTTGTGATCAGGCGGAACA 6542
         ||||||||||||||||| |||||||||||||| ||||||||||||||||||| |||||||
Db  6480 GGGACGTCTGGGCTGGGCTGAGGTGGTGACCACCAGTGGTAATCAGGCGGGACC 6539

Qy  6543 TCCGCCTACAAACTGCTCGCGCCAGCAAATCCTGTCGCGTCGTTGCTGGCTCAGCCCTATTAC 6602
         |||||||| |||||||||||||||||| |||||||| ||||||||||||||||||| ||| ||
Db  6540 TCCGCCTATAAGCTGTCGCGCCAGCAAATCCTATCGGCTGCTGTGTAGCTGAGCCCTACTAC 6599

Qy  6603 GTCGACGGCATACCGGTCTCATGGACGGCCGCGCCGAGCGCCTGCGGCCATGTCTATGGC 6662
         |||||| |||||||||||| |||||| | |||||| ||| |||||| |||||||||||||
Db  6600 GTCGACGGCAATTCCGGTCTCATGGACGCGGACGCGCTCTGCGCCGCCCATGTCTATGGC 6659

Qy  6663 CCTGGGCAAAGTGTCACCATTGACGGGGAACGCTACACCCCTTCCGCATCAACTGCGCTT 6722
         ||||||||||| |||||||| |||||||||||||||||||| ||| |||||||||||||
Db  6660 CCTGGGCAAAGTTTACCATTCATCCGAGGTGTCATCCGAGGTGTCATTGACACTTGGACGCGGACGCTC 6719

Qy  6723 AGGAATGTGCCCCTGGAGTGTCATCCGAGTGTCCATTGACATTGGACGCGGACT 6782
         ||||||||| |||||||||||| ||| |||||||||||||| |||||||||||
Db  6720 AGGAATGGCAACCCTGGAGTGTCATTCATCCGAGGTGTCATTGACATTGGACGCGGACT 6779

Qy  6783 GAAGACTCAGAACTGACTGAGGCGACTGTCCAGGCGTCAGCCCTTCAGGCTATC 6842
         |||||||||||||| |||||| |||||||| ||||| |||||||||| ||||||
Db  6780 GAAGACTTCAGAACTGACTGAGGCGACTGAGATCTGCCCGGCGATCTTCCAAGCGATC 6839

Qy  6843 GAGAATGCTGCGAGAATTCTTCACAATAGATGTCAACCTTGCAATGGAAGATTGCAGTACA 6902
         |||||| |||||||||||| ||||| |||||| |||||||| |||||||||||||||||||
Db  6840 GAGAATGTGCTGCGAGGATTCTTGAACCGCACATTGATGTCATTGATGGGGGGACTGTCAGTACA 6899

Qy  6903 CCCTCTCTTGTGGGAGTAGCCGAGAGATGCCTGTGTGGGAAGAAGAGACATACCCCGCACT 6962
         ||||||||| |||||||||||||||| |||||| ||||||||||||| ||||||| |||||
Db  6900 CCCTCTCTTGTTGGTAGTAGCCGAGAGATGCCTGTATGGGAAGAAGAGCCTGTGTGGGAAGAAGCATACCCCGTACT 6959

Qy  6963 CCATCGCCAGCACTTATCTCGGTTACCGTTAAGATGTCATGCGTGTTGAGAAGGGTG 7022
         ||||||||||||||| ||||||||| || |||| ||||||||| |||||||||||||
Db  6960 CCATCCAGCACTTATCTCGGTTACTTACCGTTACCGTTCAAGAATGTCGTTGCGTTGAAAAGAGC 7019

Qy  7023 TCTTTCCGCAGGATACCCCGTCTTTCTGACTCATTCGAGCTCATCGAGACTGTGTGAGATG 7082
         ||| ||||||| ||||||||||| |||||||||||||| |||||||||| |||||||||||
Db  7020 TCCTCCTCGCAGGATACCCCGTCTTTCTGACTCATTCGAGCTCATCGAGACTGTGTGAGATG 7079

Qy  7083 ACAGCCGAAGGGAGCCCATTGTGACAAGGCCGATTACTGTGAC 7142
         |||||||||||||||||||| |||||||| ||||||||| |||
Db  7080 ACAGCCGAAGGGGAGGGAAAGTGTCTTCTTCAACGTGCCCACGGGCCCACTTATTAAAAGCCTTATTT 7139

Qy  7143 CCACAGACGATGCCACAGAAGCTTACCGTTAAGATGTCATGCGTGTTGAGAAGAGC 7202
         ||||| ||||| ||||||||||||||||||||||| ||||||||| ||||||||||
Db  7140 CCACAGACCAGCGACGACCAGGAAGCTTACCGTTACCGTTCAAGAATGTCGTTGCGTTGGAAAAGAGC 7199

Qy  7203 GTAACACGCTTCTTTCTTTGTCATTGGATGACGGTCGCTGCAAGCCTGTGTGAGATG 7262
         || ||||||||| ||| ||||||||||| |||||||||| |||||||||||||||||
Db  7200 GTCACGCGGCTTTTTCTCATTGGGTTGACGGTGCGTGATGTTGCTAGCCTGTGTGAGATG 7259

Qy  7263 GAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCGACTTGGCCACTCCGGTTGTT 7322
         |||||||||||||| ||||||||||| |||||||||||||||||||||||||||||||
Db  7260 GAAATCCAGAACAACATACAGCCTATTGTGACAAGGTGGCCACTCCGCTTGAATTGCAGGTT 7319

Qy  7323 GGGTGCTTGGTCTGGGCAATGAACTTACCTTTGACTGCGTGTTGAGGCTAGGCAAGAGC 7382
         ||||||| ||| |||||||||||||||||||| ||||||| |||||| |||||||||||
Db  7320 GGGTGCTTGGTCTGGGCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGGTTAGGCAAGAA 7379

Qy  7383 ACCTTGGCTTCTCTTCTCTTACATTTGGTTCTTGGGTGCTGCGACGAGGGGCCACTCCGGCC 7442
         |||||||||| ||||||| |||| ||| |||||||||||||||||||||||| ||||||| |
Db  7380 ACCTTGGCGCCTCCTTCTCCTTACATTTGGTCTGCTGGGTGCTGCGAGTGCCGCTAGGCGAACAA 7439

Qy  7443 AAGCCCCGTGTGAGGCCCGGTGGCTTCCTTGTGGGCGGGT 7502
         |||| ||||||||||||||||||||||| |||||||||||
Db  7440 AAGCCCCGTGTGAGGCCCGGTGGTGGCTTCTGTGGCGGGT
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Db   7440 AAGCCTCCCGGTGAGGCCGGTTGGCTCTTTGTTAGTGGCCGACTACTAAGGTGTAT 7499

Qy   7503 GTCACCAACCCGGACAAATGTTGGGAGAAGAGTTGACAAGGTTACCTTCTGGCGTGCCCCT 7562
          || |||| ||||||||| ||||| |||| |  || ||||||||| |||||||||||||| ||
Db   7500 GTTACCAATCCAGACAATGTGGGACGGAGGGTGACAAGGTGACCTTCTGGCGTGCCTCCT 7559

Qy   7563 AGGGTTCATGACAAAATTCCTCGTGACTCCATAGAGCGCGCTAAGAGGCAGCTCAAGCC 7622
          |||||||||||||   |||| ||||| |||| |||||||| |||||||||| |||||||||
Db   7560 AGGGTTCATGATAGTACCGTGACTCTATTGAGCGCGCTAAGAGGCCGCTAAGAGCC 7619

Qy   7623 TGCCTAAGCATGGCATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCC 7682
          ||||||||||||||||| ||||||||||||||||||||  ||||||||||||||||||||||||
Db   7620 TGCCTAAGCATGGCATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCC 7679

Qy   7683 ATGGGCTGGGATCTAAGTGTCGTCAAGACCTCGCCACCCTGCGGGGAAGATGGCT 7742
          ||||||||||||||||| ||| ||||| ||||||||||||||| ||||||||||||
Db   7680 ATGGGCTGGGATCTAAGGTGTCGTTAAGGACTTAGCCACCCCGCGGGGAAGATGGCC 7739

Qy   7743 GTCATGACCGGCTCCAGGAGATACTTGAAGGGACCGCCAGTCCCTTTACTCTTACTGTG 7802
          |||||||||||||| |||||||||| |||||||| |||||||||||  |||||||||||||
Db   7740 GTCCATGACCGGCTTCAGGAGATACTTGAAGGGACTCCGTCCCCTTTACTTACTGTG 7799

Qy   7803 AAAAAGGAAGTGTTCTTCAAAGACCGAAAGAAGGAAGGAGCCCCCGCCTCATTGTGTTC 7862
          |||||||||||||||||||||||||||||||||||||||||||| |||| |||||||| |
Db   7800 AAAAAGGAGGTGTTCTTCAAAGACCGGAAGAAGGAGGAGCCCCCGCCCTCCATTGTGTTC 7859

Qy   7863 CCCCCCTGGACTTCCGGATAGCTGAAAAGCTTATTCTGGGACACCTGACGGGTAGCC 7922
          ||||||||||||||||||||||||||||| || |||| ||||||||| |||||||||||
Db   7860 CCCCCCTGGACTTCCGGATAGCTGAAAAGCTCATCTGGGAGACCCGTCTATATGGGTACAT 7919

Qy   7923 AAGGCCGGTTGTGGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCCGAATTAGGAG 7982
          |||||||||||||||||||||| |||| ||||||| |||| |||||||||||||||||||
Db   7920 AAGGCCGGTTGTGGGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCCGAGTTAAGGAG 7979

Qy   7983 ATGCTCAAAACTGTGGAATCAAAGAAGACACCATGCGCTGTGTGAGCGCCACATGC 8042
          ||||||  |||| || |||||||| ||||||||| | |||||||||||||| ||||||
Db   7980 ATGCTCAAGCTATTGGGAGTCTAAGAAGACCCCTTGCGCCATCTGTGTGACGCCACCTGC 8039

Qy   8043 TTCGACAGTAGCATAACTGAAGAGGACGTTGGCGCTGGGACAGAGCTTTATGCCCTGGCT 8102
          ||||||||||||| |||||||||||| |||| ||||||| | || ||||||||||||||||
Db   8040 TTCGACAGTAGCATAACTGAAGAGGACGTTGGCGCTGGGGACAGAGCTGGGTTATGCCCTGGCC 8099

Qy   8103 TCAGACCATCCAGAAATGCCAGTTCGGTGCTGCCCTGGGGAAATACTATGCCTCTGGCACAAATGGTA 8162
          ||  ||||| ||||||| |||||||||||||| ||||||| |||||| |||||||||||||||||||
Db   8100 TCTGACCATCCAGAATGCCAGTTCGGTGCTGCCCACTTGGGGAAATACTATGCCTCCAGCCATGGTC 8159

Qy   8163 ACCCCGAGGGGTGCCAGTGGGTCGGTGAGAGGTATTGTAGATCCTCCAGGGGTCTTGACCACC 8222
          |||||||||| || |||  ||||||||||||| | || || ||||||||| |||||||||||||
Db   8160 ACCCCGGAGGGGTGCCAGTGGGTCGGTGAGAGGTATTGCAGATCCTCGGGTGTCCTAACAACT 8219

Qy   8223 AGTCGGAGCAACTGCTTGACTTGTATATCAAGGTGAAAAGCCGCGGTGAGAGGGTGGGG 8282
          || ||||||||||||||| || |||||| |||||| |||||||| |||||||| ||||||
Db   8220 AGCGCGGAGCAACTGCTTGACCTTGAGATCATAGTGAAAGCTGCCGTGTGAGAGAGTGGGG 8279

Qy   8283 CTGAAAAATGTCTCAGCCGACGACGCTTTGGCACGAGCTTTGGCAGAGCCCTGGCCAGCCCTGGACGCATGCGAG 8342
          ||||||||||| || || |||||||||||||| ||||| ||||||||||||||||| || ||||
Db   8280 CTGAAAAATGTCTCTCTTCTCATAGCCGGCGGCGATGGGATCATAATGTGAGCGGCGCCA 8339

Qy   8343 GTGTGCGATCCTCAGCGACGCTTTGGCGACGCTTGGGCAGAGCCCTGGCCGGTACGCATGGCATGCGAG 8402
          |||||||| || ||||||||| ||||||  ||| |||||||||| |||| ||| ||||||||| ||||||
Db   8340 GTGTGCGACACCCAAGCCGACGCCTTCGGCCTATGGGCAGAGCCCTAGGGTAGCGGTATGGCATGGCGAG 8399

Qy   8403 CCTTCGTATCATGCACGACTCGGACACTGGACACGGCGCCCCTTTCTGCTGCCCACTTGGCCTTGCTGAGTGC 8462
          || |  |||||| ||||| ||||| ||||||  |||| ||||||||||||||||||||||||| |||||||||
Db   8400 CCCTCATATCATGCACGATCATGCAGCACCACTTGCTCTTCTGCTGCCCGAGGCCCCTCGCC 8459

Qy   8463 AATGCAGATGGGAAACGCCATTCTTCCTCCGACCACGAGACTTCCGGAGGCCCCTCGCC 8522
          || ||||||  ||||| || |||||||||| ||||||||||||| |||||||||||||||
Db   8460 AATCCAGATGGGAAGCGCGGCCATTTCTTCCTCGACCACGACTTCCGGAGGCCGCTCGCGC 8519

Qy   8523 ATGTCGAGCGAGTACAGTGACCCCGGT TTCGGCCATCCTCCATACCCT 8582
          ||||||||||||| ||| || ||||||||| ||||||||| ||||||| ||||||
Db   8520 ATGTCGAGCGAGTAGTAGTAGTGACCCCGGATCGGCGGATCGGTTACATCCCTTTATCCT 8579
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Qy   8583 TGGCATCCTATCACACGGTGGGTCATCATCCCTCACGTGCTCCACGTGCTGCCGTTTAGGGGT 8642
          ||||||||| ||||||||||||||||||||||||| ||||| ||||||||||| | ||||| ||
Db   8580 TGGCACCCCATCACACGGTGGGTCATCATCCCTCATGTGCTCCACGTGCTAACGTGCTGCCGTTCAGGGGT 8639

Qy   8643 GGTGGCACACCGTCTGATCCTCGTGTCTGCAGGTACATCGTACATGTGGCACGTACATGTCCA 8702
          |||||||||||||||||||||||| |||||| |||||||| ||||| |||||||||||||||||
Db   8640 GGAGGCACACCGTCTGATCCGTCTGGTGCCAGGTGCATCGTGTAACTACTACAAGTTTCCA 8699

Qy   8703 CTGGACAAACTGCCTAACATCGTGGCCCTTCCACCGGACCAGCAGCGTTGAGGGTTACC 8762
          ||||||||||| ||||||||| |||| || |||||| |||||| ||||||||||||||||
Db   8700 CTGGACAAACTGCCTAACATCGTGGCCCTTCCACCGGGCCAGCAGCGTTGAGGGGTTACC 8759

Qy   8763 GCAGACACACTAAGACAAAAATGGAGGCTGGCAAGGTGTGAGCGACCTCAAGCTCCCT 8822
          ||||||||||||||||||||||||||||||||| ||||||||||| ||||| |||| ||
Db   8760 GCAGACACAACTAAAACAAAACAAAGGTCGGTGTAAGGTTCTGAGCGACCTCAAGCTCCCT 8819

Qy   8823 GGCCTAGCAGTCCACCGGAGAAGGCCCGGGGACGTCGGTGATGCCGGTCCGGTCCGCGC 8882
          ||  | ||||||| ||||| |||||| || ||| || ||||| |||| |||||| || ||
Db   8820 GGCTTAGCAGTCCACCGGAACAAGAAGGCCGGGGCGTTGCGAACACGGCGTCCGCGC 8879

Qy   8883 GGTTGGGCTGAGTGGCTGGCTAGGGGCGTGTTGTGGCGTCCAGGCCTCCCCCTCCG 8942
          |||||||||||| |||| ||||||| |||| ||||||| ||||||||| |||||| ||
Db   8880 GGTTGGGCTGAGTGGCTGGCTAGGGGCGTGTTGTTGTGGCATCCAGGCCTTCCTCCCCT 8939

Qy   8943 GAGATTGCTGTATCCCGGGGGTTTCCCCTTTCCCCCCCTATATGGGGTGGTTCAT 9002
          ||||||||||||| |||||||||| ||||  |||||| ||||||||||||||||| ||
Db   8940 GAGATTGCTGTGATCCCGGGGGGTTTCCCTCTCTCCCCCCTATATGGGGTGGTTACAT 8999

Qy   9003 CAATTGGATTTCACAAGCCCAGAGAGCGTCGTGGCGGTGGCAAGTTAGGGAG 9062
          ||||| ||||  ||||||| ||||| ||| ||||||||| |||||||||||||
Db   9000 CAATTGGATTTCACAGACCCAGAGAGTGAACCAGAGTCGCGGTGGCAAGGTCGTGGCTGTGATC 9059

Qy   9063 ATCGTAGCCCCTTCGGTGAACTAAATTCATCTGTTGCGGTGACTGATC 9122
          || || ||||| ||||||||||||||||||||||||||||||||||||||
Db   9060 ATCGTAGCCCCTTCGGTGAACTAAATTCATCTGTTGCGGTGACTGATC 9119

Qy   9123 ATCACTGGAGGAGGTTCCCGCCCTCCCCGCTCTGGGCTAAAAAGGG 9182
          ||||| |||||||||| ||||| ||||||||| ||||||||||||||
Db   9120 ATCACCGGAGGAGGTTCCCGCCCTCCCCAGGGTCTCCCCCGCTCTGGGCTAAAAAGGG 9179

Qy   9183 CCCGGCCTTGGAGGCATGGTTACTAACCCCCTGGCAGGTCAAAGCCTGATGGTGC 9242
          ||||||||| || | |||| ||||||| |||| ||||||||||||||| |||||||
Db   9180 CCCGGCCTTGGAGGCATGGTTGGTTACTAACCCCTGGCAGGTCAAAGCCTGATGGTGC 9239

Qy   9243 TAATGCACTGCCACTTCGGTGCGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC 9302
          |||||||||||||||| ||||| |||||||  ||||||| |||| |||||||||||||||
Db   9240 TAATGCACTGCCACTTCGGTGCGGGTCGCTACCTTTATAGCGTAATCCGTGACTACGGGC 9299

Qy   9303 TGCTCCGAGCCCTCCGATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC 9362
          ||||||||||||||| |||||||||||||| |||||||| |||||| |||||||
Db   9300 TGCTCCGAGCCCTCCGATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC 9359

Qy   9363 GGTAAGAGCTCGGCCCCAAAGGCCGGGTTCTACT 9395
          |||  ||||| || |||||| ||||| |||||||
Db   9360 GGGAAGAGCTCGGCCCCGAAGGCCGGGTTCTACT 9392
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PN   US5874563-A.
XX
PD   23-FEB-1999.
XX
PF   05-JUN-1995;   95US-0485910.
XX
PR   19-MAY-1995;   95US-0444733.
PR   20-MAY-1994;   94US-0246985.
PR   03-AUG-1994;   94US-0285543.
PR   03-AUG-1994;   94US-0285558.
PR   26-OCT-1994;   94US-0329729.
PR   23-NOV-1994;   94US-0344271.
PR   16-DEC-1994;   94US-0357509.
PR   15-FEB-1995;   95US-0389886.
PR   05-JUN-1995;   95US-0485910.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fry KE,  Kim JP,  Linnen JM,  Wages J,  Young LM;
XX
DR   WPI; 1999-180067/15.
DR   P-PSDB; AAW94511.
XX
PT   Isolated polynucleotide sequences derived from the Hepatitis G Virus
PT   that encode the E2 antigen - useful for producing vaccines and
PT   inhibitors against Hepatitis G, and for assays to detect the virus
PT   in a sample
XX
PS   Claim 1; Column 97-118; 20pp; English.
XX
CC   The specification describes isolated polynucleotide sequences, derived
CC   from a Non-A, Non-B, Non-C, Non-D, Non-E (N-(ABCDE) Hepatitis virus
CC   (designated Hepatitis G or HGV). HGV is characterised by stimulating
CC   production of serum alanine aminotransferase in primates infected with
CC   the virus, being serologically distinct from the Hepatitis A, B, C, D
CC   and E viruses, and being a member of the Flaviviridae virus family.
CC   The HGV-E2 antigens, encoded by the polynucleotide sequences of the
CC   invention, may be produced by standard recombinant DNA techniques,
CC   and used in the preparation of vaccines. Anti-sense oligonucleotides
CC   (and oligonucleotide analogues which encode portions of the sequences
CC   disclosed in the specification) may be used to prevent expression of
CC   the HGV-E2 genes by blocking transcription and preventing them
CC   functioning normally in viral replication. Antisense sequences may be
CC   used in this way as part of a treatment strategy against HGV infection.
CC   The single stranded nature of the viral genome makes HGV highly
CC   susceptible to inhibition in this way. The present sequence represents
CC   the polynucleotide sequence of HGV-PNF 2161 variant.
XX
SQ   Sequence 9392 BP; 1694 A; 2551 C; 2998 G; 2148 T; 1 other;

Query Match             84.9%;  Score 7979;  DB 20;  Length 9392;
Best Local Similarity   90.7%;  Pred. No. 0;
Matches  8515;  Conservative     1;  Mismatches  876;  Indels     1;  Gaps     1;

Qy         3 ACGTGGGGGGGTTGATCCCCCCCCCCCCCCGGCACTGGGTGCAAGCCCCATAAACCGACGCCT 62
             ||||||| |||||||||||||||||||||||||||||||||||||||| |||||||||||
Db         1 ACGTGGGGGAGTTGATCCCCCCCCCCCCCCGGCACTGGGTGCAAGCCCCAGAAACCGACCCT 60

Qy        63 ATCTAAGTAGACGCCAATGACTCGGCCGCCGACTCGGCCGCCCGGCCAAAAGGTGGTGGATGG 122
             ||||||||||||||||||||||||||| || ||||||||||||| |||||||||||||||||
Db        61 ATCTAAGTAGACGCCAATGACTCGGCCGCCGACTCGGCCGCCCGGCCAAAAGGTGGTGGATGG 120

Qy       123 GTGGTGACAGGGTTGGTAGGTCGTAAATCCCGGTCATCCTGGTAGCCACTATAGGTGGGT 182
             ||| ||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db       121 GTGATGACAGGGTTGGTAGGTCGTAAATCCCGGTCACCTTGGTAGCCACTATAGGTGGGT 180

Qy       183 CTTAAGAGAAGTCAAGACTCCTCTTGTGCCTGCGCGGAGACCGCCGCACGGTCCACAGGT 242
             ||||||||||| |||| |||||||||||||||||||||||||||||||||||||||||||
Db       181 CTTAAGAGAAGTTAAGATTCCTCTTGTGCCTGCGCGGAGACCGCCGCACGGTCCACAGGT 240

Qy       243 GCTGGCCTACCGGTGAATAAGGGCCCGACGTTAAGGCCCTCAGGCTCCGTCGTTAAACCCGAGCCCGT 302
             | ||| ||||||||| ||||||||||||||| ||||| |||||| |||| |||||||||||||||||||
Db       241 GTTGGGCCTACCGGTGGAATAAGGGCCCGACGTTCAGGCTCGGTGACCGTCGTTAAACCCGAGCGCGT 300

Qy       303 CACCCACCTGGGCAAACGACGCCCACGTACGGTCGCACCTTCAATGTCTCTCTTG 362
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db       301 TACCCACCTGGGCAAACGACGCCCACGTACGGTCGCACCTTCAATGTCTCTCTG 360

Qy       363 ACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAGTGGGGGCCGGGGTTATGGGGAAG 422
             |||||||||   | |||||||||||||||||||||||||||||||||| |||  |||||
Db       361 ACCAATAGGCGTAGCCGGCGAGTTGACAAGGACCAGTGGGGGCCGGGGCT-TGGAGAGG 419

Qy       423 GACCCAAACCCTGCCCTTCCCGTGGGCCGGGAAATGCATGGGGCCACCCAGCTCCCCG 482
             ||| ||| ||  |||||||||||||| |||||||||||| ||||||||||||||||||
Db       420 GACTCCAAGTCCCGGCCTTCCCGTGGGCCGGGAAATGCATGGGGCCACCCAGCTCCGCG 479

Qy       483 GCGGCCTGCAGCCGGCGGGTAGCCCAAGAATCCTTCGGGTGAGGCGGCGGTGGCATTTCTCTT 542
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||| ||
Db       480 GCGGCCTGCAGCCGGCGGGTAGCCCAAGAATCCTTCGGGTGAGGCGGTGGGTGGCATTTCCTTT 539

Qy       543 TTCTATACCATCATGGCAGTCCTTCTGCTCCTTCTGCGAGCGAATGGCAATATTCCTCACAAATTGCTGTGCC 602
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||  ||||||||
Db       540 TTCTATACCATCATGGCAGTCCTTCTGCTCCTTCTGCGAGCGAATGGCAATATTCCTCACAAATTGTGTGCC 599

Qy       603 GCCCCGGCCACCCACGCTTGTCGAGCGAATGGCCGGGGCCCTTGTACGGGCCCTGGTCTCCGGCCGCTGTGCGCC 662
             |||||||||||||||||||||||||||| ||||||||||||||| ||||||||||| |||||||  ||||||
Db       600 GCCCCGGCCACCCACGCTTGTCGAGCGAATGGGCCGGGGCCCTTGTACGGGCCCTGGTCTCCGGCCTAT 659

Qy       663 CCGGAAGACATCGGGTTCTGCCTGGAGGCGGATGCCCTGGTGCCCTGGGGTGCACGGTT 722
             |||||| |||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       660 CCGGAGGACATCGGGTTCTGCCTGGAGGCGGATGCCCTGGTGCCCTGGGGTGCACGATT 719

Qy       723 TGCACCGACCGGTCGTGCTGGCCACTGTATCAGGCGGTTTGCTTCTGTGCCTGGCGGCCTGGCAAGTCC 782
             ||| ||||||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||
Db       720 TGCACTGACCAATGCTGGCCACTGTATCAGGCGGTTTGGCGGTGTCGCGCCTGCCTGGCGGCCTGGCAAGTCC 779

Qy       783 GCGGCCCAGCTCGTGGGAACTGGGAGCCGTACGGCGCCCTTGTCCGGTCTCCGGCTAC 842
             |||||| ||||| || |||||||||||||| ||||||| |||| ||||||||||||||
Db       780 GCGGCCCAACTGGTGGGGGAGCTGGGGAGCCGTACGGGGCCCTATACGGGCTCCGGCCTAT 839

Qy       843 GTAGCCGGGATCCTGGGTTCGGCGAGGTTTACTCCGGGGTCCTGACAGTTGGTTGTTGCGG 902
             || ||| |||| |||||||||||||||||| || ||||||||||| ||||||||||||||
Db       840 GTGCTGGGATCCTGGGCGTGGGGTGTACTCGGGGTGAGTTGGGGAGTCGCGG 899

Qy       903 TTGAGGCGCCGGGTCTACCTGAGGCCCAACCTGAAGTGCAGTAGAATGTGACGTAAG 962
             || |||||| |||||| |||| | |||||| |||||||||| ||| |||||||||||
Db       900 TTGACGCGCCGGGTCTACCCGGTGCAGTGGCCTAACCTGACGTGTGCAGTCGCGTGTGAGCTAAAG 959

Qy       963 TGGGGAAGTGAGTTTGGAAGATGGACTGAGACGAGCAGTTGGCCTCCAATTACTGGATTTTGGAA 1022
             |||| |||||||||||||||||||||||| |||||||||| ||||||| |||||||||||||||
Db       960 TGGGAAAGTGAGTTTGGAAGATGGACTGAGACGAGCAGTTGGCCTCCAACTACTGGATTCTGGAA 1019

Qy      1023 TACCTTTGGAAAGTCCCATTTGAATTTGCTGGAGGAGGAGTGATGAGCCTGACCCCTCTGTTG 1082
             |||||||||||||||||||||   |  |||||||||||||||  |   || |||||||  |||
Db      1020 TACCTCTCGAAGGTCCCATTTGATTTCTCGGAGGAGGAGTGATAAGCCTGACCCCTTGTTG 1079

Qy      1083 GTTTGGGTGGCCCGCATTGTCTTTTGCTGCTGGACCAACGGATTGTCATGGTTTCGTGGTGTG 1142
             ||||||| |||||| |||||||||||||||||||||||||||||| |||| || ||||| |||
Db      1080 GTTTGCGTGGCCGCATTGTCTTTGCTGCTGGACAACGGATTGTCATGGTTTCATGGTGGTG 1139

Qy      1143 ACGATGGCGGGATGTTGCAAGGCGCCCCTCCGGTTGCAAGGGTCCCGCCCCTTTGAC 1202
             |||||||| ||||| |||||||||| |||| ||||||||||||| ||||||||||||
Db      1140 ACGATGGCCGGGATGTGCGCAAGGTGCCCCGGCGCCCCGTTTTGGGGTCACGCCCCTTTGAC 1199

Qy      1203 TACGGGTGAAGTGCAGTCATCGTCGCGTATTCCCACTGGG 1262
             ||||||| ||||||| || || |  |||| || ||||||
Db      1200 TACGGGTTGACTTGGCAGACCTGCTTGCAGGGCCAACGGTTCGCGTTTTCGACTGGG 1259

Qy      1263 GAGAGGGTGGGATCGAGGGAATGTCACGCTTCGTGTGACTGCCCAACGGT 1322
             |||||| ||| ||||| ||||| ||| ||||  ||||  |||||||||||
Db      1260 GAGAAGGTGTGGACCGTGGGACGTTACGCTTCAGTGTGACTGCCCGTCCACAGGT 1319

Qy      1323 GTTTGGGTCCCGGCCTTTGCCAGGCGGTTGGGCGACGCCGACCCCATTGAGC 1382
             ||||||| |||||||||||||||  |||| ||||| |||  ||||||||||||
Db      1320 GTTGGTTGCCAGCCTTTTGCCAAGCAATCGCGGTGGGGTGGGGTGACCCCATCATTGGAGC 1379
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DNA sequence alignment (Qy/Db) with residue position numbers.

Left column:

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Db   3540 TGTTGGGTCATCAGATCCGACGGGGCCCTATGCCATGGCTTGAGCAAGGGGACAAGGTG 3599

Qy   3603 GAGCTGGATGTGGCCATGGGAGTGGAGGTCTTCGACTTCGTCGTCTGGTTCGTCACCGGTCCTT 3662
          ||||||||| ||| |||| | | |||| |||||  ||||||||||| | |||||| |||| ||
Db   3600 GAGCTGGATGTGGCCATGGGAGTGGAGGTCTTCGACTTCGTCGTCTGGTTCGTCACCGGTCCTA 3659

Qy   3663 TGCGACAAAGGGCACCCAGTAAGAAGTCTCCGTGCTCAGTGCTGGCGGCAGGGTT 3722
          || ||| ||||||| |||||| ||| |||| |||||||| ||||| |||| ||||
Db   3660 TGTGACGAAGGGCACGCAGTAGGAAGCGTCCGTGTCTGTGCTTCACTCCGGTGGTAGGGTC 3719

Qy   3723 ACTGCCGCGCGATTCACTAGGCCGTGGACTCCAACAGATGCCAAGACTACCACA 3782
          || || ||| ||||| ||||||| || ||| |||| || || ||| |||| |||
Db   3720 ACCGCGCACGTTCACTAGGCCGTGACCCAAGTGCCAACAGATGCCAAAACCACTACT 3779

Qy   3783 GAACCCCTCCGGTGCCGGCAAAAGGAGTTTTCAAGGAGGCCCCGTTGTTTATGCCTACG 3842
          ||||||| ||||| |||||||||||| ||||||||||||||  |||| |||||||| |||
Db   3780 GAACCCCTCCGGTGCCGGCAAAAGGAGTTTTCAAAGGAGGCCCCGTTGTTTATGCCTACG 3839

Qy   3843 GGGGCGGAAAAGAGCACCCCGCTACCGTTGGAGTACGGCAACATGGGCCACAAGGTCTTG 3902
          |||||||||| ||||| || | |||| ||| |||||||| || ||||||||||||||| |
Db   3840 GGACCGGAAAAGAGCACTGGGCCTGCGCCCCGTCCCTTGGAGTACGGCACCAAGGTCTTA 3899

Qy   3903 ATCTTGAACCCGTCGGTAGCTACCGGTGACCATGGGCCCATACATGGAGCGGGCTGGCG 3962
          ||||||||||| | | |||| || | |||| | || |||| || ||| |||| |||||
Db   3900 ATCTTGAACCCCTCAGTGCCCACTGTGGCCACTGGGCCCGTACAACATCGGGCCGGCTGGCG 3959

Qy   3963 GGGAAACACCCCAGTATTACTGTGCCATGACACACCACTGCTTTCACAGGATCACTGAC 4022
          | | |||| ||||| |||  ||||||  || || ||||||||  || ||||||||||||
Db   3960 GGTAAACATCCAAGTATATACTGTGGGACATGTCCAACTGCTTTCACAAGGATCACTGAC 4019

Qy   4023 TCGCCCCTTACGTATTCCACTTACGGAAGTTTTTTGGCCAACCCTAGGCAGAGATGCTGAGG 4082
          || | ||| ||| | || ||| || ||| ||| | || ||||| |||| |||||| ||| |
Db   4020 TCCCCCCTGACGTATTCAACCTCATGGCCAACCCTAGGCAGAGATGCTACGG 4079

Qy   4083 GGTGTGTGGTGGTCATTGTGACGAGTGCCACAGTCATGACTCAACTGTGTTGTGGGC 4142
          | ||| | ||||||  | |||||| || ||||| ||  | |||| |||| | ||||
Db   4080 GGCGTTTCGGTGGTCATTGTGATGAGTGCCACAGTCATCAACCGTGTCGTTAGGC 4139

Qy   4143 ATTGGGGCGTGTCAGGGAGCTGCGCGCAGGATGTGAGTGCAATTGCGTTCTCTACGGCCACT 4202
          |||||| | | ||||||| |||  || | ||||||||  ||||| ||||||||||||| |||
Db   4140 ATTGGGAGTCCGGAGCTCGGGAGCTGCGGGGTGCCAATTGCGTCTCTACGGCCACC 4199

Qy   4203 GCCACCCCTCCCGGATCCCCCGGATCGACCACCAGCACACCATCAATCATTGAGACAAAACTGGAC 4262
          || | ||||||||| |||| ||||| || || |||||||| ||||| ||||||||| |||||||
Db   4200 GCTACACCTCCCGGATCCCCCGGATCGACACACCCTCCCATATTTGAGACAAAATGGAC 4259

Qy   4263 GTGGGAGAGATCCCCTTCTATGGCCATGGGCCATACACCTCTTGAGCGGATGCCGACCGGAAGG 4322
          ||||| ||| ||||| || ||||| || |||||| || | | ||| ||| ||||||||||||
Db   4260 GTGGGCAGAGATTCCCTTTTATGGGCATGGGCCATACACCCCTGCAGCGCCGGATGCCGACCGGAAGG 4319

Qy   4323 CATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGACGTCCTGCGCGCGCCAGTTTTCGGCT 4382
          |||| ||||||| ||||| || ||||| |||||||| || ||||| |||||||||||||
Db   4320 CACCTCGTGTCTGCCATTCTAAGGCTGAGTGCGACGTGCTGCGCGCCCAGTTTGCCTCCGCT 4379

Qy   4383 AGGGGGCTAAATGCCATATTCAGGGGAAAGACAGTTCTATCATCAAAGATGGA 4442
          |||||||  |||| || |  || || ||| |||||| ||||||||| | |||
Db   4380 AGGGGGGTCAATGGCCATTCTAAGGCGAAAGACAGTTCTATCATCAAGGATGGG 4439

Qy   4443 GACCTGGTGTCTGCTACAGACGTCGTCGAGGAGCTGTCAGTTCCACTCGGTACACTGGTACAACTTCGATTCT 4502
          ||||| ||| || || |||||| | |||||||| || || || |||||| || ||| ||  |||||||||
Db   4440 GACCTGGTGTCTGCTACAGACGCCGTTGAGGAGGTTCGTGGCTTGGTACACTGGTACACTTCGATTCC 4499

Qy   4503 GTCACCGATTGGGGTGTGTCTACAAGACGGTGCCCGTGAAACTGTCGGGTGACCTTGATCCCACCATT 4562
          ||||| |||||||| | |||||| |||||| | |||||||||  || ||| |||| ||||||||||||
Db   4500 GTCACCGACTGGGGTGTGTCTACAAGACGCCGTGAACTGTGCGGACTGCTGATCCCACCATT 4559

Qy   4563 ACCATCTCCCTGCACAGCCGGTGCCCGTCGAACTGTCGGATGCCCGGAGGACGAC 4622
          ||||| |||||||||| | |||||||||| |||||| | | |||||||||| |||
Db   4560 ACCATCTCCCTGCCACAGTTCGGGACAGTGTCGATGCTGTCAAAGACGAGGAGCGC 4619

Qy   4623 ACGGGTAGGGCAGTTCTGGCGCTACTACGGGGCCCTGCTGGT 4682
          ||||||||||| ||||||||||||||| ||||| |||| |||
Db   4620 ACGGGTAGGGCAGTTCTGGCGCTACTACGGGGCCCTGCGGGGT 4679
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Right column:

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Qy   4683 GTGGTCGCTCAGGTCCTGTCTGTGGTCGGCGGTGTGGAGAGCCGGTGTGTGACCTGGTACGGAAATG 4742
          ||||||||||||||| | ||||| ||| ||| ||| |||| |||||||  |||||| |||||||
Db   4680 GTGGTCGCTCAGGTCCTGTCTGTGGTCGGCGGTGTGGAGAGCCGGTGTGTGACCTGGTACGGAAATG 4739

Qy   4743 GAACCTGACCTGACAGCAACTACTGAGACTTTACGACAACTGCCCTTACACCGCCAGCC 4802
          |||||||||||| | ||||| |||||| || |||||||| |||| |||||||||||||
Db   4740 GAACCTGACTTGACAGCTAACCTACTGAGACTTTACGACGACTGCCCTTACACCGCCAGCC 4799

Qy   4803 GTCGCAGCTGACAATTGGGAGAACCGCCGTGTCTTTTCGGGCCTTGCCCCGTTGAGGATG 4862
          |||||| ||||| |||  || || ||||| ||  |||| || ||| | |||||||||||
Db   4800 GTCGCGGCTGATATCGGAGAAGCCGCCGTGTCTTCTCGGGCCTCGCCCCCATTGAGGATG 4859

Qy   4863 CATCCCGATGTTAGCTGGCAAAAGTTCGGCGGCGTCAACTGCCCCTTCCTGCTGTGGGTGTT 4922
          |||| ||||| |||| |||||||| || ||||| ||||| |||| |||| | ||||||||
Db   4860 CACCCTGATGTCAGCTGGCAAAAGTTCGGCGGCGTCAACTGCCCCTTGTTGTGGGTGTT 4919

Qy   4923 CAGCGGACCATGTGCGCGGAAACACTGCTCTCCCGGCCCATGGATGACCCCAGTGGCA 4982
          |||||| |||||| |||||||||||| ||||||| || |||| |||||||||  |||
Db   4920 CAGCGGACCATGTGCGCGGAAACACTGCTCTCCCGGCCCATGGATGACCCCCAATGGCA 4979

Qy   4983 GGTCTGAAGGGCCCGAATCCTGTCCCACTCCTGCTGAGGTGGGCAATGATTTACCATCT 5042
          |||||||||||| | |||||| ||||||||| ||||| ||||| ||||||||||||||
Db   4980 GGTCTGAAGGGCCCAAATCCTGTCCCACTCCTGCTGAGGTGGGCAATGATTTACCATCT 5039

Qy   5043 AAAGTGGCCGGCCATCACATCGTGGACGACCTGGTCCGTAGGCTGGTGGCGGAGGGT 5102
          ||||||||| ||||||||||| || ||||| |||| ||||| ||||| |||||||||
Db   5040 AAAGTGGCCGGCCACCATAGTGGACGACCTGGTCCGTGGGCTCGGTGGCGGAGGGT 5099

Qy   5103 TACGTCCGTCGATGCGAGTGGGACCATCTTGATGGTGGCCTCGCTATTGCGGGGGCATG 5162
          |||||||||  ||||||| |||| || | |||||||| |||  || ||||| |||
Db   5100 TACGTCCGTCGCTGCGAGTGGGTCGGATCTTGATGATCGGTCTCGCTAGTCGTCGCGGGGGAATG 5159

Qy   5163 ATCTATGGTCATACACCGGTCTCTCGTGGTGGTTACAGACTGGGATGTGAAGGGGGGT 5222
          ||||| ||| || ||||| | || || ||||| ||||| || ||| ||||| |||||
Db   5160 ATCTACGGTCATACACCGGGTCGCTAGTGGTGGTGGACAGACTGGGACAGTGAAGGGGGGT 5219

Qy   5223 GGCAGCCCCCTTATCGGAGCGTGCAGGCACCCGCCAGTGGTTGTCAGTTCCCCC 5282
          ||  |||||| || |||| |||||||| || |||| ||||||||||||||||||
Db   5220 GGCGCCCCCTTATCGGAGCGTGCAGGCACCCGCCAGTGGTCGGTGCAGGTTCCT 5279

Qy   5283 CCGGTAGACCATCGGCCGCGGGGCCATCGGATGCCAACACAGTGACAGAT 5342
          |||||||||| |||||||| || | ||  | |||||||||||||||||||
Db   5280 CCGGTAGACCATCGGCCGCGGGGTGAATCAGCACCATCGGATGCCAAGACAGTGACAGAT 5339

Qy   5343 GCGGTGGCGGCCATCCAGGTTGATTGCGATGGTCAGTGATTGGTCAGTATCGATCGGGGAA 5402
          |||||||| || |||||||| ||| ||||| | |||| | ||||| |||| |||||||||
Db   5340 GCGGTGGCAGCCATCCAGGTTGACTGCGATTGGACTGCGATCATCGTGTCATCATCGTGTCATCAGGGAGAA 5399

Qy   5403 GTGCTGTCCTTGGCCCAGGCTAAGAACGGCGGGCGCCTACGGCTACCACCAAGTGCTT 5462
          || | |||| | ||||| || ||||| |||||||||| | || ||||||||||| ||
Db   5400 GTGTTGTCCTTGGCTCAGGCTAAGAACGGCGGGCGCCTACACAGCCAACCGCCAAGTGCTC 5459

Qy   5463 GCTGGCTGCTACGGGGCTGGGCGGCGGTGTAGGAGCGGGGTGTAGCTGCGTAATAGCTCTTC 5522
          |||||||||||||| |||||| | || |||| |||| |||||||||| | || || ||||||
Db   5460 GCTGGCTGCTACGGGGCTGGGCTGTGGGCGTGTAGGAGGTGTGTCCACTGCATTGTTACAAGCTCTTC 5519

Qy   5523 GCCGGGGCCCTCCTAGGAGCGCCGGTGTAGGAGCCCTCCATGGGGCCGCTTG 5582
          |||||| ||||  ||||| || |||| |  ||||||| |||||||||| |||
Db   5520 GCCGAGGGCTTCAAGGGAGCGGTGGCGGGCGTGTGGGCGTTGTGGGCGTTGTGGGCTTG 5579

Qy   5583 GCCTATGGGCTTGCGAGGGCAACCCCGCAAACCCGCTTAGCCTCCATCAGGGGCGCGTTG 5642
          |||||||||||| ||| ||||||||||| ||||| | | ||||||||||||| ||||||
Db   5580 GCCTACGGGGCTTCAAGGGAGCGGCAACGTCAGACGCGGTCTGCCCTCTATTTGGGGCGCGTTGGA 5639

Qy   5643 GGCGTTGGAGGCAACGCCGCAAAACCGCATGGTCGCAGCGCCGGAGGACGAC 5702
          ||||||||| ||||||||| |||| ||||| ||||||||||| |||||||||
Db   5640 GGCGTTGGAGGCAACGTCAGACGCGGTCTGTGATGCGTGCTGTCGATGGGGCTGCTGTGGA 5699

Qy   5703 ACGGGTCTGGCCACGCCGTTCGTGGGCTTAACCATGGCGCGGCGCGGAAGTGCT 5762
          |||||||||||||||||||| |  ||||||||||||||||||| |||||||  |
Db   5700 ACGGGTCTGGCCACGGCGTTCGTGGGCGTTCATGGCGCGCGGAGGGGGCC 5759
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Qy   5763  AGCGTCTCCCCCTCCTTGGTCACCATTTTACTCGGGGGCCGTCGGGGGCTGGGAGGGCCTG  5822
           ||  |||||||||||||| ||||  |||| || |   |||||| || |||||||||||| ||
Db   5760  AGTGTCTCCCCCTCCTTGGTCACCATTTTATTGGGGGCCGTCGGAGGCCTGGGAGGGGTGTT  5819

Qy   5823  GTGAATCGGCTAGCCTTGTCTTCGACTTATTGCGGGGAAACTATCATCAGAAGATCTG  5882
           |||| ||| |||||||||| ||||||| ||| || ||||||||||||||||||||||||
Db   5820  GTCAACGCGGCCTAGTCTTTGACTTCTTGCGGGGAAACTTTCATCAGAAGATCTG  5879

Qy   5883  TGGTATGCCATCCCAGTGCTAACCAGTCCGGGGGGCAGGACTTGCGGGGGATCGCCTCTCCGGG  5942
           |||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||||
Db   5880  TGGTATGCCATCCCAGTACTGACCAGGCCGGGGGGCCTTGCGGGGGATCGCCTCTCCGGG  5939

Qy   5943  TTGGTGTTGTACTCAGCTAACAACTCGGCACTACCACTTGGTTGAACCGTCTGCTGACT  6002
           |||| |||| ||| || |||||||||||||||||||||||||||||||||||||||||||
Db   5940  TTTGGTTTTGTATTCAGCTAACAACTCGGTTGAACCGTCTGCTGACT  5999

Qy   6003  ACATTGCCAAGGTCCTCATGCATCCCTGACAGTTACTTTCAGCAGGCCGATTACTGTGAC  6062
           || || |||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   6000  ACGTTACCAAGGTCTTCATGTATCCCGACAGTTACTTTCAGCAGGCCAAGTTGACTATTGCCAC  6059

Qy   6063  AAGGTCTCAGCTGCGTCCCGACGTTGAGCCGTCCACTCGCCACCGTCC  6122
           |||||||||||||||||||||||||||| |||||| |||||||||||||
Db   6060  AAGGTCTCAGCTGCGTCCCGACCGTCCCTGAGCCTCACCCGCCAAC  6119

Qy   6123  AGGGAGCCTAAGGTGGATGAGGTTCAGGTGGGGGTACGTCTGGGGACTGGGGATGGATC  6182
           |||||||||||||||||||| |||||||||||| |||||||||||||||||| ||||||||
Db   6120  AGGGAGCCTAAGGTGGATGAGGTGGGGACCGTGTCTGGGGACTGGGGATGGATC  6179

Qy   6183  ATGCGTCAAGTGCGCATGGTGATGGGCCAGACTTCGGGCCCTCTGCCCCGTGGTGTCATTA  6242
           ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   6180  ATGCGCCAAGTGCGCGGTCATGGCCAGACTCAGGGCCCTCTGCCCCGTGGTGTCACTA  6239

Qy   6243  CCCTTATGGCACTGCGGGAGGGGTGTCCGGGAGAATGGTTGTTCCGGACGGCCATGTTGAG  6302
           ||||||||||||||||||||||||| ||||||||||| ||||||| ||||||||||||| |||
Db   6240  CCCTTGTGGCATTGCGGGAGGGGTGTCCGGGAATGTCTTGCTTGACGGGTCATGTTGAG  6299

Qy   6303  AGTCGTTGTCTTTGTGGTTGTGGCTGTCGATCACCGGTGATGTTTGAATGGGCAACTCAAAGAT  6362
           ||||||| || ||||||||||||||||||| |||||||||| ||||||||||||||||||||||
Db   6300  AGTCGTCGCTCTGTGGCTGTCGATCACCGGTGATGTTTCTGAATGGGCAACTCAAAGAA  6359

Qy   6363  CCAGTTTACTCTACCAAGCTGTGCAGGCATTGTGGATGGGGACAGTCCCTGTGACATG  6422
           |||||||||| |||||||||||| |||| ||||||||||||||||||||||||||||||
Db   6360  CCAGTTTACTTTACCAAGCTGTGCCGGCACTATTGGATGGGGACAGTCCCTGTGACATG  6419

Qy   6423  CTGGGCCATGGCGAGACGTCGCCTTTGCTCGCCCTCAGACACCCGAAGGTGTGTACCATTC  6482
           |||||||||||| ||||||||||||||||| ||| |||||||||||||||||||||||||||
Db   6420  CTGGGTCATGGGTACGGTGAAACGTCCGGCTCGCCCTCCGGACACCCGAAGGTTGTGCCCTTC  6479

Qy   6483  GGGACGTCTGGGTGGCTGAGGTGGTGGATCACCCTTCCGCATCAACGGCGAACA  6542
           ||||||||||||||||||||||||||||| |||||||||||||||||||||||| ||
Db   6480  GGGACGTCTGGGTGGCTGAGGTGGTGACCACACCGCCACCGGGAATCAGGAGGACC  6539

Qy   6543  TCCGCCTACAAACTGCTGCGCGCGCCCAGACAATCCTGTGGTCGTTGTTGCGGCTGCTTAC  6602
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   6540  TCCGCCTATAAGCTGCTGCGCGCGCCCAGACAATCCTATGCGGCTGCTTAC  6599

Qy   6603  GTCGACGGCGCATACCGGTTCATGGACGTCTCATGGCCTGCCATGGTCTATGGC  6662
           |||||||||||||||| |||||||||||| |||||||||||||||||| |||||||
Db   6600  GTCGACGGCATTACGGGTTCATGGACGTCTCATGGCCTGCCATGGTCTATGGC  6659

Qy   6663  CCTGGCAAAGTGTCACCATTGCACGGGGAACGCTACACCCTTCCGCATCAACTGCGGCTT  6722
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   6660  CCTGGCAAAGTGTTACCATTGGACGGGGAGCGCTACACACCTTGCCTCAACTCGAGGCTC  6719

Qy   6723  AGGAATGTGGCGCCCTCTGAGGTGTCATCCGAGGTGTCCATTGGGACGGGAGACT  6782
           |||||| ||||| || ||||||||||||||||||||||||||| ||||||||||||
Db   6720  AGGAATGTGGCACCCTCTGAGGTGTCCATTGGGACGGGAGACT  6779

Qy   6783  GAAGACTCAGAACTGACTGAGGCGCTCGACCTGCGCGCCCTGTCCAGGCTATC  6842
           |||||||||||||||||||||||||||||||||||||||||| |||||||| |||
Db   6780  GAAGACTCAGAACTGACTGAGGCGCTGCTGCTCTCCCAAGCCGATC  6839

Qy   6843  GAGAATGCTGCGAGAATTCTTGAACCTCACATAGATGTCATGGAAGATTGCAGTACA  6902
           ||||||||||||||||||||||||||| |||||||||||||||||||||||||| ||||
Db   6840  GAGAATGCTGCGAGGATTCTTGAACCGCACATTGATGTCATCATGGAGAGACATCATGGAGGACTGCAGTACA  6899

Qy   6903  CCCTCTCTTGTGGGAGTAGCCGAGTGCCGCGAGATGCCGTGTGGGGAGAAGACATCACCCCCACT  6962
           ||||||||||||||| ||| |||||||||||||| |||||||||||||||||||||||||||||||
Db   6900  CCCTCTCTTGTGGTAGTAGCCGAGTGCCGTGATGGGGAGAGACATCCCCCGTACT  6959

Qy   6963  CCATTCGCCAGCACTTATCTCGGTTACTCGGTTACTGAGAGCAGCCCAGATGAGAAGACACCCCGTCGGTG  7022
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6960  CCATCGCCACCACTTATCTCGGTTACTGAGAGCAGCTCAGATGATGAGAGACCCCGGTG  7019

Qy   7023  TCTTCCTCCAGGAGGATACCCCGTCTTCTGACTCATTGGAGGTCATCCAAGAGTCCGAG  7082
           || |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   7020  TCCTCCTCCAGGAGGATACCCCGTCCTCTGACTCATTGGAGGTCATCCAAGAGTCCGAG  7079

Qy   7083  ACAGCCGAAGGGAGGAAAGCGTCTTCAACGTGGCTCTTCCGTACTAACGGAGTTGTTT  7142
           |||||||||||||||||||| |||| ||||||| |||||||| |||   |||||| ||||
Db   7080  ACAGCCGAAGGGAGGAAAGTGTCTTCAACGTGGCTCTTCCGTATTAAAAGCCTTATTT  7139

Qy   7143  CCACAGAGCCGATGCCACAGAAAGCTTACCGTTAAGAATGTCATGCTGTGTTGAGAAGAGC  7202
           |||||||||||| |||||||||||||||||||| ||||||| |||||||||| |||||||||
Db   7140  CCACAGAGCCGACGCGACCAGGAAGCTTACCGTTCAAGATGTCGTGGCTGTTGAGATG  7199

Qy   7203  GTAACACGCTTCTTTTCATTGGGATTGACGGTTCGCTGACGTGACGGTCGTGTGTGAGATG  7262
           || | |||||| ||| ||||||||||| ||||||||||||| || |||||||||||||||||
Db   7200  GTCACGCGCTTTTTTCTCATTGGGTTTGACGGTTGATGTTGACGGTGCGGTCGTGTGTGAGATG  7259

Qy   7263  GAAATCCAGACCATCAGCCTATTGTGCACAAGGTGCGCACTCCCGCTTGCAAGTTGCAGGTT  7322
           ||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   7260  GAAATCCAGACCATCAGCCTATTGTGCACAAGGTGCGCACTCCCGCTTGTGAATTGCAGGTT  7319

Qy   7323  GGGTGCTTGGTGGTGCAATGAACCTACCTTTGAATGTGACAAGTGTGACCAGTGTAGGCAAGAG  7382
           |||||||||||| ||||||||| |||||||||||||||||| |||||||||||||||||||||
Db   7320  GGGTGCTTGGTGGTGGCAATGAACATGGTCAATGTGACAAGTGTGACCAGTGTAGGCAAGAA  7379

Qy   7383  ACCTTGGCTTCCTTCTCTACATTGGTCTGGGGTGCCACTGACGAGGGCCACTCCGGCC  7442
           |||||||||||||||| |||| |||||||||||||||||||||| |||||||||||||||
Db   7380  ACCTTGGCCTCGTCTTCTACATTGGTCTGGAGTGCCACTAGGGCCCACGCCGGGCC  7439

Qy   7443  AAGCCCCCTGTGGTGAGGCCGGTTGGCTCCTTGGTGCCGCCGCCACCACCAAGGTGTAT  7502
           |||| ||  |||| ||||||||||||||||||||| ||||||||||||||||||||||||
Db   7440  AAGCCCTCCCGTGGTGAGGCCGGTTGGCTGTTTGTTAGTGGGCCGCCGCCACCACCAAGGTGTAT  7499

Qy   7503  GTCACCAACCGGACAATGTTGGGAGGAGAGTTGACAAGGTTACCTTCTGCCGTGCCCCT  7562
           |||| |||||||| |||| ||||||||||||||||||||||| |||||||||||||||||
Db   7500  GTTACCAATCCAGACAATGTGGGACGGAGACAGTGTGGACAAGGTGACCAAGGTGCTGCTCCT  7559

Qy   7563  AGGGTTCATGACAAATTCCGTGACTCCATAGAGGCGCCAGCTCAAGCC  7622
           ||||||||||||||||||| || ||||||||||||||||| ||||||||
Db   7560  AGGGTTCATGACAAATTCCGTGACTCCATAGAGGGCCTAAGAGGGCTAAGCC  7619

Qy   7623  TGCCTAAGCATGGGTTCACTTATTCTGGAGGAATCAGGACCCTATTAC  7682
           ||||||||||||||| ||||||||||| ||||||| ||||||||||||
Db   7620  TGCCTAAGCATGGGTTCACTTATTCTGGAGGAATCAGGACCCTACTAC  7679

Qy   7683  ATGGGCTGGGGATCTGGAAGGTGTCGGTCACACCCTCGCCACCCCCGGGAAGATGGCT  7742
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||| |||
Db   7680  ATGGGCTGGGGATCTGGAAGGTGTCGGTTAAGGACTTAGGACTCCACCCCGGGAAGATGGCC  7739

Qy   7743  GTCCATGACAAGTACACTGGTTCTCCGGAGATACTTCTTACTCTTACTGTG  7802
           |||| |||||||||||||||| ||||||||||||||| |||||||||||||||
Db   7740  GTCCATGACAAGTTCAGGAGATACTTTCAGGAGACTTGAAGGGACTCTTACTCTTACTGTG  7799

Qy   7803  AAAAAGGAAGTGTTCTTCAAAACCGAAAGGAAGAAGAAGGCCCCCCGCC  7862
           ||||||||||| ||||||||||||||||||||||||||||| |||||||||
Db   7800  AAAAAGGAGGTGTTCTTCAAAAGACCGAAGGAGAAGAAGGCCCCCCGCC  7859

Qy   7863  CCCCCCCTGACTTCCGGATAGCTTGAAAGCTGAAAAAGTCTGGTAGCC  7922
           |||||| ||||||||||||| ||||||||| |||||||| ||||||||||
Db   7860  CCCCCCCTGACTTCCGGATAGCTTCAAAAGCTCATCTTGGGGAGACCGGGGTAGCC  7919

Qy   7923  AAGGCGGTGTTGGGGGGCCTACGGGGGGTCATGCAAATCAGCCAATTAGGGAG  7982
           |||| || |||||||| |||||||||||| |||||||||||||||||||||||| ||||
Db   7920  ...
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Db   7920 AAGGCGGTGTTGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAGTTAAGGAG 7979

Qy   7983 ATGCTCAAACTGTGGAATCAAAGAGACACCATGCGCCATCTGTGTGGACGCCACATGC 8042
          |||||| ||   || |  ||| ||||||| |  |||||||||||||||| || |||||
Db   7980 ATGCTCAAGCTATGGGAGTCTAAGAGAGACCCCTTGCGCCATCTGTGTGGACGCCACCTGC 8039

Qy   8043 TTCGACAGTAGCATAACTGAAGAGACAGCGTGGCCGTCTGAGACAGAGCTTTATGCCTGGCT 8102
          |||||||||||  || |||||||||| || |||||||| ||| ||| || || |||||
Db   8040 TTCGACAGTAGCATAACTGAAGAGACGTGGCTTTGGAGACAGAGCTATACGCTCTGGCC 8099

Qy   8103 TCAGACCATCCAGAATGGGTGCGTGCCCTGGGAAATACTATGCCTCTGGCACAATGGTA 8162
          || ||||||||||| |||||   ||  |   ||| |||| ||  | || ||| ||||| |
Db   8100 TCTGACCATCCAGAATGGGTGCGGGCCCACTTGGGAAATACTATGCCTCAGGCACCATGGTC 8159

Qy   8163 ACCCCGAGGGGTGCCACTGGTGAGAGTATTGTAGATCCTCAGGGTGTCTTGACCACC 8222
          |||| || |||||  || |||||||| || ||||| || |||   || || |||||
Db   8160 ACCCCGGAAGGGTGCCCGTCGGTGAGAGTATTGCAGATCCTCGGGTGTCCTAACAACT 8219

Qy   8223 AGTGCGAGCAACTGCTTGACTTGCTATATCAACAAGTGAAAGCCGCTGTGAGAGGTGGGG 8282
          || |  |||||||||| |||| ||||||||||||||| |||||| ||| |||||| |||
Db   8220 AGCGGCAGCAACTGCTTGACCTGCTACATCAAGGTGAAAGCTGCCTGTGAGAGACTGGGG 8279

Qy   8283 CTGAAAAAATGTCTCCGCTCCTCATCGCTGGCGATGACTGTTGATCATATGCGAACGGCCT 8342
          ||||||||||| | |||| || |  |  || |  || |||| ||||  ||||||| |
Db   8280 CTGAAAAAATGTCTCTTCTCATAGCCGGCGATGACTGCTTGATCATATGTGAGCGGCCA 8339

Qy   8343 GTGTGCGGATCCTAGCGACGCGTTTGGGCGAGCCCTGGCGAGCTACGCGGTACGCATGCGAG 8402
          |||||| |||| || ||||| || |||||||||| ||| |||||| || |||| |||||
Db   8340 GTGTGCGGACCCCAAGCCAAGCCACGCGTTTGGGCCAGCCCTATGGGTACGCGGTACGGCGAG 8399

Qy   8403 CCTTCGTATCATGCATCACTGGACACGGCCCCCCTTCGTCTCCACTTGGCTAGCTGAGTGC 8462
          ||| |  |||  |||| || ||||||||||||| |  || |||| ||||  |||||  |||
Db   8400 CCCTCATATCATGCATCATTGGACACGGCCCCCCTTCTGCTCCACTTGGCTGCTGAGTGC 8459

Qy   8463 AATGCAGATGGGAAACGCCATTTTCTTCCTGACCACGACTTTCGGAGGCCCCGGCTCCGC 8522
          |||||||||||||| |||||| |||| |||||||||||| ||||| || |||| || |||
Db   8460 AATGCAGATGGGAAGCGCCATTTTCTTCCTGACCACGACTTCCGGAGGCCGCTCGCGC 8519

Qy   8523 ATGTCCAGCGAGTACAGTGCCCCAATGCCTCGGCGACATGGTTACATCCCTATACCCT 8582
          ||  |||| ||||||||||  ||| || |||| |||||| |  ||||| | ||||||
Db   8520 ATGTCGAGTGAGTATAGTGCCCCGATGGCTTCGGCGCATGGCTTCATCCCTCCTTTATCCT 8579

Qy   8583 TGGCATCCTATCACACGGCTGGGTCATCATCCCTCACGTGCTCACCTGCGCGTTTAGGGGT 8642
          |||| |  | |||||||| |   |||||||||  |||||| || |||| ||| || |||
Db   8580 TGGCACCCCATCACACGGCTGGGTCATCATCATCCCTCATGTGCTCAACGTGCGCCATTCAGGGGT 8639

Qy   8643 GGTGCACACCGTCTGATCCTGTGTGTGTGGCCAGTGAATTGGTAATTACTACAAGTTTCCA 8702
          | |||| ||||||||| || ||  |  |||||||| ||||||||||||| ||||||||||
Db   8640 GGAGGCACACCGTCTGATCCGGTTTGGTGCCCAGTGTAATTGGTAACTACTACAAGTTTCCA 8699

Qy   8703 CTGGACAAACTGCCTAACATCGTGGCCCTCCACGACGCGTTGAGGGTTACC 8762
          ||||||||| | || |||||  | |||||||| ||||||||||||||||||
Db   8700 CTGGACAAACTGCCTAACATCATCGTGGCCCTTCACGACCAGCGGTTGAGGGTTACC 8759

Qy   8763 GCAGACAAACTGCTTCCACCGGAGAAATGAGGCCTGGCAAGGTGCTGAGGCGACCTCCCT 8822
          |||| |||||||| | ||||||||||| ||||| ||||| |  ||| | || |||||||
Db   8760 GCAGACAAACTGCTTCGCACCGGAGAAGATGGGCTTGGTTCTGAGCGACGTTCTCAAGCTCCCT 8819

Qy   8823 GGCCTAGCAGTCCACCGGAAGAAGGCCGGGGGCATTGCGAACGCGTATGCTTCCGGTCGCGC 8882
          || | ||||||||||| |||||||| |||| |  | |||||||| |||| |||  ||| |
Db   8820 GGCCTTAGCAGTCCACCGGAAGAAGGCCGGGTTGGCGGTCGTTGCGAACACGCAGTCTCCGCGC 8879

Qy   8883 GGTTGGGCTGAGTTGGCTAGGGCGTCTAGGGGCTGTGTGTTGGGTGTTCCCCCGGGGGTTCAT 8942
          ||||||||| ||||||| ||||| ||  |   ||| ||||| |||  || || |||||||||
Db   8880 GGTTGGGCTGAGTTGGCTAGGGGCTGTGTGTTGTTGTGGCATCCCAGGCCTTACGGCTTCCTCCCCCT 8939

Qy   8943 GAGATTGCTTGGGTATCCCGGGGGTTCCCCGGTTTGGGGTTCTTAGCCCTGCTC 9002
          ||||||||||  ||||||| ||||||| ||| |||||||||||||||||||||
Db   8940 GAGATTGCTGTGTATCCCGGGGGTTCCCCTTATATGGGGGTTCTTAGCCCTGCTC 8999

Qy   9003 CAATTGGATTTCACAAGCCAGAGGAGTCGCCTGGGTTCTTGGGGTTGGGGTTCTTAGCCCTGCTC 9062
          ||||||||||||||| |||||||||||||| |||| | |||||||| ||| |||||||||||
Db   9000 CAATTGGATTTCACAAGCCAGAGAGTCGCTGATGCCTGTATCGGGTTGGGGTTCTTAGCCCTGCTC 9059

Qy   9063 ATCGTAGCCCCTTCGGTGAACTAAAATCATCTGTGCGGCAAGGTCCGGTGCAAGGTCGGTGACTGATC 9122
          ||||||||| ||||||||| |||||  ||||||||||||||||| ||||||  |||||||||||||
Db   9060 ATCGTAGCCCTTCGGTGAACTAAATCATCTGTGCGGCAAGGTCTGTGGTCGGTGACTGATC 9119

Qy   9123 ATCACTGGAGGAGGTTCCCGCCCTCCCGCCCCAGGGGTCTCCCCGGGGTAAAAAGGG 9182
          |||| ||||||||||| ||||||| ||||||||||||||||||||||||||||||||
Db   9120 ATCACCGGAGGAGGTTCCCGCCCTCCCCGCCCCGGGGTCTCCCCGGGGTAAAAAGGG 9179

Qy   9183 CCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCCTGGCAGGGTCAAAGCCTGATGGTGC 9242
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9180 CCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCCTGGCAGGGTCAAAGCCTGATGGTGC 9239

Qy   9243 TAATGCACTGCCACTTCGGTGCGGTGCGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC 9302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9240 TAATGCACTGCCACTTCGGTGCGGTGCGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC 9299

Qy   9303 TGCTCGCAGAGCCCTCCCGGATGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC 9362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9300 TGCTCGCAGAGCCTCCCGGATGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC 9359

Qy   9363 GGTAAGAGCTCGGCCCAAAGGCCGGGTTCTACT 9395
          ||  ||||||||| |||||| ||||||||||||
Db   9360 GGGAAGAGCTCGGCCCGAAGGCCGGGTTCTACT 9392
```

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RESULT 5
AAX02334
ID   AAX02334 standard; cDNA; 9392 BP.
XX
AC   AAX02334;
XX
DT   06-MAY-1999  (first entry)
XX
DE   US5855134 Seq ID 14.
XX
KW   Non-A Non-B Non-C Non-D Non-E Hepatitis virus; immunogen; HGV; HAV; HBV;
KW   immunoreactive; serum alanine aminotransferase; hepatitis A virus; HCV;
KW   hepatitis B virus; hepatitis C virus; hepatitis D virus; HDV; HEV;
KW   hepatitis E virus; Flaviviridae; vaccine; prophylactic; therapeutic; diagnosis;
KW   antibody; vaccine; detection; ds.
XX
OS   Hepatitis G virus.
XX
FH   Key            Location/Qualifiers
FT   CDS            459..9080
FT                  /*tag= a
FT                  /product= "HGV-PNF 2161 variant"
XX
PN   US5855134-A.
XX
PD   05-JAN-1999.
XX
PF   05-JUN-1995;
XX
PR   19-MAY-1995;  95US-0044733.
PR   20-MAY-1994;  94US-0246985.
PR   03-AUG-1994;  94US-0285543.
PR   03-AUG-1994;  94US-0285558.
PR   03-AUG-1994;  94US-0285561.
PR   26-OCT-1994;  94US-0329729.
PR   23-NOV-1994;  94US-0344271.
PR   16-DEC-1994;  94US-0357509.
PR   15-FEB-1995;  95US-0389886.
PR   05-JUN-1995;  95US-0461361.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fry KE,  Kim JP,  Linnen JM,  Wages J,  Young LM;
.XX
DR   WPI; 1999-105108/09.
DR   P-PSDB; AAW92755.
XX
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PT   New isolated hepatitis G virus antigens - used to develop products
PT   for the diagnosis, prophylaxis and therapy of hepatitis G virus
PT   infections
XX
PS   Example 6; Column 99-118; 204pp; English.
XX
CC   This invention describes a Non-A Non-B Non-C Non-D Non-E Hepatitis Virus
CC   (HGV) Immunogenic composition which comprises a purified HGV polypeptide
CC   antigen at least 10 amino acids in length which is specifically
CC   immunoreactive with HGV-positive sera, present in a carrier, where HGV
CC   is characterised by (a) production of elevated serum alanine
CC   aminotransferase levels in an infected primate (b) its serological
CC   distinction from hepatitis A virus (HAV), hepatitis B virus (HBV),
CC   hepatitis C virus (HCV), hepatitis D virus (HDV), and hepatitis E virus
CC   (HEV) (c) membership in the virus family Flaviviridae. The compositions
CC   can be used to develop products useful for prophylactic, therapeutic and
CC   diagnosis applications. The immunogenic compositions can be used for the
CC   production of antibodies, in vaccines and for detection and diagnosis.
XX
SQ   Sequence 9392 BP; 1694 A; 2551 C; 2998 G; 2148 T; 1 other;

Query Match             84.9%;  Score 7979;  DB 20;  Length 9392;
Best Local Similarity   90.7%;  Pred. No. 0;
Matches  8515;  Conservative    1;  Mismatches  876;  Indels    1;  Gaps    1;
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Qy      3 ACGTGGGGGGTTGATCCCCCCCCCGGCACTGGGTCGAAGCCCATAAACCGACGCCT 62
          |||||||||| |||||||||||||||||||||||||||||||| ||| ||||||||
Db      1 ACGTGGGGGAGTTGATCCCCCCCCCGGCACTGGGTCGAAGCCCAGAAACCGACGCCT 60

Qy     63 ATCTAAGTAGACCAATGACCTCGGCGGCCGGACTCGGCGACCGGCCAAAAGGTGGTGGATGG 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATCTAAGTAGACCAATGACCTCGGCGGCCGGACTCGGCGACCGGCCAAAAGGTGGTGGATGG 120

Qy    123 GTGGTGACAGGGTTGGTAGTCGTAAATCCGGTCATCCTGGTAGCCACTATAGGTGGGT 182
          || |||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    121 GTGATGACAGGGTTGGTAGTCGTAAATCCGGTCACCCTGGTAGCCACTATAGGTGGGT 180

Qy    183 CTTAAGAGAAGGTCAAGACTCCCTTGTGCCTGCGGCGAGACCCGCACGGTCCACAGGT 242
          ||||||||||||||| ||| |||||||||||||||||||||||| ||||||||||||
Db    181 CTTAAGAGAAGGTTAAGATTCCCTTGTGCCTGCGGCGAGACCCGCACGGTCCACAGGT 240

Qy    243 GCTGCGCTACCGGTGTGAATAAGGCCCGACGTCAGGCTCGTCGTTAAACCGAGCCCGT 302
          | |||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db    241 GTTGGCCTACCGGTGTGGAATAAGGCCCGACGTCGTCGTTAAACCGAGCCCGT 300

Qy    303 CACCCACCTGGGCAAACGACGACGCCCAGTACGGTCGCGCCCTTCAATGTCTCTTG 362
          |||||||||||||  | |||||||||||||| ||||||||||||||||||||||||
Db    301 TACCCACCTGGGCAAACGACGACGCCCAGTCGGTCGCGCCCTTCAATGTCTCTCTTG 360

Qy    363 ACCAATAGGTTTATCCGGCGAGTTGACAAGGACACCAGTGGGGGCCGGGGAAG 422
          |||||| |||   || ||||||| ||||||||| ||| | |||||||||||||
Db    361 ACCAATAGGCTAGCCGGCGAGTTGACAAGGACACCAGTGGGGGCCGGGGCT-TGGAGAGG 419

Qy    423 GACCCCAAACCCTCCCCTTCCCGGTGGGCCGGGAAATGCATGGGGCCACCCAGCTCCGCG 482
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GACTCCAAGTCCCCGGCGTCCCCGGGCCGGGAAATGCATGGGGCCACCCAGCTCCGCG 479

Qy    483 GCGGCCTGCAGCCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGGCCGGGGTGGCATTTCTT 542
          ||||||||||| ||||||||||||||||||||||||||| |||||||||||||||||||||
Db    480 GCGGCCTGCAGCCGCCGGGGTAGCCCAAGAATCCTTCGGGTCGGAGGGGCCGGGGTGGCATTTCCTTT 539

Qy    543 TTCTATACCATCATGGCCAGTCCTTCCTTCGTCTTCGTCCTTCGTGGTTGAGGGCCATTCTG 602
          ||||||||||||||||||||||||||| || |||||||||||||||||||||||||||||||
Db    540 TTCTATACCATCATGGCCAGTCCTTCCTCGTCCTTCGTGGTTGAGGGCCATTCTG 599

Qy    603 GCCCGGCCACCACGGCTTGTCGAGCGAATGGGCAATATTCCTCACAAATTGCTGTGCC 662
          |||||||||||| |||||||||||||| ||||||||| |||||||||||||||||||
Db    600 GCCCGGCCACCCACGCTTGTCGAGCGAATGGGCAATATTCCTCACAAATTGTGTGCC 659

Qy    663 CCGGAAGACATCGGGTTCTGCCTGGAAGGCGGATGCCTCGGTGGCGTGGCCACGGTT 722
          ||||||| |||||||||||||||||||||||||||| |||||||||||||||||||
Db    660 CCGGAGGCAGATCGGGTTCTGCCTGGAGGTCGGATGCCTGGGTGCCTGCCTGGGCCACGGATT 719
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Qy    723 TGCACCGACCGTGCTGGCCACTGTATCAGGCGGGTTTGGCGTGCGGCCTGGCAAGTCC 782
          ||||| |||| |||||||||||||||||||||||  |||||||||||||||||||||||
Db    720 TGCACTGACCAATGCTGGCCACTGTATCAGGCGGCGGGTTTGGCGTGCGGCCTGGCAAGTCC 779

Qy    783 GCGGCCCAGCTCGTTGGGGAACTGGGGAGCTCTGGGGGTCTACGGGCCTGTCGGCTTAC 842
          ||||||||  || ||| |||||| |||| | ||||||||  |||| |||||||||||| |
Db    780 GCGGCCCAACTGGTCGGGGGAGGTTAGCCGTATACGGGCCCCTATACCGGGCTGTCGGCTTAT 839

Qy    843 GTAGCCGGATCCTGGGTCTCGGCGAGGTTTACTCCCGGGTCCTGACAGTTGGTGTGCG 902
          || |||||||||||||||| ||||||| ||||| ||||||| ||||| |||||||||||
Db    840 GTGGCTGGGATCCTGGGCCTGGGTGAGGTGACTCCTAACGGTGGGAGTCGCG 899

Qy    903 TTGAGGCGCCGGGTCTACCTGATGCCCAACCTGAAGTGCAGTAGAATGTGACGTTAAG 962
          |||| || |||||||||| ||| |||||||||||||  |||||||||||| ||||| |||
Db    900 TTGACGCCGCCGGGTCTACCCGGCCTAACCTGACGTGTGCAGTCGCCGTGTGAGCTAAAG 959

Qy    963 TGGGAAGTGAGTTTTGGAGATGGACTGAGCAGTTGGCCTCCAATTACTGATTTTGGAA 1022
          ||||||||||| |||||| || |||| |||||| |||||| |||  || |||| |||||
Db    960 TGGGAAAGTGAGTTTTGGAGATGGACTGAACAGTCGGCCTCCAACTACTGGGAGAA 1019

Qy   1023 TACCTTTGGAAAGTCCCATTTGAATTTGGAGGAGTGATGAGCCTGACCCCCTCTGTTG 1082
          ||| || |||||||||||||| |||| ||| |||||  ||||| ||||| ||||||||
Db   1020 TACCCTGGAAGGTCCCATTTGATTTCTGAGAGGGCGTGATAAGCCTGACCCCCCTGTTG 1079

Qy   1083 GTTTGGGTGGCCGCATTGCTTTGCTGCGTTGAGCAACGACGATTGTCATGGTTCCTGCTGTG 1142
          |||||| |||||||||||||| | ||||||||||||||||||||||||||||| ||| |||||
Db   1080 GTTTGGGTGGCCGCATTGCTTTGCTGCGTTGAGCAACGATTGTCATGTTCTTCCGTTGGTG 1139

Qy   1143 ACGATGGCGGGGATGTTGCAAGGCGCCCCGGTCCGTTTGGGGTCCCGCCCTTTGAC 1202
          ||||||||||||||||| |||||||| ||||||||||||||| |||||||| |||||
Db   1140 ACGATGCCGGGGATGTCGCAAGGCGCCCCTGCCTGCGTCCTTTTGGGGTCACGCCCTTTGAC 1199

Qy   1203 TACGGGTTGAAGTGGCAGTCATGCTCCTGCAGGGCTAACGGGTCGCGTATTCCCACTGGG 1262
          ||||||||||| || ||||| || |||||||| ||  |||||| ||| ||||| |||||||
Db   1200 TACGGGTTGACTTGGCAGACCTGCTCTTGCAGGGCCAACGGTCGCGTTTTTCGACTGGG 1259

Qy   1263 GAGAGGCGTGTGGGATCGGAGGGAATGCGAGGGAAGTGCACGCTCTGTGACTGCCCCAACGGCCCCTGG 1322
          |||||| ||||||| ||| ||| || ||  ||| |||| | ||||||||| |||| ||| ||||||||||
Db   1260 GAGAAGGTGTGGGACCCTGGGAACGTTACCGGTCTTCAGTGACTGCCCTAACGGCCCCTGG 1319

Qy   1323 GTTTGGGTCCCGGCTTTTGCCGTTTAAGGCGGTTGGGTGGGGCGCACCCGCATCACCCATTGGAGC 1382
          |||||||||||| || |||||| || ||| | |||| ||||||||||| || |||||||||||||||
Db   1320 GTGTGTGGTCCCAGCCTTTGCCAAGCAATCGCTGCGGGTGACCCTGACACCCTCACTTATTGGAGC 1379

Qy   1383 CACGGACAAAACCAGTGGCCCCTATCATGCGCCTCCAATATGTCTATGGGTCTGTCGTCCGTA 1442
          |||||| |||  || ||||||||||||||  |||| |||| || || |||||| || ||||  |
Db   1380 CACGGGGCAAAATCAGTGGCCCCCATTGCATGTCATGGGTCTGCTCACAGTC 1439

Qy   1443 ACGTGCGTGTGGGGTTCCGTGTCTTCGACCGGCGTCGATTCGGATTCCGAAGATC 1502
          ||||||||||||||| ||| |||||||| || | ||| |||||  |||| ||||||
Db   1440 ACTTGCGTGTGGGGTTCCGCTGCGTTCTTGCCTCCCACCAGTGGTGTGCGCGACTCGAAGATA 1499

Qy   1503 GATGTGGAGTTGGTGCCGGTTGAGTCTCCGGGGGAAGTCTAGGGTCA 1562
          |||||||||||| || |||||||||||  ||||| |||||||||||||
Db   1500 GATGTGGAGTTAGTGCCAGTTGGCGTCTGCCACCATAGCGCACTTGGATCA 1559

Qy   1563 TCGGATCGGACACGGTGGTTGAGCTCCGGAGTCGGGGAGTCCCGGTTCGCGGTAACGTGTATT 1622
          ||||||||| ||||| |||||||| ||||||||||||||||  ||||||||||| ||| ||||
Db   1560 TCGGATCGGACACGGTGGTTGAGCTGCCGGAGTGGGGAATCCGTGCTGGCCGAAACCGGTGTGTT 1619

Qy   1623 CTTGGACCCTGCGCTGCCTTCGTCCTTCCTGGTTGGTTGAGCCTCGGGGCCGAAACCGGG 1682
          |||||||||||||||| ||| |||||||| |||||| || ||| | ||| ||||| ||||
Db   1620 CTTGGACCCTGCGCTGCCTTCGTCCTTCGTGGTTGAGGGACTCGTGCGGCCGCCCCAGACCGGG 1679

Qy   1683 TCGGTTAGATTCCTTTCCATCGTCGCGGCAATATTCCTCACAAATTGCTGTGCC 1742
          ||||| |||||||| |||||| |||||||||||||| ||||||||||||| ||||
Db   1680 TCGGTTAGGTTCCATTCCATCGTCGCGGCAATATTCCTCACAAATTGTGTGGAA 1739

Qy   1743 GCTATGCCGTCCGTTCGTCAACAGGACAACTCCCTTCAAGGGCCCCTGGGCAACCAG 1802
          || |||||||  || |||| |||||||||||| ||||| |||||||| |||||||| |
Db   1740 GCTGTGCCCCTTCGTCGTCAACAGGACAACTCCCTCAAGGGGCCCCTGGGCAACCAG 1799

Qy   1803 GGGAGAGGCAACCCGGTGCGGTCGCGCCCTGGCGTTTGGTCCTACCATGACCAAGATC 1862
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Left column (positions 1800–2942):

Db 1800 ...
Qy 1863 ... 1922
Db 1860 ... 1919
Qy 1923 ... 1982
Db 1920 ... 1979
Qy 1983 ... 2042
Db 1980 ... 2039
Qy 2043 ... 2102
Db 2040 ... 2099
Qy 2103 ... 2162
Db 2100 ... 2159
Qy 2163 ... 2222
Db 2160 ... 2219
Qy 2223 ... 2282
Db 2220 ... 2279
Qy 2283 ... 2342
Db 2280 ... 2339
Qy 2343 ... 2402
Db 2340 ... 2399
Qy 2403 ... 2462
Db 2400 ... 2459
Qy 2463 ... 2522
Db 2460 ... 2519
Qy 2523 ... 2582
Db 2520 ... 2579
Qy 2583 ... 2642
Db 2580 ... 2639
Qy 2643 ... 2702
Db 2640 ... 2699
Qy 2703 ... 2762
Db 2700 ... 2759
Qy 2763 ... 2822
Db 2760 ... 2819
Qy 2823 ... 2882
Db 2820 ... 2879
Qy 2883 ... 2942

Right column (positions 2880–4022):

Db 2880 ... 2939
Qy 2943 ... 3002
Db 2940 ... 2999
Qy 3003 ... 3062
Db 3000 ... 3059
Qy 3063 ... 3122
Db 3060 ... 3119
Qy 3123 ... 3182
Db 3120 ... 3179
Qy 3183 ... 3242
Db 3180 ... 3239
Qy 3243 ... 3302
Db 3240 ... 3299
Qy 3303 ... 3362
Db 3300 ... 3359
Qy 3363 ... 3422
Db 3360 ... 3419
Qy 3423 ... 3482
Db 3420 ... 3479
Qy 3483 ... 3542
Db 3480 ... 3539
Qy 3543 ... 3602
Db 3540 ... 3599
Qy 3603 ... 3662
Db 3600 ... 3659
Qy 3663 ... 3722
Db 3660 ... 3719
Qy 3723 ... 3782
Db 3720 ... 3779
Qy 3783 ... 3842
Db 3780 ... 3839
Qy 3843 ... 3902
Db 3840 ... 3899
Qy 3903 ... 3962
Db 3900 ... 3959
Qy 3963 ... 4022
Db 3960 ... 4019

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Qy  4023  TCGCCCTTACGTATTCCACTTACGGAAGGTTTTTGGCCAACCCTAGGCAGATGCTGAGG  4082
          |||||  |||| | ||||||| |||| ||||||||||||||||||||||||||||| ||
Db  4079  TCCCCCCTACGTATTCAACCTATGGGGAGGTTTTTGGCCAACCCTAGGCAGATGCTACGG  4079

Qy  4083  GGTGTGTCGGTCATTTGTGACGAGTGCCACAGTCATGATGCATGAGTGTTTGTTGGGC  4142
          |  | || |||||||||| |||||||||||||||| ||| | || |  | ||||||
Db  4080  GGCGTTTCGGTGTCATTTGTGATGAGTGCCACAGTCATGATGCATGAGTGTTTGTTAGGC  4139

Qy  4143  ATTGGGCGTGTCAGGGAGCTGGCGGAGGATGTGGAGTGCAATTGGTGTCTCTACGCCACT  4202
          ||||||  |||||||||||||||| |  | ||||||| |||  |  | ||||||||||||
Db  4140  ATTGGGAGAGTCCGGGAGCTGGCGGTGGGTGTGGCAACTAGTGTCTCTACGCCACC  4199

Qy  4203  GCCACCCTCCCGGATCCCGATGACCCAGCACCATCAATCATTGAGACAAAACTGGAC  4262
          |||||||| |||||||||||  | |||||| |||| |||| || |||| | ||||||
Db  4200  GCTACACCTCCCGGATCCCGATGACCCAGCAGCACCTTCCATAATTGAGACAAAATTGAC  4259

Qy  4263  GTGGGAGAGATCCCCTTCTATGGCCATGGCATACCCTCTGAGCGGATGCGGACCGGAAGG  4322
          | ||| |||| ||||| || ||  | |||||| | ||| ||||||| |||||||||||||
Db  4260  GTGGGCAGACATCCCTTTATGGGATGGCATGGCTACCCTCGAGCGGATGCGGACCGGAAGG  4319

Qy  4323  CATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGCCCTGGCGGCCAGTTTTCGGCT  4382
          ||| ||  | ||  | |||||| || ||||| |||||||||||||||| ||| |||
Db  4320  CACCTCGTGTTCTGCCATTCTAAGGCTGAGTGCGAGCCCTGGCGGCCAGTTCTCCGCT  4379

Qy  4383  AGGGGGTAAATGCCATCGCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATGGA  4442
          |||||| |||||| |||||| ||||||||  ||||||||| ||||||||||| ||||
Db  4380  AGGGGGTCAATGCCATTGCCTATTATAGGGGTAAAGACAGTTCTATCATCAAGGATGGG  4439

Qy  4443  GACCTCGTGGTGTGTCTACAGACGACCACTATCCACTGGGTACACTGGAACTTCGATTCT  4502
          |||||||||||||||| |||| |||| ||||||||||||||||||||||| | |  |||
Db  4440  GACCTCGTGGTGTGTCTACACTGACGACCACTATCCACTGGGTAAATTTCGAAATTTCGACTCC  4499

Qy  4503  GTCACCGATTGTGGGTTAGTGGTGGAGGAGTCGTCGAGGTGACCCTTGATCCCACCATT  4562
          |||||| ||||| |  |||||||||||||||||  |||||||||||||||||  ||||
Db  4500  GTCACCGACTGTGGTTAGTGGAGGAGTCGTCGAGGTGACCTGAAGTTGATCCCACCATT  4559

Qy  4563  ACCATCTCCCTGCCACGGTCGCCGCGGTCGCCTGAACTGTCGATGCAGCCGGAGGACGC  4622
          ||||||||||| |||||||||  |||||||  |||||||||||||||||||||||||||
Db  4560  ACCATCTCCCTGCCACAGTCGCCGCGGTCGCCTGAACTGTCGATGCAAAGACCAGGACGC  4619

Qy  4623  ACGGGTAGGGGCAGGTCTGGGCGCCTACTACGCGGGGCCCCCTGCTGGT  4682
          |||||||||| ||||||||||| |||||||||||||| ||||||||
Db  4620  ACGGGTAGGGGCAGGTCTGGGCGCTACTACTACGCGGGGCCAAAGCCCCTGCGGGT  4679

Qy  4683  GTGGTGCGCCTCAGGTCGCTGTCTCGGGGTGGAAGCCGGTCGACCTGGTACGGGAATG  4742
          |||||||||| |||||||||||||||||||  |||||| |||||||||||||||||||
Db  4680  GTGGTGCGCCTCAGGTCGCTGTCTCGGGGTGGAAGCCGGTCGAGCTGGTGACGGGAATG  4739

Qy  4743  GAACCTGACCTGACAGCAAAACTTACGACAACTGCCCTTACACCGCAGCC  4802
          ||||||||||||| | |||||| ||||||| | ||||| |||||||||||
Db  4740  GAACCTGACCTGACAGCAACCTTTACCGACACCTGCCCTTACACGCAGCACGCAGCC  4799

Qy  4803  GTCGCAGCTGACATTGGGGAAGCCGCCGGTGTCTTCTTCGGGGCTTGAGGATG  4862
          |||||||| ||| ||||||||||||||||||||||||||| || ||||||||
Db  4800  GTCGCAGCTGACATCGGGGAAGCCGCCGGTGTCTTCTCTCGGGGCTTGAGGATG  4859

Qy  4863  GTCGCAGCGCCGAATCCTGCCGTCTGGGCTCAACTGGCCCTTCCTGGTGGGTGTT  4922
          |||||||||| ||||||||| |||||||||||||||| ||||||||| || || |
Db  4860  GTCGCAGCGCTGATATCGGAGCTCGGGCTCAACTGGCCCTTCCTGGTGGGTGTT  4919

Qy  4923  CAGCGACCACCATGTGCCGGGAAACACTGCTCTCCCCGGATGACCCCAGTGGGCA  4982
          |||||||||||||||||||||||| |||||||||||||||||||||||| |||||
Db  4979  CAGCGACCACCATGTGCCGGGAAATCCTGCTCTCCCCGGATGACCCCCAATGGGCA  4979

Qy  4983  GGTCTGAAAGGGCCCGAATCCTGCCGGTCAACTGGTCGGGCAATGATTTACCATCT  5042
          ||| ||||||||||||||||||||| ||||| ||||||||||| || || ||||||
Db  4980  GGTCTGAAAGGGCCCAAATCCTGTCCCCACTCCTGCTGGTGGGGCAATGATTTACCATCC  5039

Qy  5043  AAAGTGGCCGGCCATCACATCGTGACGACCTTGTCCTGGTCTGGCGGAGGGT  5102
          |||||||||||||| || ||||||||||||||||||||||| ||||||||||
Db  5099  AAAGTGGCCGGCCACCACATAGTGACGACCTGGTCCTCCCGGAGACTCGTGCGCGGAGGGT  5099
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Qy  5103  TACGTCCGCTGCGATGCGGGACCACCATCTTGATGGTGGGCCTCGCTATTGCGGGGGCATG  5162
          |||||||||||||||| |||| | | ||| |||||||||||||| | ||||||||| |
Db  5100  TACGTCCGCTGCGACGCGTGGCCGATCTTGATGATGCTGGTGATCGGGATGTATCGGGGGAATG  5159

Qy  5163  ATCTATGGTCATACACCGGTCTCTCGTGTGGTTACAGACTGGAGTGAAGTGAAGGGGGGGT  5222
          |||||||||||| |||||||| | ||| |  | | ||||||| ||| ||||||| ||| |
Db  5160  ATCTACGCGTCATACACCGGTCGCCTCGCTCGTGTGGTGTGACAGACTGGGGATGTGAAGGGGGGGT  5219

Qy  5223  GGCAGCCCCCTTATCGGCATGGCACGGCCACGCCCGTGTGTCAGGTCCCC  5282
          ||||  || ||| |||||||||| || || ||||| |||||||||||| |
Db  5220  GGCGCCCCCCTTTATCGGCATGGCACAGGCCACGCCCCAGCCCGTGTGGCAGGTGCAGGTTCCT  5279

Qy  5283  CCGGTAGACCATCGCCGATGACCCGGGGGGGAGAGTCTCGGCCCATCGGATGCCAACACAGTGACAGAT  5342
          ||||| ||||||||||||||||||  |||||||||||||||||| |||| ||||||||||||||||||
Db  5280  CCGGTAGAACCATCGCCGATCCCGCGGGGTGAATCAGCAGCATCAGATGCCAAGACAGTGACAGAT  5339

Qy  5343  GCGGTGGCGGCCATCCAGTGGATTGGCGATTGCGATTGGTCAGTGTCGATCGGGGAA  5402
          |||||||| ||||| |||| | ||||| ||| | |||| ||||| |||||||| |||
Db  5340  GCGGGTGGCAGCCATCAGGTGGACTGGCGATTGGACTATCATGACTGTGTCGATCGGAGAA  5399

Qy  5403  GTGTCTGCTTGGCCCCAGGCCTAGACGGCGGCTACCAGCTACCACCAAGTGGCTT  5462
          |||||||||||||||||| ||||| ||||||| || ||||||||||||||||||||
Db  5400  GTGTTGTCTGCTTGGCTCAGGGTGACGGCCTAAGACGCGCCGAGCCCTACCACCAAGTGGCTC  5459

Qy  5463  GCTGCCTGCTACACGGGACGCGGCCGTCCCCCACTGTTTCAATTGTTGACAAGCTCTTC  5522
          |||||||| || ||| ||||||||||| ||||||| || ||| ||||||||||| ||||
Db  5460  GCTGGCTGCTATACGGGGACGCGGCCGTTCCCACTGTTCCCAGTTGTTGACAAGCTCTTC  5519

Qy  5523  GCCGGGGTCGGGGGGCGGTGAGGGCGGCGTGGGCCATTGCCACAGTGTAAATAGCTGGCGCG  5582
          |||||  | ||||||  | |||| |||||||||| ||||||||||||||| ||||||||||
Db  5520  GCCGGAGGGTGGGGCGGCCGTGTGGCGGCGTGGGCCATTGCCACAGCGTGATAGCTGCTGGCGCG  5579

Qy  5583  GCCTATGGGGCTTCTCTAGGAGCCCCTCCATTGGCCTCGCGCCTTCGCCCGCTCATGGGTTG  5642
          ||| |||||||||||  |||||| |||||||||||||||||||||||| ||| ||||| ||
Db  5580  GCCTACGGGGCTTCAAGGAGCGCCCTCCATTGGCGCGCCGTTGGGCAGCCGTGATGGGGTTG  5639

Qy  5643  GGGCTCGGAGGCAACGCGCAAACCCGCTTAGCCTGGGGGCCCTGGG  5702
          |||| |||||||||||||| ||||||| |||||  | |  |||||||
Db  5640  GGGCTTGGAGGCAACGCGCTCAGACCGCTCTGCCTTCCATTGGGGGCTGCTGGA  5699

Qy  5703  ACCCTCTGGCACGCCCTGTGTGGGTTAACCATGGGGCGCGTTCATGGGAAGTGCT  5762
          |||| |||| ||||| ||||||||| ||||| ||||||||||||||| ||||| |
Db  5700  ACCGCCTGGCACTCCTCGTGTCGTGTGGCTCATGCAGTGCGTCATGGGGGGGGCC  5759

Qy  5763  AGCGTCTCCCCCTCCTTGGTCACCATTTTACTGGGGCGGGGCGTG  5822
          | ||||| |||||||||||| | |||||| |||||||||||| | |
Db  5760  AGTGTCTCCCCCTTGGTCACCATTTATTTATTGGGGCGGGGTGTT  5819

Qy  5823  GTGAATGCGGCTAGCCTTGTCTTCGACTTTTATGGCGGGAAACTATCATCAGAAGATCTG  5882
          | || ||| | |||| ||| ||| | | |||| ||||||||||||||||||||||||| |
Db  5820  GTCAACGCGGCGAGCCTAGTTTGACTTTGACTTTCATGGGGGGAAACTTTCATCAGAAGATCTG  5879

Qy  5883  TGGTATGCCATCCCAGTGCTAACCAGTCCGGGGGCTTGCGGGGGGATCCGCCTCTCGGG  5942
          |||||||||||||||||| |||||||||  ||||||||| || | |||| || ||||||
Db  5880  TGGTATGCCATCCCAGTACTAACAACTCCCGTGACTGAAGCCTTGCGCGGGATCGCCTCTCGGG  5939

Qy  5943  TTGGTGTTACTCAGCTGGCCCTTCGGGGTCAACTGGCCCTTCCTGGTGGGTGTT  6002
          ||||||| || ||||| ||||| |||||||||| |||||||||||| ||||| |
Db  5940  TTGGTTTTTGTTATTCAGCTAACAACTCTGCTGGTTGGTTGAACCGGTCTGCTGACT  5999

Qy  6003  ACATTGCCAAGGTCCTCCATCGCCATCCCTGACATCCCCGATTACTTGTGAC  6062
          || | ||||||||| ||||| ||||| ||||| || |  |||| || |||||
Db  6059  ACGTTACCAAGGTCTTCATCGTATCCCGGACAGTTACTTTCAGCAGTTATTGCGAC  6059

Qy  6063  AAGGTCTCAGCTTGTGCTCCTGGTTGAGCCTCGCCACCGTTGGTTGCCGTGTGACT  6122
          ||||| ||||| |||||||| |||||||||||||||| |||| ||||| ||| |||
Db  6119  AAGGTCTCAGCGTTCAGCCGTTCTCCGCGCCTGAGCCTCGCCACAGTGTTGTCCGTGACT  6119

Qy  6123  AGGAGCCTAAGGTGGACTTCAGGTCGGGTACGGCCGATTGGATGGATGATC  6182
          |||||||||||| |||| ||||||| |||||| ||| |||||| |  ||||
Db  6179  AGGGAGCCTAAGGTGGATGAGGTTACAGTGGGGTATGTCTGGGACCTGTGGGAGTGGATC  6179

Qy  6183  ATGGCTCAAGTGCCCATGGTGATGGCCGTGATGCGGCCAGACTTCGGGCCCCTCGCCCCGGTGTCATTA  6242
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Right column:

Db   GAAATCCAGAACCATACAGCCTATTGTGACCAGGTGCGCACTCCGCTTGAATTGCAGGTT 7319
Qy   7323 GGGTGCTTGGTGGGGAGGGGTGGTCCGGACGAATGTGTTGACAAGTGTGAGGCTAGGCAAGAG 7382
           ||||| | ||||||||||||| ||||||||||||||||| |||||| ||||||||||
Db   7320 GGGTGCTTGGTGGGGCAATGAACTTACCTTTGAATGCACAAGTGTGAGGCTAGGCAAGAA 7379

Qy   7383 ACCTTGGCTTCCTTCTCTTACATTGGTCTCGGGTGCCACTGACGAGGGCACTCCGGCC 7442
           ||||||||| || ||||||||||||||||||| ||||||||||||||||||||||||
Db   7380 ACCTTGGCCTCCTTCTCTTACATTGGTCTCGGAGTGCCGCTGACTGAGGGCCACGCCGGCC 7439

Qy   7443 AAGCCCCTGTGGTGAGGCCGGTTGGCTCCTTGTCGGTTGGTGGCCGACCACCAAGGTGTAT 7502
           |||||||||||| | ||||||||||||||||||||| ||||||||||||||||||||||
Db   7440 AAGCCTCCCGTGGTGAGGCCGGTTGGCTCTTTGTTGTAGTGGCCGACACTACTAAGGTGTAT 7499

Qy   7503 GTCACCAACCCGGACAATGTTGGAGAAGAGTTGACAAGGTGACCTTCTGGCGTGTCCCCT 7562
           ||||||||| | || | |||| ||||||||||||||||| ||||| ||||||||| ||
Db   7500 GTTACCAATCCAGACAATGTGGGACGAGGGTGGACAAGGTGACCTTCTGGCGTGCTCCT 7559

Qy   7563 AGGGTTCATGACAAATTCCTCGTGGACTCCATAGAGCGCGCTAAGAGGCCAGCTCAAGCC 7622
           |||||||||||| || || |||||||| ||||| || ||||| |||||||||||||||||
Db   7560 AGGGTTCATGAAGTACCTCGTGACTCTTATTGAGCGCGCTAAGAGGGCCGCTCAAGCC 7619

Qy   7623 TGCCTAAGCATGGTTACACTTATGAGGAGCAATAAGACTGTAAGGCCACATGCTGCC 7682
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7620 TGCCTAAGCATGGTTACACTTATGAGGAGCAATAAGACTGTAAGGCCACATGCTGCC 7679

Qy   7683 ATGGGCTGGGGATCTAAGGTGTCGGTCAAGGACCTTCGGGGGAAGGACTGGGAGTGGCT 7742
           |||||||||||||||||||||||||| || ||||| ||||||||| ||||||||||
Db   7680 ATGGGCTGGGGATCTAAGGTGTCGGTTAAGGACTTAGCCCACCCCGCGGGGAAGATGGCC 7739

Qy   7743 GTCCATGACCGGCTCCAGAGATACTTGAAGGGACGCCAGTCCCCTTTACTCTTACTCTGTG 7802
           |||||||| | ||||||||||||| |||||| | ||||||||||||| ||||||||
Db   7740 GTCCATGACCGGCTTCAGAGATACTTGAAGGGACTTCCGGTCCCCTTTACTCTTACTCTGTG 7799

Qy   7803 AAAAAGGAAGTGTCTTCAAAGACCGAAGGAGGAAGGAAGGCCCCCGCCCCTCATTGTTC 7862
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7800 AAAAAGGAAGTGTTCTTCAAAGACCGAAGGAGGAAGGAAGGCCCCCGCCCCTCATTGTGTTC 7859

Qy   7863 CCCCCCTGGACTTCCGGATAGCTGAAAAGCTTATTCTGGACGGGGTAGCC 7922
           ||||||||||||||||||||||| |||||||||| | |||||||||||
Db   7860 CCCCCCCTGGACTTCCGGATAGCTGAAAAGCTCATCTGGAGACCGGGTAGCC 7919

Qy   7923 AAGGCGGTGTTTGGGGGGGGGCCTTCCAGTCACCCCAAATCAGCGAATTCAGGGAG 7982
           |||||||| ||||||||||||| | ||| ||||||||||| ||| ||||| |||||
Db   7920 AAGGCGGTGTTTGGGGGGGGGCCCTCCAGTCACCCCAAATCAGCGAGTTAAGGAG 7979

Qy   7983 ATGCTCAAACTGTGGGAATCAAAGAGACACCATGCTGTGTGGACGCCACATGC 8042
           ||||||| || ||||||||||||||||| ||||||||||||||||||||||
Db   7980 ATGCTCAAGCTATGGGAGTCTAAGAAGAGACCCCCTGCCGCATCGTGTGGACGCCACCTGC 8039

Qy   8043 TTCGACAGTAGCATAACTGAAGAGGACGTGCGCGTCGGACGCTTTATGCCCTGGCT 8102
           ||||||||||||||||||||||||||| ||||||| | | |||||||||||||
Db   8040 TTCGACAGTAGCATAACTGAAGAGGACGTGCGCGTCGGACGCTATACGCTCTGGCC 8099

Qy   8103 TCAGACCATCCAGAATGGTTGCGTGCCCTGGGAATCACTTATGCCTCTGGCACAATGGTA 8162
           ||| ||||||||||||||| || ||||||||||| | |||||| ||||||||||| |
Db   8100 TCTGACCATCCAGAATGGTTCGCGGCACTTGGGAAATACTATGCCTCAGGCACCATGGTC 8159

Qy   8163 ACCCCCGAGGGGGTGCCCAGTGGTGAGAGGTATTGTGACTTGTCCTAAAACT 8222
           ||||| | |||| ||||||||| ||||||||||||||||||||| |||| |||
Db   8160 ACCCCCGGAGGGGTGCCCGTCGGTGGCTTTGGGAATCCTCAGGGGTGTCCTAACAACT 8219

Qy   8223 AGTGCCGGAACTGCTTGACTTGCTATCAAGGTGAAAGCCGCCTCGAGAGGTGGGG 8282
           | |||||||| ||||||| ||||| |||||||| ||||| |||||||||||||
Db   8220 AGCCCGGAGCAACTGCTTGACCTGCTCAATCAAGGTGAAAGCTGCCTCGTGGAGAGTGGGG 8279

Qy   8283 CTGAAAAATGTCTCGCTCCTCATCGCTGGCCAATGGTCGTTTGATCATATGCGAACGGCCT 8342
           || ||| | || |||||||||| |||||||||||| || ||||||||||||||||||
Db   8280 CTGAAAAATGTCTCTCTTCTCATAGCCGGCCGATGACTGCTTGATCATATGTGAGCGGCCA 8339

Qy   8343 GTGTCGCGATCCTAGCGACGCGTTTGGGCGACCCTGGGCGCAGAGCCCTTCAGCGAGTCACGCGT 8402
           ||| || | | ||||||| | ||||||||||||||| | ||| ||||||||||||||||
Db   8340 GTGTCGCACCCCAAGCGACGACGCTTTGGGCGACCCTGGGCGCAGAGCCCTCAGCGAGTCACGCGT 8399

Left column:

Db ||||| |||||||| |||| ||||||||||||||||||||||||||||| || 6239
6180 ATGCGCCAAGTGCGCGTGGCTGCGTCATGGCCAGACTCAGGGCCCTGCCCCGTGTGTCACTA

Qy   6243 CCCTTATGGCACGTGCGGGGAGGGGTGGTCCGGACGAATGTTGTTGACCGCCATGTTGAG 6302
           |||| | ||| || || |||||||||||||||||| || ||||||||||||||||||||
Db   6240 CCCTTGTGGCATTCGGGGAATGTTCCTGGCCGGGGAATGGTTGCTTGACGGTCATGTTGAG 6299

Qy   6303 AGTCGTTGTCTTTGTGGTTGCGTGATCACCGGTGATGTTTTGAATGGGCAACTCAAAGAT 6362
           ||| ||| | | |||| ||||| ||||||||||||||||| ||| ||| ||||||||||
Db   6300 AGTCCTTGCCGCTCTGTGGCGTGGATCACTGGTGACGTTCTGAATGGGCAACTCAAAGAA 6359

Qy   6363 CCAGTTTACTCTACCAAGCTGCAGGCCATTATTGATGGGGACAGTCCTGTGAACATG 6422
           ||||||||||| ||||||||||||||| |||| |||||||| ||||||||||||||
Db   6360 CCAGTTTACTCTACCAAGCTGCCGGACTGTTGGATGGGGACTGTCCTGTGAACATG 6419

Qy   6423 CTGGGCTATGGCGAGACGTGCGCCTTTGCTCGCGTCAGACACCCCGAAGGTGGTACCATTC 6482
           |||| | | || | | ||||| | | |||||||||||| || |||||| |||| ||
Db   6420 CTGGGTTACGGTGAAACGTCGCGCTCCTCCCGACACCCCGAAGGTTGTGCCCCTC 6479

Qy   6483 GGGACGTCTGGGTGGCTGAGGTGGTGTTGACCCCTACCCACGTTGTGATCAGCCGAACA 6542
           ||||||||||||||| |||| ||||||||||||| |||| |||||||||||||||||
Db   6480 GGGACGTCTGGGTGGCTGAGGTGGTGACCACTACCCACCGCTGGTAATCAGGAGGACC 6539

Qy   6543 TCCGCCTACAAACTGCTGCCCAGCAAATCCTGTCGCGTGCTGTTGTGCTGCAGCCCTATTAC 6602
           ||||| |||| || ||||||||||||| |||| ||| || |||| |||||||||||||
Db   6540 TCCGCCTATAAGCTGCTGCCCAGCAAATCCTATCGGGTGCTGCTGTAGCTGCTGCAGCCCTACTAC 6599

Qy   6603 GTCGACGGCATACCCGGTCTCATGGGACGCGCCGAGCGCGCCTGCATGGTCTATGGC 6662
           |||||||||| || |||||||||||||||||| |||| | | ||| ||||| |||||
Db   6600 GTCGACGGCATTCCGGTCTCATGGGACGCGACGCCGCTCGTGCGCCCATGGTCTATGGC 6659

Qy   6663 CCTGGGCAAAGTGTCACCATTGACGGGAACGTCTACACCCTTCCGCATCAAACTGCGGCTT 6722
           ||||||||||||||||||||| |||||||||||| || |||| |||||||||||||| |||
Db   6660 CCTGGGCAAAGTGTTACCATTGACGGGAACGTCTACACCCTTGCCTCATCAAACTGCGAGCTC 6719

Qy   6723 AGGAATGTGGCGCCCTCTGAGGTGTCATCCGAGGTGTCATTGACACATTGGGACGGAGACT 6782
           ||||||||||||| || ||||| | |||||| |||| |||||||||||||||||||||||
Db   6720 AGGAATGTGGCACCCTCTGAGGTTTCATTCCGAGGTGTCATTGACACATTGGGACGGAGACT 6779

Qy   6783 GAAGACTCAGAACTGACTGAGGCCGAGCGCCTGCCCCGGGGCGCTTCCAGCGCTTCAGGCTATC 6842
           |||||||||||||||||||||||| || ||| | | |||| |||||||||||| | || | ||
Db   6780 GAAGACTCAGAACTGACTGAGGGCGAGCGCCGATCTCGCGCCGCGCTGCTCTTCCAGCGGATC 6839

Qy   6843 GAGAATGCTGCGAGAATTCTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTACA 6902
           |||||||||||||||||||| ||||| |||| ||||||| ||| ||||||||||||||||
Db   6840 GAGAATGCTGCGAGGATTCTGAACCGCACAGCATGTCATCATGGAGGACTGCAGTACA 6899

Qy   6903 CCCTCTCTTGTGGGAGTAGCCGAGATGCCGTGTGTGGGGAGAAGACATACCCCGCACT 6962
           |||||||| ||||||||||| |||| |||| ||||| |||||||| |||||| |||
Db   6900 CCCTCTCTTGTGGTAGCCGAGATGCCGTATGGGGAGAAGAAGACACAATCCCCGTACT 6959

Qy   6963 CCATCGCCAGCACTTATCTCGGTTACTGGTTACTGAGAGCAGCCAGATGAGAAGAGGAGTACCA 7022
           |||||||| || ||||||||| ||||||||||||||||||| |||||| | |||||||||
Db   6960 CCATCGCCAGCACTTATCTCGGTTACTGGTTACTGGGAGAGCAGCTGTTGGGAAGAAGAGTACCA 7019

Qy   7023 TCTTCCTCCAGGAGGAGGGGATACCCCGTCATCCGAGGTCATCCAAGAGTCCGAG 7082
           ||| ||||||||| | || ||||||| ||||||||||||| |||| |||||||||
Db   7020 TCCTCCTCCAGGAGGGGGGAAAGGTCATCAGAGGTCATCCAAGAGTCCGAG 7079

Qy   7083 ACAGCCGAAGGGGAGGGAAAGCGTCTTCAACGTGCTCTTTCCGTACTAAAAAGCCTTGTTT 7142
           |||| |||||||||| ||||||| ||||||| || |||||||| | ||||||| ||| |
Db   7080 ACAGCAGCGAAGGGGAGGGGAAAGTGTCTTCAACGTGCTCTTTCCGTATTAAAAGCCTTATTT 7139

Qy   7143 CCACAGAGCGATGCCACAGAAAGCTTACCGTTAAGATGTCATCGTGTTGCAGAAGAGC 7202
           |||||||| |||| || |||||||||||||| ||||||| |||||||||||||||||||
Db   7140 CCACAGAGCGACGACCAGAAAGCTTACCGTCAAGATGTCGTGCGTTGCAGAAAAGAGC 7199

Qy   7203 GTAACACGCTCTTTTCATTGGATTGAGGCGTCGCTGCTGCCAAGCCTTGTGTGAGATG 7262
           || || | | | |||||| ||||||| ||||||||| |||||||| ||| ||||||
Db   7200 GTCACGCGCTTTTTCTCATTGGGTTGACGTTGCTCCGCGTGTTGCCAAGCCTTGTGTGAGATG 7259

Qy   7263 GAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCGCACTCCGCTTGAATTGCAGGTT 7322
           |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   7260 GAAATCCAGAACCATACAGCCTATTGTGACCAGGTGCGCACTCCGCTTGAATTGCAGGTT

```
Qy  8403  CCTTCGTATCATGCATCACTGGACACGGCCCCCTTTCTGCTCCACTTGGCTAGCTGAGTGC  8462
          || |  ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  8400  CCCTCATATCATGCATCATTGGACACGGCCCCCTTCTGCTCCACTTGGCTGCTGAGTGC  8459

Qy  8463  AATGCAGATGGGAAACGCCATTCTTCTGCTGACCACGGACTTTCCGGAGCCCCTCGCTCGC  8522
          |||||||||  |||||||||||||||||| ||| |||||||||| |||||||||||||||||
Db  8460  AATGCAGATGGGAACGCCATTCTTCCTGACCACGGACTTCCGGAGCCCGCTCGCTCGC  8519

Qy  8523  ATGTCGGAGCGAGTACAGTGACCCAATGGCTTCGGCCATCGGTTACATCCTCCTATACCCT  8582
          ||||||| |||| ||||| |||||||||||||||||||||| |||||||||| || |||
Db  8520  ATGTCGGAGTGAGTATAGTGACCCGATGGCTTCGGCGATCGGTTACATCCTCCTTATCCT  8579

Qy  8583  TGGCATCCTATCACACGGTGGGTCATCATCCCTCACGTGCTCACCTGGCGCTTAGGGGT  8642
          |||||| || ||||||||||||||||| ||||||||| || ||| ||| || || |||||
Db  8580  TGGCACCCCATCACACGGTGGGTCATCATCCCTCATGTGCTAACGTGCGCATTCAGGGGT  8639

Qy  8643  GGTGGCACACCGTCTGATCCTGTGTGGTGCCAGTACATGGTAATTACTACAAGTTTCCA  8702
          ||    |||||||||||||||||||  |||||||||||| |||| |||||||||||||||
Db  8640  GGAGGCACACCGTCTGATCCGGTTTGGTGCCAGTGCATGGTAACTACTACAAGTTTTCCA  8699

Qy  8703  CTGGACAAAACTGCCTAACATCATCGTGGCCCTCCACGGACCAGCAGCGTTGAGGGTTACC  8762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8700  CTGGACAAAACTGCCTAACATCATCGTGGCCCTCCACGGACCAGCAGCGTTGAGGGTTACC  8759

Qy  8763  GCAGACACAACTAGACAAAAATGGAGGTGGCAGGTGCTGGCGACCTCAAGCTCCCT  8822
          |||||||||||| |||||||||||||||||||||||||| || ||||||||||||||
Db  8760  GCAGACACAACTAAAACAAAGATGGAGGTCTGAGCGACCTGGTAAGTTCTGAGCGACCTCAAGCTCCCT  8819

Qy  8823  GGGCTAGCAGTCCACCGGAAGAAGGCCGGGGCATTGCGAACGCGTATGCTCCGGTCGCGGC  8882
          || | |||||||| ||||||||||||||| |||||||||||||||||| |||| ||||||||
Db  8820  GGCTTAGCAGTCCACCGGAAGAAGGCCGGGGCGTTGCGAACACGCATGCTCCCGCTCCGCGGC  8879

Qy  8883  GGTTGGGCTGAGTTGGCTAGGGGCTGTTGTGGCGGCCTTCCCCGCTCCCCCTCCG  8942
          |||||||||||||||||||||  ||||||| |||||||||||||||||||| || |
Db  8880  GGTTGGGCTGAGTTGGCTAGGGGCTGTTGTGTGGCGGCCTACGGCTTCCTCCCCCCT  8939

Qy  8943  GAGATTGCTGGTATCCCCGGGGTTCCCCCTCTATATGGGGGGTGGTTCAT  9002
          ||||||||||||||||||||||||||||||||  |||||| ||| || ||
Db  8940  GAGATTGCTGGTATCCCCGGGGTTCCCCTCTATATGGGGGGTGGTACAT  8999

Qy  9003  CAATTGGATTTCACAAGCCAGAGAGAGTCGCTCGCCGCGGGTCTCCCCGCTGGGTAAAAAGGG  9062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9000  CAATTGGATTTCACAAGCCAGAGAGAGTCGCTCGCCGCGGGTCTCCCCGCTGGGTAAAAAGGG  9059

Qy  9063  ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGCAAGGTCCGGTGACTGATC  9122
          ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  9060  ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGCAAGGTCTGGTGACTGATC  9119

Qy  9123  ATCACTGAGGAGTTCCCGCGTCTCCCCCAGGGGTCTCCCCGCTGGGTAAAAAGGG  9182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9120  ATCACCGGAGGAGTTCCCGCGTCTCCCCAGGGGTCTCCCCGCTGGGTAAAAAGGG  9179

Qy  9183  CCCGGGCCTTGGGAGGCAGCATGGTGGTTACTAACCCCCTGGACAGGGTCAAAGCCTGATGGTGC  9242
          |||||||| ||||||||||||||||||||||| |||| || |||||||||||||||||||||
Db  9180  CCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCTGGACAGGGTCAAAGCCTGATGGTGC  9239

Qy  9243  TAATGCACTGCCACTTCGGTGGCCGGGTCCGGCTCCTACCTTATAGCGTAATCCGTGACTACGGGC  9302
          |||||||||||||||||||||||||||||||||||| || |||||||| ||||||||||||||
Db  9240  TAATGCACTGCCACTTCGGTGGCCGGGTCCGGCTCCTACCTTATAGCGTAATCCGTGACTACGGGC  9299

Qy  9303  TGCTCGCAGAGCCCTCCCCCGATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC  9362
          ||| |||||||||||||||||||| |||| ||||||||||||||||||||||||||||||
Db  9300  TGCTCGCAGAGCCCTCCCCCGATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC  9359

Qy  9363  GGTAAGAGCTCGGCCCCAAAGGCCCGGGTTCTACT  9395
          || ||||||||||||||||| |||||||||||||||
Db  9360  GGGAAGAGCTCGGCCCCGAAGGCCCGGGTTCTACT  9392
```

```
XX
AC   AAV82093;
XX
DT   29-MAR-1999  (first entry)
XX
DE   Hepatitis G virus PNF 2161 variant cDNA.
XX
KW   HGV; hepatitis; diagnosis; therapy; vaccine; ds.
XX
OS   Hepatitis G virus variant PNF 2161.
XX
FH   Key             Location/Qualifiers
FT   CDS             459..9080
FT                   /*tag= a
XX
PN   US5849532-A.
XX
PD   15-DEC-1998.
XX
PF   06-JUN-1995;  95US-0464134.
XX
PR   19-MAY-1995;  95US-0444733.
PR   20-MAY-1994;  94US-0246985.
PR   03-AUG-1994;  94US-0285543.
PR   03-AUG-1994;  94US-0285558.
PR   03-AUG-1994;  94US-0285561.
PR   26-OCT-1994;  94US-0329729.
PR   23-NOV-1994;  94US-0344271.
PR   16-DEC-1994;  94US-0357509.
PR   15-FEB-1995;  95US-0389886.
PR   06-JUN-1995;  95US-0464134.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fry KE, Kim JP, Linnen JM, Wages J, Young LM;
XX
DR   WPI; 1999-069731/06.
DR   P-PSDB; AAW89452.
XX
PT   Vector containing hepatitis G virus nucleic acid - and transformed
PT   cells for producing recombinant HGV polypeptide
XX
PS   Claim 1; Column 99-118; 204pp; English.
XX
CC   This is a consensus sequence of variant PNF 2161 of a newly
CC   discovered non-A/non-B/non-C/non-D/non-E hepatitis-associated
CC   viral agent, designated hepatitis G virus (HGV). The sequence was
CC   deduced from partial clone 470-20-1 (see AAV82094), which was
CC   obtained by immunoscreening a recombinant library constructed from
CC   patient PNF2161 serum cDNA, and from overlapping extension clones
CC   (see AAV82113-32). A vector containing an HGV nucleic acid composed
CC   of this 9392 bp sequence linked to a control sequence and encoding a
CC   product at least 10 amino acids in length is claimed.  Also claimed
CC   are a cell transformed with the vector (especially E. coli where the
CC   vector is phage lambda, or a Spodoptera frugiperda cell where the
CC   vector is a baculovirus transfer vector), and a method of producing
CC   HGV polypeptides (see AAW89452) by culturing such cells. HGV is
CC   characterised by: (i) producing elevated serum alanine
CC   aminotransferase levels in infected primates; (ii) its serological
CC   distinction from hepatitis A, B, C, D and E viruses; (iii)
CC   membership of the family Flaviviridae; and (iv) a viral genome
CC   having a region that is selectively hybridisable with the 470-20-1
CC   clone sequence.  The recombinant HGV polypeptides can be used as
CC   antigens for diagnosis of HGV infections, in vaccines and for
CC   antibody production.  Methods are presented for the nucleic acid-
CC   based detection of HGV in samples and for the isolation of further
CC   HGV genomic sequences.
XX
SQ   Sequence 9392 BP; 1694 A; 2551 C; 2998 G; 2148 T; 1 other;
```

```
Query Match             84.49%;  Score 7979;  DB 20;  Length 9392;
Best Local Similarity   90.78%;  Pred. No. 0;
Matches 8515;  Conservative 1;  Mismatches 876;  Indels 1;  Gaps 1;
```

```
RESULT 6
AAV82093
ID   AAV82093 standard; cDNA; 9392 BP.
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Qy      3 ACGTGGGGGGGTTGATCCCCCCCCCCGGCACTGGGTGCAAGCCCCATAAACCGAGCCT    62
          |||||||||  |||||||||| |||||||||||||||||||| ||||||||||  |||
Db      1 ACGTGGGGGAGTTGATCCCCCCCCCGGCACTGGGTGCAAGCCCCAGAAACCGACGCCT    60

Qy     63 ATCTAAGTAGACGCCAATGACTCGGCCGACCGACGGTCGTGGTGGATGG           122
          ||||||||||||| |||||| |||||||||||||||||||||||||||||
Db     61 ATCTAAGTAGACGCCAATGACTCGGCCGACCGACGGTCGTGGTGGATGG           120

Qy    123 GTGGTGACAGGGTTGGTAGGTCGTAAATCCCGGTCATCCTGGTAGCCACTATAGGTGGT   182
          ||  ||||||||||||||||||||||||| |||||||| |||||||||||||||||||
Db    121 GTGATGACAGGGTTGGTAGGTCGTAAATCCCGGTCACCTTGGTAGCCACTATAGGTGGT   180

Qy    183 CTTAAGAGAAGGTCAAGACTCCTCTGTGCCTGCGCGGCGAGACCGGCCACCGGTCCACAGGT   242
          |||||||||||||  ||||   |||||||||| ||||| ||||||||||||||||||||
Db    181 CTTAAGAGAAGGTTAAGAATTCCTCTGTGCCTGCGCGGCGAGACCGGCCACGCGTCCACAGGT   240

Qy    243 GCTGGCCTACCGGTGTGAATAAGGGCCCGACGTCAGGCTCGTAAACCGAGCCCGT       302
          |||||||||||| |||  ||||| ||||||||||||||||| |||||||||||||
Db    241 GTTGGCCCTACCGGTGGGAATAAGGGCCCGACGTCAGGCTCGTAAACCGAGCCCGT      300

Qy    303 CACCCACCTGGGCAAAACGAGCGCCCACGTACGGTCCACGTGCCCTTCAATGTCTCTCTTG   362
          ||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||
Db    301 TACCCACCTGGGCAAAACGAGCGCCCACGTACGGTCCACGTGCCCTTCAATGTCTCTCTTG   360

Qy    363 ACAAATAGGTTTATCCGCGAGTTGACAAGGACCAGTGGGGCCGGGGGTTATGGGGAAG   422
          ||||||||||| ||| |||||||||||||| ||||||||||||||||||||
Db    361 ACCAATAGGCGTAGCCGCGAGTTGACAAGGACCAGTGGGGCCGGGGGCT-TGGAGAGG   419

Qy    423 GACCCCAAACCCTGCCCTTCCCGGTGGGCCCGGGAAATGCATGGGGCACCCAGCTCCGCG   482
          |||||| || | |||||| ||||||||||||||||||||||||| ||||||||||||||
Db    420 GACTCCAAGTCCCGCCCTTCCCGGTGGGCCCGGGAAATGCATGGGGCACCCAGCTCCGCG   479

Qy    483 GCGGCCTGCAGCCGCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGTGGCATTTCTCTT   542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GCGGCCTGCAGCCGCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGTGGCATTTCTCTT   539

Qy    543 TTCTATACCATCATGGACAGTCCTTCCTTCGTGGTTGAGGCCCGGCCATTCTG       602
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    540 TTCTATACCATCATGGACAGTCCTTCCTTCGTGGTTGAGGCCCGGCCATTCTG      599

Qy    603 GCCCCGGCCACCCAGCCGCCGCTGTCTGCGAGCCAATGGGCAATATTCCTCACAAATTGCTGTGCC   662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    600 GCCCCGGCCACCCAGCCGCCGCTGTCTGCGAGCCAATGGGCAATATTCCTCACAAATTGTTGTGCC   659

Qy    663 CCGGAGACATCGGGTTCTGCTGGAAGGCGGATGGCCGGGTTGGTCGCCCTGGGGTGCACGGTT   722
          |||||||||||||||  |||| |||||||| ||||||||||||||||||||||||||| ||
Db    660 CCGGAGGCCATCGGGTTCTGCTGGAGGGTGATGGCCGGGTTGGTCGCCCTGGGGTGCACGATT   719

Qy    723 TGCACCGACCGTTGCTGGCCACTGTATCAGGCGGTTGGCTGCAGTAGAATGTACGGTTAAG   782
          |||| ||||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Db    720 TGCACTGACCGTGGCTGGCCACTGTATCAGGCGGTTGGCTGCAGTAGAATGTACGGTTAAAG   779

Qy    783 GCGGGCCCAGCTCGTTGGGGAACTGGGAGCCTGTACGGGGAGCCCTGTCGGCTCGGCTTAC   842
          ||||| |||| ||||||||||||||||||||||||| ||||||||||||||||||||||
Db    780 GCGGGCCCAACTCGTTGGGGAGCTGGGAGCCTGTACGGGGAGCCCTGTCGGCTCGGCTTAT   839

Qy    843 GTAGCCGGGATCCTGGGGTCTCTGGGCGGAGGTTTACTCCCGGTCCTGACAGTTGGTGTTGCG   902
          || ||||||||| |||| |||| ||| |||||||||||||||||||||||||||||||||
Db    840 GTTGGTCGGGATCCTGGGGTCTCTGGGCGGAGGTGTTCCTGACAGTGGGAGTGCGG         899

Qy    903 TTGAGGCCCGGCTCACCTGGGGTCTCACCTGAAGTGCAGTAGAAGTGTACGGTTAAG   962
          |||| |||||||| || ||||||||| ||||||||||||||||||||||||||||
Db    900 TTGACGGCACTTGGGGGTCTCACCTGAAGTGCAGTAGAAGTGTACGGTGTGAGCTAAAG   959

Qy    963 TGGGGAAGTGAGTGTTGGAGAATTTTGAATTTTGGAGATTACTGGATTTTTGGAA      1022
          ||||||| |||||||||||||| |||| |||||| ||| |||||||| ||||||
Db    960 TGGGGAAGTGAGTGTTGGAGAATGTTTGAATTTTGGAGATTTCTGGATTCTGGAA      1019

Qy   1023 TACCTTGGGGGTCGGGGGACTGAATCAGCCTGACCCCTCGTTG        1082
          |||||| || |||||||||||| ||| |||||||||||||| |||
Db   1020 TACCTTGGGGGTCGGGGGACTGAATCAGCCTGAATAAGCTGACCCCCCCTTG        1079

Qy   1083 GTTTGGGTGGCCCCATTCGTTTTGCTGAGCAACGGATTGTCATGGTTTCCTGCTGTGTG   1142
          ||||||||||||||||||||  ||||||||||||||||||||||| |||| |||||||||
Db   1080 GTTTGGGTGGCCGCATTGGTGCTGCTTGAGCAACGGATTGTCATGGTTCATGGTCTTGCTGTGTGTG   1139

Qy   1143 ACGATGGCGGGGATGGTTGCAAGGCGCCCCGGCTTCCGTTTTGGGGTCCCGGCCCCTTTGAC   1202
          ||||||||| |||||| ||||||||||| ||||||||| |||||||||||| ||||||||
Db   1140 ACGATGGCGGGGATGGTCGCAAGGCGACCCCGGCCTCCGTTTGGGGTCACGCCCCTTTGAC   1199

Qy   1203 TACGGGTTGAAGTGCAGTCATGCTCCTCTGCAGGGCTCGCGTATTCCCACTGGG        1262
          ||||||||||||||||||||||| ||||||||||| |||| || |||||||
Db   1200 TACGGGTTGACTTGGCAGACCTTGCTTGTGCAGGGCCAACGGTTTTCGACTGGG        1259

Qy   1263 GAGAGGGTGGGGATCGAGGGAATGTCACGCTTGTGTGACTGCCCACCTGG        1322
          ||||| ||  |||| |||||| || ||||| |||||||||||||||||||
Db   1260 GAGAAGGTGGGGACCGTGGGAACGTTACGGTTTACGGCTTGACTGTGACTGGCCCCCTGG        1319

Qy   1323 GTTTGGGTCCCGGCCTTTGCCAGGCGGTTGGGCGCCGACCCCATCACCCATTGGAGC   1382
          |||||||||||||||||| |||| |||||||||| |||||||||| || ||||||||
Db   1320 GTGTGGTTGCCACGCTTTTGCCAGCAATCGGCGTGGGGTGACCCCATCACTCATTATTGGAGC   1379

Qy   1383 CACGGACAAAACCAGTGCCCCCTCATCATGCCCCTTTCAATGTGTCTCTGTGTCCGTA   1442
          |||||||||| || ||||||||| |||||||| ||||| ||||| |||| |||||
Db   1380 CACGGGCAAAATCAGTGCCCCTTCATGCCCCCAGTATGTCTCTATGGTCTCTACAGTC   1439

Qy   1443 ACGTGCGTGGGGTTCCGTGTCTTGGTTGGTTGCCTCGATTCGAAGATC        1502
          | ||||||||||| ||  ||| ||| | || ||||||||| |||||||
Db   1440 ACTTGCGTGTGGGGTTCCGTTCCTCTTGGTTGGTTCCACCAGTGGTCGCGACTCGAAGATA   1499

Qy   1503 GATGTGTTGGAGTTTGGTGCGGTTGGTGGATCCTGCCAGCTGCACCATAGCCGCTCTAGGGTCA   1562
          |||||||||||| || ||||| |||| || ||||||||||||||||||||||||||  |||
Db   1500 GATGTGTGGGAGTTTAGTGCGCTGGCTCCTCGCTCTCCGAGTGGGGTGCCACCATAGCCGCACTGGATCA   1559

Qy   1563 TCGGATGCGACACGGTGGTTGAGCTGCTCCGAGTGGGACCTGCTAACGTGTATT   1622
          | |||||||| ||||||  |||||||| ||||||||| | | ||||||||||||
Db   1560 TCGGATCGCGACACGGTGGCTGGCTCGCTCGAGTGGGAATCCCGTGCGTGACGTGTGTT   1619

Qy   1623 CTGGACCCGTCGGCCTGCTTCATGTGGCACCTGTGTCGCGGGACTGCTGGCCCGAAACCGGG   1682
          ||||||||||||||||||| |||| | | ||||||||||| ||||| |||||||||| |||
Db   1620 CTGGACCCGTCGGCCTGCTTCTCGTGTGCGCCGCCCTGTGTGAGGGCGTCTGCCCGAGACCGGG   1679

Qy   1683 TCGGTTAGATTCCTTCCATCCGTGCACCTCGGCCTCGGTCGCACAAAGGACTTGAA   1742
          ||||||| ||| ||| | ||| |||| |||| |||||  || ||||||||||||||
Db   1680 TCGGTTAGGTTCCCATTCCATCCGTGCGCCGCTCGGTGGCTCGCACAAAGGACTTGAA   1739

Qy   1743 GCTGTGCCCTTCGTCAACAGGACGAACTCCCTGGGCCCCCTGGGCCAACCAG   1802
          ||||||||||| ||||||||||| |||||||||| |||| |||||||||||
Db   1740 GCTGTGCCCTTCGTCAACAGGACGAACTCCCTTAGGGCGGTCTCCTGGGCCAACCAG   1799

Qy   1803 GGGAGGAGGCAACCCGTGCGGACTCGCCGGAGCTGGGGTTTGGGTCTTCCACCATGACCAAGATC   1862
          ||  ||||||||||||||| ||||| |||| ||| |||||||| |||| |||||||||| |||
Db   1800 GCCGAGGCGACCCGGTGCGCGCCCGTTGGGTTTTGGGTCCTCCATGACCAGGATC   1859

Qy   1863 CGGGATTCCTGCATTTGGTGAAAATGTCCCACCAGCCATAGAGCCTTGGGAACG   1922
          |  ||||| ||||| |||||||||||| |||||||| ||||| ||| |||||||
Db   1860 CGAGATACCCGTACATCTGTGAGTGTCCACCACCAGCCATTGAGCCTCCCACCGGGACG   1919

Qy   1923 TTCGGGTTCTTCCCGGATCCTGGGGGTCCTGACAGTTGGTGTTGCGG   1982
          || ||||| |||||||| ||||| |||| |||||| || ||||||||
Db   1920 TTTGGGTTCTTCCCGGGACCGCGCCTCTCAACAACTGCATCGATGACAGGTGCGG   1979

Qy   1983 TCTGAGGCATTGGGCGGCTCGGAGCTGGGGGTTCGCAGG        2042
          | ||||| ||||||||||||| |||||||| |||||||
Db   1980 TCCGAGGCACTTGGGCGGGCTGCCCCGGGGGGTTCTCAGG        2039

Qy   2043 TGTTCGGAGCTGATGGAGACGGCCGAAATCCGGTTGCCCGGGGTACGCATGGCTGTCTCT   2102
          || ||||||| |||| |||||||||||| ||| ||||||||||| |||| |||| ||||
Db   2040 TGTTCGGAAGCTGATGGGAAGCCCAAATCCGGTTGTCTCTATGACCCCTGGGCGCAGG   2099

Qy   2103 GGTAGACCTGACGGGTTCATCACGCCTGAATCAGCCTGACCCCTCGTTG           2162
          || ||||| |||||||||||||| ||||||||||||||| ||||||  ||
Db   2100 GGCAGGCCTGACGGGTTCATGGGTTTATACATGTCCAGGGTCACTTGCAGGAGGTGGATGCCGGCGGCAAC   2159

Qy   2163 TTCATCCCCTCCTCCACGCTGGTTGCTCTTGGATTTGTATTTGTCTCCTCTCATCTGATG     2222
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Db  2160  |||||| ||  ||||||||||||||||||  |||||||||  ||  |||||||||
          TTCATCCCGCCCCCGCTGGTTGCTCTTGGACTTGATCTTGCCTGTTATTGTTCCTGTTATACCTGATG  2219

Qy  2223  AAGCTGGCTGAGGCACGGTTGGTCCCGTTGATCTTGCTTCGTGCTGTGGTGTGGGTGAAC  2282
          |||||||||||||||||||||||||||||  ||||  ||||| ||||| ||||||||||||
Db  2220  AAGCTGGCTGAGGCACGGTTGGTCCCGCTGGTGGTCCCGCTGCTGCCGCTATGGGTGGAAC  2279

Qy  2283  CAGTTGGGCGGTTCTAGGACTGCCCGGTGTGACGCTGCCGTGGCCGGTGAAGTTTTTGCG  2342
          ||||| ||||||||| ||||||||||||||||||||| ||  |||||||||||  |||||
Db  2280  CAGCTGGCAGTCCTAGGGCGTGTGGAAGCGCCGTGGGAGCGTGAGGTCGAGGTCTTCGCG  2339

Qy  2343  GGCCCTGCTGTCATGGTGTTGGGCCCTTCCCACTGTCAGTATGATGATACTAGGTCTAGCA  2402
          |||||||| ||| |||| ||||||||||  ||||||||||||| ||| ||||||||| |
Db  2340  GGCCCTGCCCGTCCCGGTGTCTGGGACTGCCCGGTCGTCAGTATGATGATATTGGGTTGGCA  2399

Qy  2403  AACCTGGTGTGTACTTTCGGTGGATGGGCCCTCAGCGGCCTCAGCTTCCTCGTTGTGTGG  2462
          |||||||||||||  |||||||||||||| ||||||||||| |||||||||||||||||
Db  2400  AACCTGGTGCGTATTTTAGATGTGGTGGGACCCCAACGCCTGATGTTCCTCGTTGTGTGG  2459

Qy  2463  AAGCTCGCTCGGGGAGCTTTCCCCTGGCACTTTTGATGGGGATTTCGGCGACCCCGCGGG  2522
          ||||||||||||||||||| ||||||||||||| ||||||| || |||||||||||||||
Db  2460  AAGCTCGCTCGGGGAGCTTTCCCCTGGCACTTTGATGGGGATTTCGGCGACCCCGCGGG  2519

Qy  2523  CGCACCTCTGTCTCGGGGCCGAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCG  2582
          |||||||  ||||||||||||||||||||||||||| |||||| |||||||||||||||
Db  2520  CGCACCTCAGTGCTCGGGGCCGAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCG  2579

Qy  2583  GTGTTGGGCTGGGTGGTGGCCAGCGCTGGTGCCTTGGGCCATAGCGCCTCCTGAGCTCAATG  2642
          ||||||||||||||||||||||||||||| |||| |||||||||||||||||||||| |||
Db  2580  GTGTTGGGCTGGGTGGTGGCCAGTGTGGTGGCCAGTGTGTGGCCATTGGGCTCCTGAGCTCGATG  2639

Qy  2643  AGGCAGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGTGTACCAG  2702
          |||||||||||||||| |||||||||||||||| |||||| |||||||| ||||||||||
Db  2640  AGGCAGGGGGTGGAGGCACAAAGCCGTGATCTATAGGACGTGGTAAGGGTGTACCAG  2699

Qy  2703  GCTGTGCCAGAGGGTGGTGCCGAGCCCCCCGGGGAGGGGGCCTCCTACCAAGCTTCTG  2762
          ||  | |||||||||| ||||||||||||||||||||||||||||| ||||||||||||
Db  2700  GCAATCCGTCAAAGGTGGTGAGGAGCGTGTCCGTCTACATCTGTGTGATGGTGGTGGTT  2759

Qy  2763  ACGTTCGCGTTCGTCCTCCTCCGCCGCTGTTCGACGCACTGGACCTCGGGACGACTCCTG  2822
          || |||||||||||||||||||||||||||||| ||||| |||| ||||||||||||| |
Db  2760  ACCTTTGGGTCGGTGTCCTCGTCTTCGGCTGGCTGGCCAGATCGTGTGATGAATGGTCGTGTTGTT  2819

Qy  2823  GCCTTGGTTCCTCCTCTTCGCCGTGCTGTTCGACGCACTGGCACTGGAGGAGCTCCTG  2882
          ||||||||||||||||||| ||||||||||| |||||||||||||| |||||||||||
Db  2820  GCCTTGGTTCCTCCTCTTCCTTCGCCGTGTGGGATTGGGGCTTGGATTGGGGAGATCTTG  2879

Qy  2883  GTCTCCCGGGCCCTCGTTACGGCACCGACTGGCACGGGTGGTTGAGTGCTGTGATGGCGGC  2942
          ||  |||||||||||||  |||||||||||||| |||||||||||||||||||||||||||
Db  2880  GTGTCCCGGGCCCTCGTTGGCTGTTCGGCGTTCGGCGTGGTTGAGTGCGTGTGATGGCGGGT  2939

Qy  2943  GAGAAGGCCACCACCATCCAGCTGTCTCCAAGATGTGCGCAAGAGGGGCTCACCTGTTT  3002
          ||||||||||||||||||||||||||||||||| ||| |||| |||||||||||| |||
Db  2940  GAGAAGGCCACCACCAACCGTCCGGTGTTTACCCGCGCCGTCCGTTGATGGGGAGCTTATTTGTTC  2999

Qy  3003  GACCACATGGCTCTTTCTCGCGCGTCAAGGAGCGCTTGGAATGGACGCGGCT  3062
          |||||| |||||||||||||||||||||||||||||||||||||||||||||
Db  3000  GATCATATGGGCTCTTTTGCCTCGCGCGTCAAGGAGCGCTTGGAATGGGACGCAGCT  3059

Qy  3063  TTGGAGCCCTTGCATTCACTCACTAGGACGGACTGTCGCCATCATCAGAGATCGCGGAGGACC  3122
          || ||  |||||||||||| ||||||||||  |||||||||||||||||||| ||||||||||
Db  3060  CTTGAACCTTCGTGTTCATTCAACCTTCGTGCCTGGTTACCCGTCGGCGTCGCCATCATACGGGATGCCGCGGAGGACT  3119

Qy  3123  CTGTCCTGCGGACAGTGCCGGTTTACCCGGTCATGGGGGCGTAGCACCGGCCGGCGTGATGAGGTT  3182
          ||||||||||||||| |||| |||||||||| |||||||||||||||||| |||||||||| |||||
Db  3120  TTGTCCTGCGGGCAGTGCTGGTTTACCCGGTGCATGGGTTGCGCGCCGCCGTTGGTTGATGAGGTT  3179

Qy  3183  CTCATCGGCGTCTTTCTCGCGCGTCAGGATGTGAATCATTTGTCCCGACTGCACCA  3242
          |||||||||||||||||||||||||||||| |||||||||||| |||||||||| |
Db  3180  CTCATCGGCGATGTGCTTCCAGGAGTGAATCATTTGTCCTGTTGTCCACCGCGCCT  3239

Qy  3243  GTTGTCATCCCGCCGGTCGCGGAAAGGGCTTCCTGGGGTCACGAAGGCAGCCTTGACAGGT  3302
          ||||| |||||||| ||||||  ||||||||||||||||| |||||||||||||||||||
Db  3240  GTTGTCATCCCGACGGTGCGGAAAGGGCTTCTTGGGGGTCACAAAGGCTGCCTTGACAGGT  3299

Qy  3303  AGGGATCCTGACTTACATCCAGGAGACGTCATGGTGGTTGGGGACGGCTACGTCACGAAGC  3362
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  3300  CGGGATCCTGACTTACATCCCAGGGGAACGTCATGGGTTGGGGACGGCTACGTCGCGAAGC  3359

Qy  3363  ATGGGCACATGTCTGAATGGCCTGCTGTTCACAACTTCCATGGGGCTTCATCCCGAACC  3422
          |||| ||||| ||  |||||||||| ||||||||||| |||||||||||||||||||||
Db  3360  ATGGGAACATGTCAGATCTGAACGGCCTGCTGTTCACGACCTTCATGGGGCTTCATCCCGAACC  3419

Qy  3423  ATCGCCACGCCCGTGGGGCGCCCTTAATCCCAGGTGGTGTCAGCGAGTGATGACGTCACG  3482
          ||||||||||||||||||||||||||||  |||||||||  |||||||||||||||||||
Db  3420  ATCGCCACCACCACCGTGGGGCGCCCTTAATCCCAGATGGTCAGCCAGTGATGATGTCACG  3479

Qy  3483  GTGTACCGGCTTCCAGATGGGGCAACTTCGTTGACCGCCCTGCACTTGCCAGGCGGAGTCC  3542
          ||| | |||| |||||||| |||||||||| ||||| |||||| |||| |||||||||||
Db  3480  GTGTATCCACTCCCCGATGGGGCTACTTCGTTAACACCTTGTACTTGCCAGGCTGAGTCC  3539

Qy  3543  TGTTGGGTTATTAGATCCGACGGGGCTTGTCCATGGCTTGACGAGCAGGGGACAAGGTT  3602
          ||||| ||| ||||||||| |||||||||||||||||||||| ||||||||||||||||
Db  3540  TGTTGGGTCATCAGATCCGACGGGGGATTTCGGCATGGCTTGAGCAAGGGGACAAGGTG  3599

Qy  3603  GAGCTGGATGTGGCCATGGAGGTCTCTGACTTCCGTTGGTTCGTCGTCTGCTGTTCACCGGTCCTT  3662
          |||||||||||||| |||||||||||||| ||||| ||||||||||||||| ||||||||||| ||
Db  3600  GAGCTGGATGTGGCCATGGAGGTCTCTGACTTCCGTGGTTCGTCGTCTGCTGCTATTATGCCTCCTA  3659

Qy  3663  TGCGACAAAGGCCACCGCAGTAAGAATCGTCGTGTCAGTGCTTCGGCCGGCCAGGGTT  3722
          || ||| ||||||||||||||||| |||| | || |||||||| |||||||||||| |
Db  3660  TGTGACGAAGGGCACCGCAGTAGGAATTGCTCGTCGTGTCTGTGCTTCACTCCCGGTGGTAGGGTC  3719

Qy  3723  ACTGCGCGCGATTCACTAGGCCGTCAAGACTGTCAAGACTACCACAGATGCCAACAGACTACCACA  3782
          || ||||||||  |||||||| |||| |||| |||||| ||||| || ||||||||||||||||
Db  3720  ACCGCGCACGGTTCACTAGGCCGTGACGATGCCAACAGATGCCAAGATGCCAAACCACTACT  3779

Qy  3783  GAACCCCTCCGGTGCCGGCAAAAGGAGTTTTCAAGGAGGCCCCGTTGTTTATGCCTACG  3842
          ||| ||||||||||||||||||||||||| ||||||| | || ||||||||||||||||
Db  3780  GAACCCCTCCGGTGCGGCGCGGCCCAAAGGAGTTTTCAAAGAGGGCCCGTTGTTTATGCCTACG  3839

Qy  3843  GGGGCGGGAAAGAGCACCCCGTACCGTGAGGGCGGATGGTGTGGTG  3902
          ||||| |||||||||||||||||||||||||| ||||||||||||||
Db  3840  GGAGCGGGAAAGAGCAGCACTCCGTACCGTGAGGGCACGATAACATGGGCACAAGGTCTTA  3899

Qy  3903  ATCTTGAACCCGTACCGTCGGTAGCTGGCCACTGGACCGCTGGAGGGCCCTGAGGAGGTG  3962
          ||||||||||||||   ||||||||||||||||||| || |||||||||||||||||||
Db  3900  ATCTTGAACCCCCAGTATTCAACCTATGGAGGTTTTGGCCAACCAGCAGATGGGCTGGCCG  3959

Qy  3963  GGGAAACACCCCAGTATTACTGTGGCCATGAACCACTGCTTTCACAAGGATCACTGAC  4022
          |||||||||||||||||| ||||||||||||||||||||| || ||||||||||||||
Db  3960  GGTAAACATCCAAGTATATGTGGGCATGCATGATACAACTGCTTCACAAGGATCACTGAC  4019

Qy  4023  TCGCCCCTTACGTATTCCACTTACGGAAGTTTTTGGCCAACCCCTAGGCAGAGATGCTGAGG  4082
          ||||||  ||||||||||||||||| ||||||||| ||||||||||||||||| ||||||||
Db  4020  TCCCCCCTGACGTATTCAACCTATGGAGGTTTTTGGCCAACCCCTAGGCAGATGCTACGG  4079

Qy  4083  GGTGTGTCGGTGGTCATTGTTGACGAGTCATGACTCAACTGTGTTGTTGGGCG  4142
          |||||||||||||||| |||  ||||||||||| ||||||||| ||||||||||
Db  4080  GGCGTTTCGGTGGTCATTTGTCATTTGTGATGGGCATGGAATGCCACAGTCTGTTAGGC  4139

Qy  4143  ATTGGGCGTGTCAGGGAGCTGGCGCGGAGGATGTGAATTGGTGCTCTACGCCACT  4202
          ||||  |||| | ||| |||||| ||||||| |||| |||| |||| | |||||||
Db  4140  ATTGGGAGAGTCCGGGAGCTGGCGCGCCGATGACCCTAGTGCTCTACGCCACC  4199

Qy  4203  GCCACCCTCCCGGATCCCCGATGACCCGCCAGCACCGTCATTGAGACAAAACTGGAC  4262
          ||  |||||||| |||||||||| || |||||||||| ||||||||| ||||||||
Db  4200  GCTACACCCTCCCGGATCCCCGATCCCCTATGACGCAGCACCCTTCCATAATTGAGACAAAATTGGAC  4259

Qy  4263  GTGGGAGAGATCCCCTTCTCATTGTGACGAGTCATGGCATGCGGACCGGAAGG  4322
          |||||||| |||||||| |||||||||| |||| ||||| ||||||||||||
Db  4260  GTGGGAGAGATTCCCTTTATGGGCATGGAATGAATACCCCGAGCGATGGAGCGGAAGG  4319

Qy  4323  CATCTCGTATTCTGCCACTCCAAGGCCGTTTCGGCT  4382
          |||||||||| ||||||  ||||||||||||||||
Db  4320  CACCTCGTGTTCTGCCATTCTAAGGCTGAGTGAGTGCGAGCGCGTCGCAGCGCGCCCTTGCTGCCAGTTCTCGCGCT  4379
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Qy   4383 AGGGGGTAAATGCCATCGGCCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATGGA 4442
          ||||||||||| ||||||| |||||||| |||||||| |||||||||||||||| |||||
Db   4380 AGGGGGTCAATGCCATTGCCTATTATAGGGGTAAAGACAGTTCTATCATCAAGGATGGG 4439

Qy   4443 GACCTGGTGGTGTGTGCTACAGACGCACTATCCACTGGGTACACTGGAACTTCGATTCT 4502
          |||||||||||| ||||||||||||| || |||||||||||||||||| |||||||  ||
Db   4440 GACCTGGTGGTCTGTGTGCTACAGACGCGCTTTCCACTGGGTACACTGGGAACTTCGACTCC 4499

Qy   4503 GTCACCCATTGTGGGTTAGTGGTGGAGGAGTCGTCGAGGTCGACCCTTGATCCCACCATT 4562
          |||||||||||  |||||  ||||  ||||||||||||||||||||||||||  |||||||
Db   4500 GTCACCGACTGTGGGATTAGTGGTGGAGGAGTCGTTGAGGTGGACCCTTGATCCCACCATT 4559

Qy   4563 ACCATCTCCTGCGCACGTTGCCCGCTCGGCTGACCGTGTCGATGCAGCGGCGGAGGACGC 4622
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   4560 ACCATCTCCTGCGCACGTTGCCCGCTCGGCTGACCGTGTCGATGCAGCGGCGGAGGACGC 4619

Qy   4623 ACGGGTAGGGGCAGGTCTGGGCGCTACTACTACGCGGGGTCGGCAAGGCCCCTGCTGGT 4682
          |||||||||||||||| |||||||||||||||||||  |||||||||| |||||  |||
Db   4620 ACGGGTAGGGGCAGGTCTGGCACGTCTACTACTACGCGGGGTCGGCAAAGCCCCTGCGGGT 4679

Qy   4683 GTGGTGCGCTCAGGTCCTGTCTCGGCGGTGGAAGCCGGTGTGACCTGGTACGGCGAATG 4742
          ||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db   4680 GTGGTGCGCTCAGGTCCTGTCTCGGCGGTGGAAGCCGGTGTGACCTGGTACGGCGAATG 4739

Qy   4743 GAACCTGACACTGACAGCAAACCTACTGAGACTTTACGACAACTGCCCTTACACCGCAGCC 4802
          ||||||||||| |||  |  |||||||||||||| |||||||||||||||||||||||||
Db   4740 GAACCTGACTTCTTGACTTTACGACAACTGCCCTTACACCGCAGCC 4799

Qy   4803 GTCCAGCTGACATTGGGGAAGCCGCGGTGTTCTTTCGGGGCTGTCCCCGTGAGCGATG 4862
          ||||||||||||  | | |||||||||||||||| |||||||||  | || |||||||
Db   4800 GTCGCGGCTGATATCGGGATAGCCGCCGTGTCCTCGCTGCTTCCTGGGCTCGGGCCATGCGGGG 4859

Qy   4863 CATCCCGGATGTTAGCTGGGCAAAAGTTCGCGGCGTCAACTGCCCTTCCTGTGGGTGTT 4922
          |||||||||| | |  |||||||||||||||||||||||||||| |||||||||||||||
Db   4860 CACCCTGATGTTCAGCTGGGCAAAAGTTCGCGGCGTCAACTGCCCTTCTGTGGGTGTT 4919

Qy   4923 CAGCGGACCATGTGCCGGATGCGGGGAACCATCTGTCTCCCGGCCATCGGATGACCCCAGTGGCA 4982
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   4920 CAGCGGACCATGTGCCGGATGCGGGGAACCATCTGTCTCCCGGCCATCGGATGACCCCAATGGGCA 4979

Qy   4983 GGTCTGAAGGGCCGAATCCTGTCCCACCTGCTCGTGAGGTGGGCAATGATTTACCATCT 5042
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   4980 GGTCTGAAGGGCCCAAATCCTGTCCCACTCCTGCTAGTGTGGGTAGTGGTGGGCAATGATTTACCATCT 5039

Qy   5043 AAAGTGGCCGGCCATCACATCGGACGACCTGGTCCGGTTCGCGGTGCGGAGGGT 5102
          |||||||||||||||||||| |||| |||||||||| |||||||||||||||
Db   5040 AAAGTGGCCGGCCACCACCATATCGGACGACCTGGTCCGGTTCGCGGTGCGGAGGGT 5099

Qy   5103 TACGTCCGCTGCGATGCGGGGACCATCTTGATGGTGGGCCTTCGCTATTGCGGGGGGCATG 5162
          |||||||||||||||||||  |  |||||||||  ||||||||||  |||||||||||||
Db   5100 TACGTCCGCTGCGACGCGGGGGTGGGTCATTGCGTGTATCGTCAGCTATCGCGGGGGGAATG 5159

Qy   5163 ATCTATGCGTCATACACCGGGTCTCTCGTGGTGGTTACAGACTGGGATGTGAAGGGGGGT 5222
          ||||||||||||||||||||||||| ||| ||||| ||||||| |||||||||||||||||
Db   5160 ATCTACGCGTCATACACCGGGTCGCTAGTGGTGGTGACTGTGTTGGGATGTGAAGGGGGGT 5219

Qy   5223 GGCAGCCCCCTTTATCGGCCATCGGAGACCACGCCCAGCCGGTTGTCGCGAGGGT 5282
          ||| ||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   5220 GGCGGCGCCCCTTTATCGGCCACCACACAGCGCCCCAGCCGGTTGTCGCGAGGGT 5279

Qy   5283 CCGGGTAGACACATGCGGGGGAGAGTCTCGCCCATCGGATGCCAACACCCTGTCGACAGAT 5342
          ||||||||| ||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   5280 CCGGGTAGACACATGCGGGGGAGAGTCTCGCCCCATCGGATGGCCCAAGACACCATGGCACAGAT 5339

Qy   5343 GCGGGTGGCGGCCATCACCGGGTCTGATTGCGATTGGCGATCATGACCCTGTCCGATCGGGGAA 5402
          ||||||||||||||||||||||| |||||||||||||||||  |  | ||||||||||||||
Db   5340 GCGGGTGGCGGCCATCCAGGTGGCTAAGACCGCCTATCATGACTCTGTCCGATCGGGGAGA 5399

Qy   5403 GTGCTGTCCTTGGCTCAAGACCGGCTAAGACGGCTACCACCAAGTGGCTT 5462
          ||||||||||||||||||||| ||| ||| | |||||||||||||||||
Db   5400 GTGTTGTCCTTGGCTCAAGACCGGGCTAAGACCGCCACAGCAACCGCCAAGTGGCTC 5459
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Qy   5463 GCTGGCTGCTACACGGGGACGCGGCCGTCCCACTGTTCAATTGTTGACAAGCTCTTC 5522
          ||||||||||| |||||||||||||||||| ||  |||||||||||||||||||||||
Db   5460 GCTGGCTGCTATACGGGGACGCGGCCGTTCCACTGTATCCATTGTTGACAAGCTCTTC 5519

Qy   5523 CCCGGGGGCTGGCGCCGGTGGTAGCGCCATTGCCACAGTGTAATAGCGTCGGCAGTGGCG 5582
          |||| ||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db   5520 CCGGAGGTGGCGGCGGTGGTGGCGCCATTGCCACAGTGCCACACGTGCGCGGCGGTGGCG 5579

Qy   5583 GCCTATGGGGCTTCTAGGAGCCCTCCATTGGTCGTGCTGCTCCTACCTCATGGGGGTTG 5642
          |||| ||||||| ||||||| |||||||||||  ||||||||||| ||||||||||||
Db   5580 GCCTACGGGGGTTCAAGGAGCCCTAGGTTGGCAGCGCCCGGCTTCCTACTATGGGGCGTGGG 5639

Qy   5643 GGCGTCGGAGGCAACGCGCCAAACCCGCTTAGCCTCCGTCTCCCTACTAGGGCGCTGGG 5702
          ||| ||||||||||||||||||||||||||||| ||| ||| |||||||||||||||||
Db   5640 GGCGTTGGAGGCAACGCCTCAGACGCGCCTGGCGTCTCGCCCCTATTGGGGGCGCTGCTGGA 5699

Qy   5703 ACCGCTCTGGCACGCCTGTCGTGGGGTTAACCATGGCGGCGCGTCATGGGAAGTGCT 5762
          |||| |||||||| |||||||||||  ||| ||||||||||||||  ||||||||||
Db   5700 ACCGCCTGGCACTCGTCGTGGGGCTTGGCCTTGACCATGGCAGTGCGGTTCATGGGGGGGCC 5759

Qy   5763 AGCGTCTCCCCCTCCTTGGTCACCATTTACTGGGGCGTGACCTGTTGACGGAATG 5822
          ||| ||||||||||| ||||||||||||||| |||| ||||||||||||||||||
Db   5760 AGTGTCTCCCCCTTGGTCACCATTTTATTTATTGGGGCCGTCCGAGGTTGGGAGGGGTTT 5819

Qy   5823 GTGAATGCGGCTAGCCTTGTCTTCGACTTTATGGGGGGAAACTATCATCAGAAGATCTG 5882
          ||  |||||||||||| ||||||||||| ||||||||||||||  ||||||||||||||
Db   5820 GTCAACGCGGCGAGCCTAGTTCTTGACTTCATGGCGGCGAAACTTTCATCAGAAGATCTG 5879

Qy   5883 TGGTATGCCATCCCAGTGCTAACCAGTCTACCACCAGCCCGGGGATCGCCCCTGGGG 5942
          |||||||||||||||||||| |||  || |||||||||||||| ||||| |||||||
Db   5880 TGGTATGCCATCCCAGTGCTACCAGCCGCCCGGGGGATCGCCCTGGGG 5939

Qy   5943 TTGGTGTGTACTCAGCTAACAACTCTGGCACTCGGTGGTGACCGGTGCTGCTGACT 6002
          ||||| | ||| ||||||| ||||||||||| ||||||||||||||| ||| ||||
Db   5940 TTGGTTTTGTATTCAGCTAACAACTCTGGCACTCGGTGGTGACCGGTGCTGCTGACT 5999

Qy   6003 ACATTGCCAAGGTCCTCATGCAATCCGTCATGTTTCAGCAGGGCGATTACTGTGAC 6062
          |   | || |||||| |||||| ||||||| |||||||||||||| | || |||||
Db   6000 ACGTTACCAAGGTCTTCATGGCGTCCTATGTCTGGGGCACCTATTGACTATTGCGAC 6059

Qy   6063 AAGGTCTCAGTTGCTCTGCGACGCTGCTTCACTCGCCACCGTGGTTGCCCTGGTCAAC 6122
          |||||||||  |||||||||| || | |||||| |||||||||||||||||||||||||
Db   6060 AAGGTCTCAGCTGCTCTGCGACCGCTGCTTCACCGCCACCGTGGTTGCCCTGGTCAAC 6119

Qy   6123 AGGGAGCCTAAGGTGGATGAGGTTCAGGTGGGACTTGTGGGAGTTGATC 6182
          ||||||||||||||||||||||||  |||| |||||| |||||||||||
Db   6120 AGGGAGCCTAAGGTGGATGAGGTACAGGTGTGGGACCTGTATGCTGTGGGACCGTGGGAGTTGATC 6179

Qy   6183 ATCGTCAAGTGCGCATGGTGATGGCCAGACTTCGGCGCCCTCGCCCGTGTCATTA 6242
          | ||||||||||||||||  || ||||| |||| |||||||||||||||||| ||
Db   6180 ATCGTCAAGTGCGCGTGGTGATGGCCAGACTTCAGGGGCCCTCGCCCCGTGTCTGTACTA 6239

Qy   6243 CCCTTATGGCACTGCGGGGAGGGGTCGGGGGAGGGGTGTTGGACGGGCCATGTGAG 6302
          ||||| ||||| || |||||||||||||||||| ||||||||||| |||| |||||
Db   6240 CCCTTGTGGCATTGCGGGGAGGGGGTGTGCGGGAGGGGTGTTGGACGGGTCATGTGAG 6299

Qy   6303 AGTCGTTGTCTTTGTGTGGCTGCCTGATCACCGGTGATGTTTTGAATGGGCAACTCAAAGAT 6362
          |||| |||| ||  |||||||||| | |||||||||  |||  | |||||||||||||||
Db   6300 AGTCGCTTGCCTTGTGTGGCTGCGCGATCACTGGTGACGTTCTGAATGGGCAACTCAAAGAA 6359

Qy   6363 CCAGTTTACTCTACCAAGCTGCAGGCAGTTATTGGATGGGACAGTCCCTGTGAACATG 6422
          ||||||||||||||||| |||||| ||  |||||||| |||| |||||||||||||||
Db   6360 CCAGTTTACTCTACCAAGCTGCCGCAGTTATTGGATGGGACTGTCCCTGTGAACATG 6419

Qy   6423 CTGGGCTATGGCGAGACGTCGCCGCTTTGCTCCTCAGACACCCGAAGTGTACCATTC 6482
          |||| | | | || ||||| ||| ||||  |||||||||||||||||| |||||||
Db   6420 CTGGGTTACGGTGAAACGTCGCCGCTCTCCTGCGGCTCCTCCGACACCCCGAAGGTTGTGCCCTTC 6479

Qy   6483 GGGACGCTGGGTGGGCTGGGTGAGGTGGTGGACCCCGTGATCAGGTGTTGATCAGGCGAACA 6542
          ||| ||||| ||| |||||||||||||| ||||| ||| |||  | ||||  |||||||||
Db   6480 GGGACGTCTGGCTGGGTGAGGTGGTGGACCACCTCCCCACCGTGGTAATCAGGAGGAGACC 6539

Qy   6543 TCCGCCTACAAACTGCTGCGGCCAGCAAATCCTGTCGCGGCTGCGTGTTGCTGAGCCCTATTAC 6602
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Left column:

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Db  6540  |||||| || |||||||||||||||||||||| |||||||||||| |||  6599
          TCCGCTATAAGCTGCTGCGCCAGCAAATCGTCTATCGGCTGCTGTGTAGCTGCCCTACTAC
Qy  6603  GTCGACGGCATACCGGTCTCATGGGACACCGGACGCGCAGCGCCTGCCATGGTCTATGGC  6662
          |||||||||||| ||||||||| ||||||||||||||||| || |||| ||||||||||||
Db  6600  GTCGACGGCATTCCGGTCTCATGGGACGCGCGGACGCTCGTGCGCGCCGGCCATGGTCTATGGC  6659

Qy  6663  CCTGGGCAAAGTGTCACCATTGACGGGGAACCTACACCCTTCCGCATCAACTGCGGCTT  6722
          |||||||||||||| ||||||||||||||||||||| ||||||||| |||||||||||||
Db  6660  CCTGGGCAAAGTGTTACCATTGACGGGGAGCGCCTACACCTTGCCATCTCATCAACTGCGGCTC  6719

Qy  6723  AGGAATGTGGCGCCCCTGAGGTGTCATCCGAGGTGTCATTGACATTGGGACGGAGACT  6782
          ||||||||| ||||||||||||| || |||||||||||||| |||||||||||||||||
Db  6720  AGGAATGTGGCACCCCTGAGGTTTCATCCGAGGTGTCCATTGACATTGGGACGGAGACT  6779

Qy  6783  GAAGACTTCAGAACTGACTGAGGCGCACCTGCCCGGGGCCTTCAGCCTCTATC  6842
          ||||||||||||||||||||||||||| || || |||| |||||||||||||
Db  6780  GAAGACTGACTGAGGCGCACCTGCCCGGGGCCTGCGCCCTGCTCTCCAAGCGATC  6839

Qy  6843  GAGAATGCTGCCAGAATTCTTGAACCTTCACATAGATGTCATCATGGAAGATTGCAGTACA  6902
          ||||||||||||||||| || ||||||| |||||||||||||||| |||||||||||||||
Db  6840  GAGAATGCTGCCAGGATTCTTGAACCTTCATCATGTCATCATGGAGGACTGCAGTACA  6899

Qy  6903  CCCTCTCTTTGTGGAGTAGCCCGAGAGATGCCTGTGTGGGAGAAGACATACCCCCGCACT  6962
          |||||||| || |||||| || |||| |||||||||||||||||| ||||||||||||||
Db  6900  CCCTCTCTTTGTGTAGTAGCCCGAGAGATGCCTGTATGGGAGAAGACATACCCCCGTACT  6959

Qy  6963  CCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCCCAGATGAGAAGACCCCGTCGGTG  7022
          |||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||||
Db  6960  CCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCTCAGATGAGAAGACCCCGTCGGTG  7019

Qy  7023  TCTTCCTCGCAGGAGGATACCCCGTCTTCTGACTCATTCGAGTCATCCAAGAGTCCGAG  7082
          || ||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||
Db  7020  TCCTCCTCGCAGGAGGATACCCCGTCTTCTCGACTCATTCGAGTCATCCAAGAGTCCGAG  7079

Qy  7083  ACAGCCGAAGGGAGGGAGGAAAGCGTCTTCAACGTGGCTCTTCCGTACTACTAAAAGCCTTGTT  7142
          |||||||||||||||||||||||||||||| ||||||||||||||| |||| |||||||||
Db  7080  ACAGCCGAAGGGAGGGAGGAAAGTGTCTTCAACGTCTTCAACGTGGCTATTAAAAGCCTTATTT  7139

Qy  7143  CCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGATGTCATGCGTGTTGAGAGAGC  7202
          ||||||||||||||||||||||||||  ||||||||||||||||||||||| | ||||||
Db  7140  CCACAGAGCGACGCGCACAAGAAGAAGCTTACCGTCAAGATGTCGTTGCGTGTTGAAAAGAGC  7199

Qy  7203  GTAACACGCTTCTTTTTCATTGGGATTGACGCTGTCGCTGACGTTCGTCAGCCTGTGTGAGATG  7262
          || | || || |||||||||||| ||||| |||||||||| ||||||||||||||||||||
Db  7200  GTCACGCGCTTTTTTCATTGGGGTTGACGGTGCCTATTGGACCCTTGAAATTGCAGGTT  7259

Qy  7263  GAAATCCAGAACCATACAGCCTATTGTGACAAGTGCACGAGGCCTAGGCAAGAG  7322
          |||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db  7260  GAAATCCAGAACCATACAGCCTATTGTGACAAGTGCACGAGGCCTAGGCAAGAA  7319

Qy  7323  GGGTGCTTGGTGGCGGCGCCAATGAACTTACCTTGGTCTGGGTCTGACAAGTGTAGGCAAGAG  7382
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  7320  GGGTGCTTGGTGGCGGCGCCAATGAACTGACTTTGAAATGTGGGTCTGACAAGTGTAGGCAAGAA  7379

Qy  7383  ACCTTGGCTTCCTTCTCTTACATTTGGTCTCGTGGACTCCATAGAGGGCGTAAGAGGCGTCAAGCC  7442
          |||| |||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  7380  ACCTTGGCTTCCTTCTCTTACATTTGGTCTCGTATTGGAGTCGTGAGCGCGTCTATTGAGCGCGTCAAGCC  7439

Qy  7443  AAGCCCCCGTGTGTGAGGCGGTTGGCTCCTTGCTGGTGGCCGCCACCAAGGTGTAT  7502
          |||| |||||||||| |||||| |||||| ||||| |||||||||||||||||||
Db  7440  AAGCCTCCCGTGTGTGAGGCGGTTGGCTCTTTGTTAGTTGGCCGACACTACTAAGGTGTAT  7499

Qy  7503  GTCACCAACCCGGACAATGTTGGGAGAAGAGTTACCTTCTCGGCCTGCCCCT  7562
          ||||| |||||||| ||||||||||| || ||||||||||| |||||||
Db  7500  GTTACCAATCCAGACAATTCCAGAGGGACGGAGGGTCGACCCTTCTCGGCCTGCTCCT  7559

Qy  7563  AGGGTTCATGACAAATTCTCTCGTGGACTCCATAGAGGGCGTAAGAGGCAGTCAAGCC  7622
          |||| ||||||||||||  |||||||||  || ||||||||||||||||||||||||
Db  7560  AGGGTTCATGAATGACTACCTCGTATTGGAGTCGTGAGCGCGTCTATTGAGCGCGTCAAGCC  7619

Qy  7623  TGCCTAAGCATGGTTACACTTATGAGGAGCAATAAGGACTGTAAGGCCACATGCTGCC  7682
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7620  TGCCTAAGCATGGTTACACTTATGAGGAGCAATAAGGACTGTAAGGCCACATGCTGCC  7679
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Right column:

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Db  7620  TGCCTAAGCATGGTTACACTTATGAGGAGCAATAAGGACTGTAAGGCCACATGCTGCC  7679
Qy  7683  ATGGGCTGGGGATCTGGGGATCTTAAGGTGTCGGTCTCGGTCAAGGACCTTCGCCACCCTGCGGTGGAAGATGGCT  7742
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  7680  ATGGGCTGGGGATCTGGGGATCTTAAGGTGTCGGTCTCGGTCTAAGGACTTAGCCACCCCCGGGGAAGATGGGCC  7739

Qy  7743  GTCCATGACCGGCTCCAGGAGATACTTGAAGGGACGCCAGTCCCCTTTACTCTTACTGTG  7802
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  7740  GTCCATGACCGGCTTCAGGAGATACTTGAAGGGACTCCGGTCCCCTTTACTCTTACTGTG  7799

Qy  7803  AAAAGGAGTGTTCTTCAAAGACCGAAAGAAGAAGGAGAAGGCCCCCGCCTCATTGTGTTC  7862
          ||||||||||||||||||||| |||||||||||||||| |||||||||||||||||||||
Db  7800  AAAAGGAGTGTGTTCTTCAAAGACCGAAAGGAGGAGGAAGGCCCCCGCCTCATTGTGTTC  7859

Qy  7863  CCCCCCCTGACTTCCGGATAGCTGCTGAAAAGCTTATTCTGGGACGGCCACCTGGACCGGTAGCC  7922
          |||||||||||||||||||||||| |||||||||||| ||||||||||||||||||||||||||
Db  7860  CCCCCCCTGACTTCCGGATAGCTGCTGAAAAGCTCATCTTGGGAGACGCCCACCTGGACCGGTAGCC  7919

Qy  7923  AAGGGGGTGTTGGGGGGGGGCCTAGCCTTCCAGCCTTCCAAATCAGCGAATTAGGGAG  7982
          ||||| ||||| || |||||||||||| ||||||||||||||||||||||||||||||
Db  7920  AAGGCGGTGTTGGGGGGGGGCCTAGCCGTTCCAGCCTTCCAAATCAGCGAGTTAAGGAG  7979

Qy  7983  ATGTCAAACTGTGGGAATCAAAGAAGACACCATGCGCCATCTGTGTGGACGCCACATGC  8042
          ||||||| |||||||||| |||||||||| |||||||| |||||||||||||||||||
Db  7980  ATGCTCAAGTCATGGGAGTCTAAGAGAACCCCTGCGCCCATCTGTGTGGACGCCACCTGC  8039

Qy  8043  TTCGACAGTAGCATAACTGAAGAGAGACGTGGCGTGGAGACAGCTTTATGCCTGGCT  8102
          |||||||||| ||||||||||||||||| |||||||||||||| || |||||||||||
Db  8040  TTCGACAGTAGCATAACTGAAGAGAGACGTGGCGTGGAGACAGCTGCTGCTTTGGCGCC  8099

Qy  8103  TCAGACCATCCAGAATGGGTGCGTGCCCTGGGGAAATACTATGCCTGGCACAATGGTA  8162
          || ||||||| |||| || |||||||||||| ||||||||||||||| ||||| ||
Db  8100  TCTGACCATCCAGAATGGGTGCGTGCCACTGGGGAAATACTATGCCACCAGGTC  8159

Qy  8163  ACCCCGAGGGGTGCCAGTGGGTGAGAGTTATTGTAGATCTGTAGATCCTCAGGGGTCTTGACCACC  8222
          |||||||||||||||||||||||| || |||||||| |||||||||||||||||||||||||||
Db  8160  ACCCCGGAAGGGGTGCCACTGGGTCGGGTATTGCAGATCCTGCGGTGTCGGGTGTCTAACAACT  8219

Qy  8223  AGTGCCGAGCAACTGCTTGACTTGTCATATCAAAGGTGAAAGCCGCGTGTGAGAGGGTGGGG  8282
          || ||| || |||||||||||||| || ||||||||||||||||||||||||||||| |||
Db  8220  AGCCGCGAGCAACTGCTTGACTTGTCATCAAGGTGAAAGCTGCGTGTGAGAGTGGGGG  8279

Qy  8283  CTGAAAAATGTCTCGCCTCCATCGCTGGCAGCGTGTTGATCATATGCGAACGGCCT  8342
          ||||||||||||||||||||||| ||||| ||||||||||| |||||||||||||
Db  8280  CTGAAAAATGTCTCGCCTCCATAGCCGGCAGCCCAGGCTTGATCATGTGAGCGGCCA  8339

Qy  8343  GTGTGCGATCTCCAGCGACGCTTTGGGCCAGAGCCCTTCGCCAGAGTCGAGTCGCATGCGAG  8402
          |||| ||||||| ||||||||||| |||||||||||| |||||||||||||||||||||| |
Db  8340  GTGTGCGACCCAAGCGACGCGTTTGGGCAGCCCTAGCCCTCGCCAGAGTGTACGCGTGCGAG  8399

Qy  8403  CCTTCGTATCATGCGAAAGCGCATTCTTCTCGCCACGGACTTCGGAGGCCCCCTCCGCGC  8462
          ||| | |||||||| ||| ||||||| ||| |||||||||||||||| ||||||||||||
Db  8400  CCCTCATATCATGCGAAGCGCATTCTTCTCTTCGCCACGGACTTCCGGAGGCCCCCGTCGCGC  8459

Qy  8463  AATGCAGATGGAAACGCCATTCTTCCTGACCCAATGGCTTCGGCGTTCATCCTCTATACCCT  8522
          ||||||||||||||||| ||||||| ||||||||||||| |||||||||||| ||| ||||
Db  8460  AATGCAGATGGAAGCGCCATTCTTCCTGACCACGCGATGGCTTCGGCATCCGGTTACATCCTTTATCCT  8519

Qy  8523  ATGTCGAGCGACGTACAGTGACCAATGGCTTCGGCGTTCATCCTCTATACCCT  8582
          ||||||||||| |||| ||||||| || |||||| |||| |||| ||||| ||
Db  8520  ATGTCGAGTCAGTATAGTGACCCGATGGCTTCGGCGTTCATCCTTTATCCT  8579

Qy  8583  TGGCATCCTATCCACACGGTGGCTCATCATCCTGCTCACGTGCTCCACGTGCTTAGGGGT  8642
          |||| |||| |||||||||||||| ||||||||||| | ||| || |||||||||||
Db  8580  TGGCACCCCCATCCACGGTGGGTGGCATCATCCTCATGTGCTCAACGTGCGCCATTCAGGGGGT  8639

Qy  8643  GGTGGCACACCGTCTGATCCGTCTGTGTGTCCAGTGACATGGTAATTACTACAAGTTTCCA  8702
          ||||| || ||||| |||| || |||||| ||||||||||| ||||||| |||||||||
Db  8640  GGAGGCACACCGTCTGATCCGGTTTGGTGGCCGTTGGTGGCATGGTCATGTCAACTACTACAAGTTTCCA  8699

Qy  8703  CTGGACAAACTGCCTAAACTCAACATCATCGTGGCCCTCACGGACGCCACGCAGTCGTTGAGGGTTACC  8762
          ||||||||||||| ||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  8700  CTGGACAAACTGCCTAACATCATCAACATCATCGTGGCCCTCACGGACGCCACGCAGCAGCGTTGAGGGTTACC  8759
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Qy   8763  GCAGACACAACTAAGACAAAAATGAGGTGGCAAGGTGCTGAGCGACCTTCAAGCTCCCT   8822
           |||||||||||||  |||| ||||  ||||||||||||||    ||||| |||||||||||
Db   8760  GCAGACACAACTAAAACAAAAGATGAGGTGGCACCTTGAGCCACCTTCAAGCTCCCT     8819

Qy   8823  GGCCTAGCAGTCCACCGGAGAAGGCCGGGCATTGCGAACGCGTATGCTCCGGTCGCGC   8882
           ||| |||||||||||| |||||  ||||||| | ||||||| ||| |||||| ||||||
Db   8820  GGCTTAGCAGTCCACCGAGAAGAAGGCCGGGCCGTTGCGAACACGCATGCTCCGCTCGCGC  8879

Qy   8883  GGTTGGGCTGAGTTGGCTAGGGGCTGTTGTGGCCGTCCAGGCCTTCCCCCTCCG        8942
           ||||||||||||||||||||||||||||||||||  |||||||||||||||| ||
Db   8880  GGTTGGGCTGAGTTGGCTAGGGGCTGTTGTGGCCATCCAGGCCTTCCCCCTCCCCCT     8939

Qy   8943  GAGATTGCTGCTGTATCCCGGGGGGTTTCCCCCTTTCCCCCCCTATATGGGGTGTTCAT   9002
           |||||||||||||||||||||||||| |||||  |||||||||| ||||| ||||| |||
Db   8940  GAGATTGCTGCTGTATCCCGGGGGGTTTCCCTCTCTCCCCCCCTATATGGGGTGGTACAT   8999

Qy   9003  CAATTGGATTTCACAAGCCAGAGGAGTGCGCTGGCGTGGTTGGGGTTCTTAGCCCTGCTC   9062
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   9000  CAATTGGATTTCACAAGCCAGAGGAGTCGCTGGCGTGGTTGGGGTTCTTAGCCCTGCTC   9059

Qy   9063  ATCGTAGCCCCTTCGGTGAACTAAATTCATCTGTTGCGCAAGGTCCGTGACTGATC     9122
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   9060  ATCGTAGCCCCTTCGGTGAACTAAATTCATCTGTTGCGCAAGGTCGTGGTGACTGATC    9119

Qy   9123  ATCACTGGAGGAGGTTCCCGCCTCCCCGCCCAGGGGTCTCCCCGCGTGGGTAAAAAGGG   9182
           |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   9120  ATCACCGGAGGAGAGTTCCCGCCTCCCCGCCCAGGGGTCTCCCCGCGTGGGTAAAAAGGG   9179

Qy   9183  CCCGGCCTTGGGAGGCATGTGGTTACTAACCCCTGGCAGGGTCAAAGCCTGATGGTGC   9242
           ||| ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   9180  CCCGGCCTTGGGAGGCATGTGGTTACTAACCCCTGGCAGGGTCAAAGCCTGATGGTGC    9239

Qy   9243  TAATGCACTGCCACTTCGGTGCGGGGTCGCGGGTCGTAATCCGTACGGGGC          9302
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9240  TAATGCACTGCCACTTCGGTGCGGGGTCGCGGGTCGTAATCCGTACGGGGC          9299

Qy   9303  TGCTCGCAGAGCCCTCCCCCGATGGGGCACAGTGACTGTGATCTTGAAGGGGTCCACCCC   9362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9300  TGCTCGCAGAGCCCTCCCCCGATGGGGCACAGTGACTGTGATCTTGAAGGGGTGCACCCC   9359

Qy   9363  GGTAAGAGCTCGGCCCCAAAGGCCGGGTTCTACT                           9395
           ||||||||||||||||||||||||||||| |||||
Db   9360  GGGAAGAGCTCGGCCCCGAAGGCCGGGTTCTTCTACT                        9392
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RESULT 7
AAT08812
ID   AAT08812 standard; cDNA; 9392 BP.
XX
AC   AAT08812;
XX
DT   12-AUG-1996 (first entry)
XX
DE   Hepatitis virus open reading frame sequence from clone 470-20-1.
XX
KW   Hepatitis G virus; HGV; Flaviviridae; viral capsid protein; probe;
KW   viral envelope protein; non-structural protein; RNA helicase; antibody;
KW   chymotrypsin-like serine protease; RNA dependent RNA polymerase;
KW   HGV genome; ds.
XX
OS   Hepatitis G virus clone 470-20-1.
XX
FH   Key   Location/Qualifiers
FT   misc_feature   271..456
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FT   /note= "clone GE57"
FT   /tag= b
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FT   /note= "varial capsid region GE-Cap"
FT   /tag= c
FT   CDS   459..9077
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FT   misc_feature   2904..3254
FT   /note= "NS2b region (GE-NS2b)"
FT   /tag= u
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FT   /note= "PEP5/NS2B"
FT   /tag= v
FT   misc_feature   3168..3305
FT   /note= "clone GE17"
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FT   /note= "PEP5/NS3"
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FT   misc_feature   3615..3935
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FT   /note= "PEP6/NS3"
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FT   /note= "NS4a region (GE-NS4a)"
FT   misc_feature   5082..6536
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Query Match          84.9%;  Score 7977.4;  DB 17;  Length 9392;
Best Local Similarity 90.6%;  Pred. No. 0;
Matches 8514;  Conservative 1;  Mismatches 877;  Indels 1;  Gaps 1;

Qy      3 ACGTTGGGGGGTTGATCCCCCCCCCCGGCACTGGGTGCAAGCCCCATAAACCGACGCCT  62
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACGTTGGGGGGTTGATCCCCCCCCCCGGCACTGGGTGCAAGCCCCAGAAAACCGACGCCT  60

Qy     63 ATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCGCCGACCGGCCAAAAGGTGGTGGATGG  122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCGCCGACCGGCCAAAAGGTGGTGGATGG  120

Qy    123 GTGGTGACAGGGTTGGTAGGTCGTAAATCCGGTCATCCTGTAGCCACTATAGGTGGGT  182
          |||  |||||||||||||||||||||||||||| | |||||||||||||||||||||||
Db    121 GTGATGACAGGGTTGGTAGGTCGTAAATCCGGTCACCTTGTAGCCACTATAGGTGGGT  180

Qy    183 CTTAAGAGAAGGTCAAGACTCCTCTTTGTGCCTGCGGCGACACCGGCGACCGTCCACAGGT  242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTAAGAGAAGGTTAAGATTCCTCTTGTGCCTGCGGCGACACCGGCGACCGTCCACAGGT  240

Qy    243 GCTGGCCCTACCGGTGTGAATAAGGGCCCGACGTCGCTCGTTAAACCGAGCCCCGT  302
          ||  ||||||||||||||||||||||||||||||||||||||| | ||| |||||||
Db    241 GTTGGCCCTACCGGTGGGAATAAGGGCCCGACGTCGCTCGTTAAACCGAGCCCCGT  300

Qy    303 CACCCACCTGGCAAACGACGCCCACGTACGGTCCCCCTTCAATGTCTCTCTTG  362
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Db    301 TACCCACCTGGCAAACGACGCCCACGTACGGTCCCCCTTCAATGTCTCTCTTG  360

Qy    363 ACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAGTGGGGGCCGGGGGTTATGGGGAAG  422
          |||||||||||||||||||||||||||||||||||||||||||||||||| | ||||||||
Db    361 ACCAATAGGCTAGCCGGCGAGTTGACAAGGACCAGTGGGGGCCGGGGGCT-TGGAGAGG  419

Qy    423 GACCCCAAACCCTGCCCTTCCGGTGTGGGGGAAATGCATGGGGCCGGGCCACCGGCGTCCGCG  482
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Db    420 GACTCCAAGTCCCGCCCCTTCCCGGTGGGGGGCGGGGGGGCACCCAGCTCCGCG  479

Qy    483 GCGGCCTGCAGCCGGGGTAGCCAAGAATCCTTCGGGTGAGGGGGTGGCATTTCTCTT  542
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Db    480 GCGGCCTGCAGCCGGGGTAGCCAAGAATCCTTCGGGTGAGGGGGTGGCATTTCCTTT  539

Qy    543 TTCTATACCATCATGGCAGTCCTTCGTGCCTCCTTCTCGTGGTTGAGGCCGGGGCCATTCTG  602
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Db    540 TTCTATACCATCATGGCAGTCCTTCGTGCCTCCTTCTCGTGGTTGAGGCCGGGGCCATTCTG  599
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Qy   603  GCCCCGGCCACCCACCGCTTGTCGCGCAATATGGGCAATATTCCTCACAAATTGCTGTGCC   662
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Db   600  GCCCCGGCCACCCACCGCTTGTCGCGCAATATGGGCAATATTCCTCACAAATTGTGTGCC    659

Qy   663  CCGGAAGACATCGGTTCTGCTGGCCACTGTATCAGGCGGGATGCCTGGTGGTGGCCTGGTTGCGCACGGTT   722
          |||| ||||| ||||||||||||| |  |  ||||||||||||||||||||||||||||| ||  |||
Db   660  CCGGAGGACAATCGGTTCTGCTGGCCACTGTATCAGGCGGGATGCCTGGTGGTGGCCTGGTGGCACGATT    719

Qy   723  TGCACCGACCGTTGCTGGCCACTGTATCAGGCGGGTTTGGCTGTGCGGCCTGGCAAGTCC             782
          |||| |||| |||||||||||||||||||||||| |||||||||||||||||||||||||
Db   720  TGCACTGACCAATGCTGGCCACTGTATCAGGCGGGTTTGGCTGTGCGGCCTGGCAAGTCC              779

Qy   783  GCGGCCCAGCTCGTTGGGAACTGGGAGGCCTGTACGGGCCCCTGTCGGTCTCGGCTTAC               842
          || |||||||||| ||||||||||||| |||||||||||||||||||||| |||||||||
Db   780  GCGGCCCAACTGGTGGGGAACTGGGAGGCTGGTAGCCTACTAGGGCCCTGTCGGTCTCGGCCTAT          839

Qy   843  GTAGCCGGGATCCTCGGGTCTGGGGCCGAGGTTTACTCCGCACAGTTGGTGTTGGTGCG              902
          || | |||||| ||||||||||||||||||||||||||| ||||||||||||||||||
Db   840  GTGGCTGGGATCCTGGGGTCTGGGGTCTGAGGTGTCCTAACGGTGGGAGTGCGCG                    899

Qy   903  TTGAGGCGCCGGGTCTACCTGATGCCAAGTGAAGTGTGCAGTAGAAATGTGACGTTAAG                962
          ||||||||||| |||||||||||||||||| ||  ||||||||||||||||||||| ||
Db   900  TTGAGGCGCCGGGTCTACCTGCGCTGCCGTAACCTGTAAGCCTGACGGTGCAGTGTGAGCTGTAAAG         959

Qy   963  TGGGAAGTGAGTTTTGGACGATGACGAGCAGTTGGCCTCCAATTACTGGATTTGGAA                 1022
          |||||||||||| |  |||| ||||||||  ||||| ||||| ||||||||||||||
Db   960  TGGGAAGTGAGTTTTTGGAGAGTGGACTGGCCTGCTGCCTGAGCAACTACTGGATTCTGGAA             1019

Qy  1023  TACCTTTGGAAAGTCCCATTTGAATTTGGAGAGGAGTGATGAGGAGGCTGACCCCTGTTG              1082
          ||||| |||||  ||||||| ||||| |||| | |||||||  |||||||||||||||||
Db  1020  TACCTCTGGAAGGTCCCATTTGATTTCTGGAGAGGAGGCTGATAAGCCTGATAAGGCCTTTTCGCCTGTTG    1079

Qy  1083  GTTTGGGTGGCCGCAGTTGCTTTTGCTGGAGCAACGATTGTCATGGTTTTCTGCTGGTG              1142
          |||||||||| ||   |||||||| | ||||||||||||||||||| | ||||||||||
Db  1080  GTTTGGGTGGCCGCATTTGCTTTTGCTGGAGCAACGATTGTCATGGTCTTCTGCTGGTG               1139

Qy  1143  ACGATGGCGGGGATGTTGCAAGGCCCCTCCGTTTTGGGTTCCCGCCCCTTGAC                    1202
          |||||||| | ||||| |||||| |||||||| |||||||||||||||||| |||
Db  1140  ACGATGGCGGGGATGTCGCAAGGCGCGCCCCTCCGTTTTGGGTCTCCGCCCCCTTGAC                1199

Qy  1203  TACGGGTTGAAGTGGCAGTCATGCTGCCAGCTCTGCTGAGCTCGGCGTAATGGGCCCACTGGG          1262
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Db  1200  TACGGGTTGACTTGGCAGTCATGGTCTGGGGCCAACGGTTCGCGTTTTCGCCGTTTTCGACTGGG          1259

Qy  1263  GAGAGGGTGTGGGAATGTCGAGGGAATGTCACGCTTCTGTGTGCTGCCCCAACGGCCCCTGG           1322
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Db  1260  GAGAAGGTGTGGGAACTGGTCAGTGTCAGTTAGGCCTCAGTGTGCTGCCCCAACGGTGCCCCTG          1319

Qy  1323  GTTTGGGTCCCCGGTTTTGCCAGGCGGTTGGTGGGGCGGACCCCGACCCCATCCCATTGGGAGC         1382
          ||||| | ||||||||||||||||||| ||| ||||| |  ||||||||||||||||||||||
Db  1320  GTGTTGGGTTCCCGGTTTTGCCAAGCAATCGGCTGGGTGGCTGACCCTGTGGGTGACCACTTATTGGGAGC    1379

Qy  1383  CACGGGACAAAACCAGTGGCCCCTATCATGCCCCATAATGTCTATGGTGTCTGTCCGTA              1442
          |||||||| ||||  |||||||| || | ||||||| |||||||||| ||||||||
Db  1380  CACGGGTGGGTGCAAAATCAGTGGCCCCTTTCATGCCCCAGTGTGTCTATGGTGTCTGTACAGTC         1439

Qy  1443  ACGTGCGTGTGGGTTTTGCGTCCGGTTCCGTGTTTGCCTGTCTTGGTGTCTGATTCGAAGATC         1502
          |||||| || ||||||||  |||||||||||||||||||| |  |  |||||||||||||||| |
Db  1440  ACTTGCGTGTGGGTTTTGCCGTGTTTGCCTTTGCCTGTCTCAGTGGTGTCGGACTGGAAGATA          1499

Qy  1503  GATGTTCGTGGAGTTTTGTGTGACTCGCCAGTGCTTCGCCAGCTGGCACCTATAGCCGGTCAGGGTCA     1562
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Db  1500  GATGTGTGGGGAGTTTAGTGCCGTGGCTCTTGGGCTCTGGCAGTGGTTGCCACCTATGGTGCGTGTGATCA   1559

Qy  1563  TCGGATCGGCGACACGTGGTTGGTGAGCGCTGTCTCCCGTGTTGGCCTCGGTAACGTGTATT           1622
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Db  1560  TCGGATCGGCGACACGTGGGCGCCTGGGCTCTCGGGAGTCCCGTGTTGGCCTCGGTAAGGGTACCGTGTGT    1619

Qy  1623  CTGGACCGTGCGCCTGCTTGCTCATGTGGCACCCACCCTGTTGTGAGGGTCTTGGCCCGAAACCCGGG     1682
          |||| ||| | ||  || |||||| | ||||||||| ||| | |||||  |   |||||||||||
Db  1620  CTGGACGTTCGCGACCTGCGCCTGCTCCTCCTGCGCCACCCTGTTGTGAGGGACTGCTGGGCCGAGACCGGG    1679
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Qy  1683  TCGGTTAGATTCCTTTCCATCGGTGCGGCACGGGGCACGGGGCCTCGGCGCTGACAAAGGGACTTGGAA     1742
          |||||| ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  1680  TCGGTTAGGTTCCCATCCATCGGTGCGGCACGGGGCACGGGGCCTCGGCGCTGACAAAGGGACTTGGAA      1739

Qy  1743  GCTGTGCCCCTTCGTCAACAGGACAACTCCCTTCACCCTCGGCGGGCCCCCTGGCAACCAG             1802
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1740  GCTGTGCCCCTTCGTCGTCAACAGGACAACTCCCTTCACCCTCTAGGGGGCCCCCTGGCAACCAG         1799

Qy  1803  GGGAGGAGGCAACCGGTCGGCGTCGGCCTCTACACCATGACCAAGATC                          1862
          | || | |||||| |||  | |||||||  ||||||||||||||| |||
Db  1800  GGCCGAGGCAACCGGTCGGCGTCGGCCTCTACCAGGATGACCAGGATC                          1859

Qy  1863  CGGGATTCCCTGCATTGGTGAAATGTCCCGGGTACCGGTTGCCCAGACCTGGGAACG                 1922
          || | ||||| ||||||||||||||||| ||||  ||  |||  ||| | |  |||| |
Db  1860  CGAGATACCCTACATGTCTGGTGAGTGTCCCAGCAGCCATTGAGCCTCCCACCGGGACG                1919

Qy  1923  TTCGGGTTCTTCCCCGGAGTCCGCGTCCATTTAACAACTGCATGCCGCTAGGCACGGAAGTG            1982
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Db  1920  TTTGGGTTCTTCCCGGAGTCGCCTCACGTCTCTTGGGGGCCTGGTTCTACGAGCTCCGGCAGG           1979

Qy  1983  TCTGAGGCATTGGGCGGAGCTGGGTTCTCCTACGGGGGTTCTACGAGCTCCGCAGG                  2042
          ||  || |||||||||||| | |  |||| ||||| || ||||| ||||||||||||
Db  1980  TCCGAGGCACTTGGGCTGCCTCAGTGGGTTCTATCAACCCCTGTCGCCAGG                       2039

Qy  2043  TGTTCGGAGCTGATGGGACGCGCGAAATCCGGTTGCCCGGGGTACGCGTCTCCTCT                  2102
          ||||||||||||||  ||||   |||| |||||| ||  ||||| |||||| ||  |
Db  2040  TGTTCGAAGCTGATGGGGGAAGCCGAAATCCGGTTGTCCGGGGTTTGCATGGCTCTTCG               2099

Qy  2103  GGTAGACCTGACGGGTTCATACACGTCCAGGGGCCAGGAGTTGGATGCGCAGGAAC                  2162
          |||| | ||||| |  || | ||||| ||||||||| |||||||||| | |||||||
Db  2100  GGCAGGCCGTGATGGGTTTATACATGTCCAGGGGCCAGGAGGTGGATGGCCAGGCAAC                 2159

Qy  2163  TTCATCCCTCCTCCACGCTGGTTGCGTCTGGATTTGTATTTGTCTGCTATCTGATG                  2222
          ||||| ||| ||||||||||| || |  |||||||| ||||  ||| ||||||||||
Db  2160  TTCATCCCGCCCCCACGCTGGTTGCTCTTGGACTTTGTATTTGTATTTGTCCTTATAACCTGATG         2219

Qy  2223  AAGCTGCTGAGGCACGGTGGCTTCGCTTGTCTCGCGTGTGGGGTGAAC                          2282
          |||||||||| |||||||||||||||||| | |||||| |||||||||
Db  2220  AAGCTGCTGAGGCACGGTGGCTTGTCGTTGTCGGATCTTCGCTGCTATGGTGGTGGGTGAAC            2279

Qy  2283  CAGTTGGCGGTTCTAGGACTGTGTGGACCTGTCCGGTCTGTGGCGTGGCGTGAAGTTTTTGCG          2342
          ||||||||||||||| ||||||||| |||   || |||| || ||||| || ||||  ||||
Db  2280  CAGCTGGCAGTCGCTCTAGGGCTGTCGTGCTGTGTGAAGCCGCCGTCGTCAGTGAGGTCTCGCG          2339

Qy  2343  GGCCCTGCCTTGTCATGTGTTTGGGCCTCAGTATGATACTAGTCTAGCA                         2402
          ||||||||| | || | |||||| ||||| |||||||| |||  |||| |
Db  2340  GGCCCTGCCTGTCCGGTGCTGTCGGGGACTCCGGTCAGTGTAGCTATGATGATTGGGTTTGGCA           2399

Qy  2403  AACCTGGTGTTCGTGTACTTTCGGTGGATGGGCCCTCAGCGCCTCATGTTCCTGTGTGTGG             2462
          |||||||||| ||   ||||||||||||| |||  |||| | ||  ||||||||||||| |||
Db  2400  AACCTGGTGCTGTACTTTTGAGATGGTTGGCCTGGCACCCCAACGCCTGTGATGTTCCTCGTGTTGTGG     2459

Qy  2463  AAGCTCGCTCTGGGGAGCTTTCCCGGGCCCAGTCACTTTGATGGGATTTCGGGACCCGCGGG           2522
          ||||||| ||| ||||||||| ||||||||| ||| | ||||| |   |  ||||||||||||
Db  2460  AAGCTTGCTCTGGGGAGCTTTCCCGGGCCCAGTCACTTTGATGGGATTTCGGGACCCGCGGG           2519

Qy  2523  CGCACCTCGTGTCCGGGCCCCAGTTCTGCTCTCGGCTCCACATTCGAGGTGACACTTCG              2582
          |||||||||| |  |||||||||||||||||||||||| |||||| ||| ||| ||||||
Db  2520  CGCACCTCAGTGCTCGGGGCCCCAGTTCTGCTCTCGGCTCTACACTCGAGGTGACACTTCG             2579

Qy  2583  GTGTTGGGCTGGTGGTGGTGTCCGTGGCCAGCGTGGGGCCCATAGCGCTTCCTCAGCTCAATG           2642
          |||| ||||||||| ||| |  ||  ||||||| |||  ||||||||||||||||| ||||
Db  2580  GTGTTGGGCTGGTGGGTGGTGCCCGTGCTAGCTTCAGTGGGGCCCATTGTGGGCCTCCTCGAGCTCGATG    2639

Qy  2643  AGCGCAGGGGGTGGAAGCAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCAG           2702
          ||||||| || |||||| ||| | ||| |||||||  |||| |  |||||||||||||||||
Db  2640  AGCGCAGGGGGTGGAGGCAGCAGAAAGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCAG           2699

Qy  2703  GCTGTCGCGCCAGAGGGTGGTGCGCCTCCTACCAAGCTTCTG                                2762
          ||  | ||| | ||| ||||| | ||| |||| || |||  |
Db  2700  GCAATCCGTCAAAGGCGTGGTGAGGAGCGCCGCCTGCCAAACCCCTG                           2759

Qy  2763  ACGTTCGCCTGTGCTGCTTGCCTCATACAATCGGCCGATGCTGTGATGTGGTGGTG                  2822
          ||| | ||| |||||||| |  ||||  | |||  |||||||||| | || ||||||
Db  2760  ACGTTCGCCTGTGCTGCTTGCCTCATACATCGGCCGATGCTGTGATGTGGTGGTG                   2822
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Qy  4983 GGTCTGAAGGGCCGAATCCTGTCCCACTCCTGCTGAGGTGGGCAATGATTACCATCT 5042
         ||||||||||||||  |||||||||||||||||||||||  |||||| ||||||||||
Db  4980 GGTCTGAAGGGCCAAATCCTGTCCCACTCCTGCTGAGGTGGGCAATGATTACCATCT 5039

Qy  5043 AAAGTGGCCGGCCATCACATCGTGGACGACCTGGTCTCGGGTCCGGTGGTGCGGAGGGT 5102
         ||||||||||||||| || ||||||||||||||||| |||| |||||||||||||||||
Db  5040 AAAGTGGCCGGCCACCACATGGACGACCTGGTCTCCGGAGACTCGGTGTGCGGAGGGT 5099

Qy  5103 TACGTCCGCTGGATGCGGGACCATCTTGATGGTGGCCCTTCGCTATTGCGGGGGCATG 5162
         |||||||||||||||||||||||  || ||||||||||||| ||| || ||||||| ||
Db  5100 TACGTCCGCTGCGACGCTGGGCCGATCTTGATGGTGGCCCTTCGCTATCGCGGGGGAATG 5159

Qy  5163 ATCTATGCGTCATACACCGGGTCTCGTGGTGGTTACAGACTGGGATGTGAAGGGGGGT 5222
         ||  ||||| |||||||||||||||||||||||| ||  || |||||||||||||||||
Db  5160 ATCTACCGCGTCATACACCGGGTCGCGCGTAGTGGTGGTGACAGACGTGGGATGTGAAGGGGGGT 5219

Qy  5223 GGCAGCCCCTTATCGGCATGGGAGGAACCAGGCCACCCGCGCGGTCGTGCCAGGTCCCC 5282
         |||||||||||| || ||||||||| |||||||||| |||| ||| | ||||||||| ||
Db  5220 GGCGCCCCCTTTATCGGCATGGGAGGAACCAGGCCACCCGCGCGGTCGTGCCAGGTCCT 5279

Qy  5283 CCGGTAGACCATCGGCCGCGGGGAGAGCTCTGCGGCCATCGGATGCCAACACAGTGACAGAT 5342
         ||||||||||||| ||| |||||| | |||||| || || |||||| | ||||||||||||||
Db  5280 CCGGTAGACCATCGGCCGCGGGGGTGAATCAGCACCATCGGATGCCAACACAGTGACAGAT 5339

Qy  5343 GCGGTGCGGCCATCCAGGTGGATTGGCTCAGTTGGTCATGACCCTGTCGATCGGCGGAA 5402
         |||||||||||||||||||||||| || |||| | |||| | |||||||||||| |||| |
Db  5340 GCGGTGCGGCCATCCAGGTGGACTGCGATTGCGACTCGTCGATCGGCGGAGAGAA 5399

Qy  5403 GTGCTTCCTTGGCCCCAGGCTAAGACGCGGCCAGGCCTACCACCAGTGGCTT 5462
         || || |||| | ||||||| |||||||||||||||||||| ||||| ||||||| |
Db  5400 GTGTTGTCCTTGGCCTGCAGGGACCGGGCCAGGCCTACACAGCAACCGCCAAGTGGCTC 5459

Qy  5463 GCTGGCTGCTACACGGGCGGCGGGCCCGTCCCACTGTTTCAATTGTGACAAGCTCTTC 5522
         || |||||||| |||||||| |||||| | ||||| |||||||||||| |||||||||| |
Db  5460 GCTGGCTGCTATACGGGCGGCGGGCCCGTTCCCACTGTATCCATTGTTGACAAGCTCTTC 5519

Qy  5523 GCCGGGGGCGGCGGCTGTGAGGCCATTGCCACAGTGTAATAGCTGCGCGCAGTGGCG 5582
         |||||||||| || || | || ||||||||||||| | | | ||||| ||||| ||||
Db  5520 GCCGGAGAGGTGGGGCGCGTGTGTGTGGCCATTGCCACAGTGTATAGCTGCGCGCATGGCG 5579

Qy  5583 GCCTATGTGGGCTTCTAGGAGCCCTCCATTGCCTGCTGCTTCCTACCTCATGGGGGTTG 5642
         ||| |||| |||||| ||||||||||||||| | | ||||||||||||||| |||||||
Db  5580 GCCTACGGGGCGTTCAAGGAGCCGTTGCAGCCCGTGGCTTCCTACCTCGATGGGGTTG 5639

Qy  5643 GGCGTGGAGGCGAAGCGCAAACCCGCTTAGCCTTCCGCTCCGCTCCTACTAGGGGGCTGGG 5702
         |||||||| | | |||| ||||| ||||| | ||| |||||||| | || |||||| |||||
Db  5640 GGCGTTGGACGAACGCAGCTCAGAGCGGCTAGTGTCCATTGGCGGCTCCTATTGGGGCTGGA 5699

Qy  5703 ACCGGCTCTGCTGGCACGCGGGTTAACCATGGCGGGGATCGCGTTCATGGGAAGTGCT 5762
         ||| |||||||||||| |||| |||||||| ||| |||||| ||||||||| ||||| |
Db  5700 ACCGGCTCTGTCGTCGGGGACTTGCGTGGGCTTGGGGGATCGCGTTCATGGGGGGGCC 5759

Qy  5763 AGCGTCTCCCCCTCCTTGGTCACCATTTACTGGGGGCGTGGGGGCGTGGAGGGGCGTG 5822
         || |||||||| ||||| |||||||| ||||||||||| | ||||| |||| ||||| |
Db  5760 AGTGTCTCCCCCTCCTTGGTCACCATTTTATTGGGGGCCGTCGGAGGTTGGGGAGGGTGTT 5819

Qy  5823 GTGAATCGCGGCTAGCCTTGTCTTGACTTTATGGCGGGAAACTATCATCAGAAGATCTG 5882
         || |||||||||| |||||| || |||||||| || ||||||||| ||||||| ||||||
Db  5820 GTCAACGGCGGCGCTAGTGTTTGACTTCTGGGGAAACTTTCATCAGAAGATCTG 5879

Qy  5883 TGGTATGCCATCCCAGTGCTAACCAGTCCGGGGGATCGCCCTCGGG 5942
         |||||| ||||||||||||| || |||||||||||||| || |||||
Db  5880 TGGTATGCCATCCCAGTGCTAACCAGTCCGGGGGATCGCTCTCGGG 5939

Qy  5943 TTGGTGTGTACTCAGCTAACAAACTCGGTTGCAGCGCCGTTCGCTGCTGACT 6002
         |||  | | |||| ||||||||||||| ||||||| ||| |||||||||||||
Db  5940 TTTGGTTTTATTCAGCTAACAAACTCTGGACTACCACTTGGTTGACCGGTCGACTATTGCGAC 5999

Qy  6003 ACATTGCCAAGGTCTTCAATGCATCCCCTGACAGTTACTTTCAGCAGGCCGATTACGTGAC 6062
         | |||| || |||| |||||||||||| ||||||||| |||||||||| |||||||| ||
Db  6000 ACGTTACCAAGGTCTTCATGTATCCCGACACGTGGCTTTTCAGCAAGTTGACTATTGCGAC 6059
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Qy  6063 AAGGTCTTCAGCTGTGCTCCGACCTTGAGCCTCGCACCGTGGTTGCCCTGGTCAAC 6122
         ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  6060 AAGGTCTTCAGCGCCTGCTCCGGCCTGAGCCTCGCCACAGTGGTTGCCCTGGTGTCAAC 6119

Qy  6123 AGGAGCCTAAGGTGGATGAGGTTCAGGTGGGTACGTCTGGGACTTGTGGGGAGTGATC 6182
         |||||||| |||||||||| ||  ||||||| ||||||| |||||||| ||||||||| |
Db  6120 AGGAGCCTAAGGTGGATGAGGTTCAGGTGGGTATGTCTCGGGACTTGTCGGGAGTGGGATC 6179

Qy  6183 ATGCGTCAAGTGCCATGTGGATGGCCAGAGTTCGGGCCCCTCCCCCGTGTCGTCATTA 6242
         ||| | |||||  | ||||| ||||||||| || ||||||||||| |||| |||||| |
Db  6180 ATGCGCCAAGTGCCGGTGGTGTGGCCAGACTTCAGGGCCCTCGCCCGTGTGTGTCACTA 6239

Qy  6243 CCCTTATGCACTCGCGGAGGGGTGGTCCGGAGGAATGTGTTGTTGACGGCCATGTTGAG 6302
         |||| |||||| | |  ||||||||| ||| ||||||||||||| |||| ||||||||||
Db  6240 CCCTTGTGGCATTGCGGGGTGGTCCGGGGAATGTGTTGCTTGACGTGCTCATGTTGAG 6299

Qy  6303 AGTCGTTGTCTTTTGTGTTGCTGATCACCGGTGATGTTTTGAATGGGCAACTCAAAGAT 6362
         |||| ||||| | | | |||||||||| |||||||| |||| |||||||||||| || |
Db  6300 AGTCGCTGTCCTCCTGTGTGCTGATCACCGGTGGTTCTGATCACTGGCGTTCTCAAAGAA 6359

Qy  6363 CCAGTTTACTTCTACCAAGCTGTGTCCAGCATTATTGGATGGGGACAGTCCCTGAACATG 6422
         ||||||||||| ||||||||||||||||||| || |||||||| ||||| ||| || |||
Db  6360 CCAGTTTACTTCTACCAAGCTGTGCCGCCACTATTGGGGACTGTCGGCTGTCGCTGAACATG 6419

Qy  6423 CTGGGCTATGGCCGAGACGTCGCGCCTTTGCTCGCCTCCGGACACCCCGGAAGCTGTACCATTC 6482
         || | |||  |||| ||||||||||||| |||||||| | |||| ||| |||||||||| |||
Db  6420 CTGGGGTACGTGGGTGAAAGCTCGCGCTCCTCCGGACACCCCGAAGGTTGTCCCTTC 6479

Qy  6483 GGGACGTCTGGGTGGGCTGAGGTGGTGGTGACCCCTACCACGTTGTGATCAGGCGAACA 6542
         |||||||||||| ||||||||||| | |||||| |||||||||||| ||||||||||| |
Db  6480 GGGACGTCTGGGCTGGGCTGAGGTGGTGGTGACCACTACCACGTTGGTAATCAGGAGACC 6539

Qy  6543 TCCGCTACAAACTGCTGCGCCAGCAAATCCTGTCGCGGACGCGGCGCCATATTAC 6602
         ||||| || || |||||| ||||||||| || || | ||||||| |||||||| |||
Db  6540 TCCGCCTATAAGCTGCTGCGCCAGCAAATCCTATCCATCGGCTGCTGCTGTCTAC 6599

Qy  6603 GTCGACGGCATACGGGTCTCATGGGACCGGCGCCGAGCCGCCTGCCATGTCTATGGC 6662
         |||||||| ||||||||| ||| |||||||| ||||||||||||| || |||||||| ||
Db  6600 GTCGACGGCCATACGGGTCTCATGGGACGGCGCCGAGCGCTGCCGCCCATGTCTATGGC 6659

Qy  6663 CCTGGGCAAAGTGTCACCATTGCACCACCCTTCCGCATCAACTGCGGCTT 6722
         || |||||||||| |||||||||| | |||||||| || | |||||| |||
Db  6660 CCTGGGCAAAGTGTTACCATTGACGGCGGAGCCGCTTGCCTCATCAACTGAGGGCTC 6719

Qy  6723 AGGAATGTGGCGCCCTCGAGGTGTCATCCGAGGTGTCACATTGGACGACGAGACT 6782
         |||||||||||| |||  |||| | ||| ||||| | |||| ||| ||||| |||||
Db  6720 AGGAATGTGGCCACCCTCTGAGGTTCATCCGAGGTGTCATTGACATTGGGACGCGGAGACT 6779

Qy  6783 GAAGACTCAGAACTGACTGAGGCCCTTGCAGCCCCTTCAGGCTT 6842
         |||||||||||||| ||||||||| || |  | |||||| |||||
Db  6780 GAAGACTCAGAACTGACTGAGGCCGATCTGCCGCGTCTCCCAAGCGATC 6839

Qy  6843 GAGAATGCTGCGAGAATTCTTCACATAGAGTTGCAGTGACATGCAGTACA 6902
         ||||||||||| ||| | ||||||| ||| ||||||||| | || |||||||
Db  6840 GAGAATGCTGCGAGATTCTTGAACCGCACCATTGATGTCATCGAGGACTGCAGTACA 6899

Qy  6903 CCCTCTCTTGTGTGGGAGTAGCCGAGGATGCCTGTGTGGGAGAAGACATACCCGCACT 6962
         |||||||| | |||||| ||| |||||| |||| ||||| ||||||||||  |||| ||
Db  6900 CCCTCTCTTTGTTGGTAGTAGCCGAGGATGCCTTGTATGGGGAGAAGAAGCACATCCCCGTACT 6959

Qy  6963 CCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCCAGATGAGAACGACCCCGTGTG 7022
         |||||||| | | ||| |||||||| ||||||| ||||| || ||||| ||| |||||||
Db  6960 CCATCGCCAGCAGCTCGGTTACTGAGATGAGCCAGTCGAGATGAGAACGACCCCGTCGTG 7019

Qy  7023 TCTTCCTCGCAGGAGATACCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCGAG 7082
         ||||||||| ||||| || |||||| | ||||| ||||||| |||| || |||||||||
Db  7020 TCCTCCTCGCAGGAGGATAACCCGTCTTCTGACTCCTCTGAGGTCATCCAAGAGTCCCGAT 7079

Qy  7083 ACAGACCGAAGGGAGGAAAAGCTGCTCTTCAACGTGGTCCTTCCTTCCGTAAAAAGCTTGTTT 7142
         | | || |||||||||||| |||| | || |||||| | ||| || | |||| |||| ||||
Db  7080 ACAGCCCAAGGGGAGGAAAGTGTCTTCAACGTGGTCTTTTCAACGTGGCTCTTTTATTT 7139

Qy  7143 CCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGATGCATCGTGTTGAGAAGAGC 7202
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Db   8220  AGGCGGAGCAACTGCTTGACCTGCTCCATCATCAAGGTGCTACATCAAGGTGAAAGCTGCCTGTGAGAGAGTGGGG  8279
Qy   8283  CTGAAAAATGTCTCCTCCTTCATCATCATGCGTGCTGCTGTTTGATCATATGCGAACGGCCT  8342
           |||||||||| || |||||  ||||| ||||  ||||||| ||||||||||| || ||||||
Db   8280  CTGAAAAATGTCTCTCTTCATAGCCGGCGATGACTGCTTGATCATATGAGCGGCCA  8339

Qy   8343  GTGTCGATCCTAGCGACGCTTTGGGCAGAGCCCTTGGCGAGCTACGGGTACGCATGCGAG  8402
           ||||| || ||||||||| |||||  ||||| ||||| ||||||| ||||| ||||||||
Db   8340  GTGTCGCACCCAAGCGACGCGCTTTGGGCAGAGCCCTAGCGAGCTATGGGTACGCGTGCGAG  8399

Qy   8403  CCTTCGTATCATGCATCACTGACACGGCCCCCTTCGTCTCCACTTGGCTAGCTGAGTGC  8462
           ||||| ||||||||||| ||| ||||||||||||| |||||||| ||||||| |||||
Db   8400  CCCTCATATATGCATCATTGGACACGGCCCCCTTCGTCTCCACTTGGCTGCTGAGTGC  8459

Qy   8463  AATGCAGATGGGAAACGCCATTCTTCCTACCACGGACCTTCGGAGGACTTCGGCCC  8522
           |||||||||| ||||| ||||||||||||||| | ||||||||| |||||| ||||
Db   8460  AATGCAGATGGGAAGCGCCATTTCTTCCTGACCACGGACTTCCGGAGGGCCGCTCGCTCGC  8519

Qy   8523  ATGTCGAGCGAGTACAGTGACCCAATGGCTTCGGCCATCGGTACATCCTCCTATACCCT  8582
           ||||| |||| ||||||| || ||||||||||||||||||| ||||||||||| |||||
Db   8520  ATGTCGAGTGAGTATAGTGACCCGATGGCTTCGGCCATCGGTACATCCTCCTTTATCCT  8579

Qy   8583  TGGCATCCTATCACACGGTGGGTCATCATCCCTGCTCACGTGCTCACCTGGGGGT  8642
           |||||||| ||| || |||||||||||||| ||||| ||||||||| | |||||||
Db   8580  TGGCACCCCATCACACGGTGGGTCATCATCCCTCATGTGTCATCAACGTGCCGCATTCAGGGGT  8639

Qy   8643  GGTGGCACACCGTCGATCCTGTGTTGGTGCCCAGTGCCATGGCTACATGGTAATTACTACAAGTTCCA  8702
           |||||||||||||| ||||  |  ||||||| ||||||||||||||||||| |||||||| ||||||||
Db   8640  GGAGGCACACCGTCGATCCGTTTGGTGCCAGTGCCATGGCTACATGGTAACTACTACAAGTTTCCA  8699

Qy   8703  CTGGACAAACTGCCTAACATCATCGTGCCCTCCACGGACCAGCGAGGGTACC  8762
           ||||| |||||||| || || ||||||||||| |||||||| ||||||||||
Db   8700  CTGGACAAACTGCCTAACATCATCGTGCCCTCCACGGACCAGCGAGGGTACC  8759

Qy   8763  GCAGACACAACTAAGACAAAAATGGAGGCTGGCAAGGTGCTGAGCGACTCCAAGCTCCCT  8822
           |||| |||||||||| ||||||| ||||||||||||||||||||||||||| ||||| ||
Db   8760  GCAGCACAACTAAGACAAAAACAAAGATGGAGGCTGGTAAGGTTCGAGCGACCTCAAGCTCCCT  8819

Qy   8823  GGCCTAGCAGTCCACAAGCCAGAGAAGGCCGGCATTGCGAACGGCGTATGCTCCGGTCGCGGC  8882
           ||| ||||||| | ||||||||||| || ||||||| |||||||||||| ||||||||||||
Db   8820  GGCTTAGCAGTCCACCAGCCAGAGAAGGCCGGCACTGCGGCGTTGCGAACACCGGTCGCTCGCGGC  8879

Qy   8883  GGTTGGCTGAGTTGGCTAGGGGGTGCTTGTGCGCCCTTCATCTGTTGCGCCAAGGTCCGGCTGATC  8942
           ||||||||||||||||| || |||||| ||||||||| ||  | | |||||||| ||||||| ||
Db   8880  GGTTGGCTGAGTTGGCTGAGGGGGTGCTTGTGCGCATCCAAGGTCCGGCAAGGTCCGGCTGATC  8939

Qy   8943  GAGATTGCTGGTATCCCGGGGGTTTCCCGCCCTTTCCCGCCCCCTATATGGGGGTGGTTCAT  9002
           |||||||||||||||||||| || ||||||||||||||||||||||||||| ||||| |||
Db   8940  GAGATTGCTGGTATCCCGGGGGTTTCCCGCCCTATATGGGGGTGGTGGTACAT  8999

Qy   9003  CAATTGGATTTCACAAGCCCAGAGAGTGGTTACTAACCCCTGCTC  9062
           |||||||||||||||||| |||||| || |||||||||| |||||
Db   9000  CAATTGGATTTCACAAGTCAGAGAGTGGTTACTAACCCCTGCTC  9059

Qy   9063  ATCGTAGCCCTTCGGTGACTTAAATTCATCTGTTGCGCGACTGATC  9122
           ||||| ||||||||||||| ||||||||| |||||||||| |||||
Db   9060  ATCGTAGCCCTTCGGTGACTTATAGCGTTATACCGTGGTCTGTGACTACGGGC  9119

Qy   9123  ATCACTGGAGGAGGTTCCCGCCCTCCCCGCCTAAAAAGGG  9182
           |||| ||||||||||||||||||||||||| ||||||||
Db   9120  ATCACCGGAGGAGGTTCCCGCCCCCCGCCTGGGTAAAAAGGG  9179

Qy   9183  CCCGGCCTTGGGAGGCATGGGGGAAATACTATGCCTCTGGCACAATGGTA  9242
           |||||||||||||||||||| |||||| |||||||| ||||||||||||
Db   9180  CCCGGCCTTGGGAGGCATGGGGGAAATACTATGCCCTCTGGCACAATGGTGTC  9239

Qy   9243  TAATGCACTCCACTTCGGTGGGTCGGGGTATTGTAGATCCTTCAGGGGTCTTGACCACC  9302
           |||| ||||||||||||||| ||||| ||| ||| |||||| ||||||||| |||||||
Db   9240  TAATGCACTCCACTTCGGTGGGTCGGCGGTATTGTAGATCCTTATACCGTGGTCTTGACTACGGGC  9299

Qy   9303  TGCTTCGCAGAGCCCTTCCCCGATGGGCACAGTGGGCACACCCC  9362
           ||||| |||||||||||||||||| |||||||||||||||||||
Db   9300  TGCTTCGCAGAGCCCTTCCCCGATGGGCACAGTGGGCACACCCC  9359
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Db   7140  |||||||| || || |||||||| ||||||| ||||| ||||||  7199
           CCACAGAGCGACGCGACCCAGGAGCTTACCGTCAAGATGTCGTTGCTCGCGTTGAAAAGAGC

Qy   7203  GTAACACGCTTCTTTTCATTGGATTGACGGTCGCTCGCGTCGCGTCTGCTGGCAAGCCTGTGTGAGATG  7262
           || ||||||||||||| |||||||| ||||||| |||||||| |||||
Db   7200  GTCACGCGGCCTTTTCTCATTGGGGTTGACGGTTGACGGTTGCTAGCCGTGTGAGATG  7259

Qy   7263  GAAATCCAGAACCATACAGCCTATTGTGACAAGCGCCATCGCTTGACAATTGCAGGTT  7322
           ||||||| || |||||||| |||||||||||||| ||| |||||||| ||||||||||
Db   7260  GAAATCCAGAACCATACAGCCTATTGTGACCAGGTGGCCACTCCGCTTGAATTGCAGGTT  7319

Qy   7323  GGGTGCTTGGTGGTGGCAATGAACTTACCTTGATGTGACAAGTGTGAGGCTAGGCAAGAG  7382
           |||||| |||||||||||||||||| ||||||||| |||| |||| ||||||||||||||
Db   7320  GGGTGCTTGGTGGTGGCAATGAACTTACCTTTGATGTGACAAGTGTGAGGCTAGGCAAGAA  7379

Qy   7383  ACCTTGGCTTCCTTCCTTCTTACATTTGGTCTCGGGGGTGCCACTGACGAGGGCACTCCGGCC  7442
           ||||||||||| ||||||||||| || |||||||||||||||| |||||||||||||| ||||
Db   7380  ACCTTGGCTCCCTCCTTCTTCTACATTTGGTCTCGGGAGTGCCGCTGACTACGAGGGCCACGCCGCC  7439

Qy   7443  AAGCCCCCTGTGTGAGGCCGGTTGGCTTCCTCGGTGGCCGACACCACCAAGGTGTAT  7502
           ||| | ||||  | |||| ||||||||||| || || || ||||||||||||||||
Db   7440  AAGCCTCCCGTGGTGGCCGGTTGGCTTCTTTGTTGTGGTGGCCGACACTACTAAGGTGTAT  7499

Qy   7503  GTCACCAACCCGACAATGTTGGGAGAGAGTTGACACAGGTTACCTTCTGGCCGTGCCCCT  7562
           ||| | |||| || | ||||||||||||| | ||||||||||||| ||||||||| |||
Db   7500  GTTACCAACCCAGACAACAATGTGGGGACGAGGGTTGACAAGGTGACCTTCGGGCCGTGCTCCT  7559

Qy   7563  AGGGTTCATGACAAATTCCTCGTGGACTCCATAGAGCGCGTAAGAGGGCAGCTCAAGCC  7622
           ||| |||||||| | |||||||| || || || ||||| ||||||||||||||||||||
Db   7560  AGGGTTCATGACAACAATCCGTCGATCCGTTATTGAGCGCCTATTCGAGAGGGCCGCTCAAGCC  7619

Qy   7623  TGCCTAAGCATGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCC  7682
           ||||||||||||||| ||||||||||||| ||||||||||||| |||||||||||||||
Db   7620  TGCCTAAGCATGGTTACACTTATGAGGAAGCAATAAGGACTGTAAGGCCACATGCTGCC  7679

Qy   7683  ATGGGCTGGGGATCTAAGGTGTCGGTCAAGGTCAAGGCTTCGGTTAAGGACTTAGCCACCCCGGGGAGATGGCT  7742
           |||||||||| || || |||||||| |||||||||| |||||||  ||||||| |||||||||||||||||
Db   7680  ATGGGCTGGGGATCTAAGGTGTCGGTCGGTTAAGGACTTAGCCACCACCCCGCGGGGAGATGGCC  7739

Qy   7743  GTCCATGACGCGGCTCCAGGAGATACTTGAAGGGACGCCAGTCCCTTTCCCCTTTTCACTCTTACTGTG  7802
           ||||||||| || ||||||||| |||| |||||| || ||||| |||| | |||||||| ||||| |||
Db   7740  GTCCATGACCGGGCTTCAGGAGATACTTGAAGGGACTCCGGTCCCGTTCCCGTCCCTTTTCACTCTTACTGTG  7799

Qy   7803  AAAAAGGAAGTGTTCTTCAAAGAACCGAAAGAGGAGAAGGAGGAGCCCCCCCGCCTCATTGTGTTC  7862
           |||||||||||||| ||||||||||| |||| ||||||||||||||||||| |||||||||||||
Db   7800  AAAAAGGAAGTGTTCTTCTTTCAAAGACCGGAAGAGGAGAAGGAGGAGCCCCCCCGCCTCATTGTGTTC  7859

Qy   7863  CCCCCCTGGACTTCCGGACTGAAAAGCTTATTCTGGGAGACCCTGGACGGGGTAGCC  7922
           ||||||| || ||||||| ||||||||||||||| |||||||||| ||||||||||
Db   7860  CCCCCCCTGGACTTCCGGACTGAAAAGCTGATCTTTGGGAGACCCCAGGCCGGGGTAGCC  7919

Qy   7923  AAGGCGGTGTTGGGGGGGCCTACCCTTCCCAGGGGAAATCAGCGAATTAGGGAG  7982
           ||||||||||||||| || ||||  ||||||||| |||||||||||||||||||
Db   7920  AAGGCGGTGTTGGGGGGGCCTACCCTTCCCAGAATCAGCGAGTTAAGGAG  7979

Qy   7983  ATGCTCAAACTGTGGGAATCAAAGAAGACACACCAGCCATCGTGTGGGACGCGCACATGC  8042
           |||| ||||||||| ||| || |||||||||| |||||||||||||| ||||| ||||||
Db   7980  ATGCTCAAGCTATGGGGGTCTAAAGAGAGACCCCTGCGCCATCGTGTGGACGCGCCACCTGC  8039

Qy   8043  TTCGACAGTAGCATAACTGAAGGAGGCACGTGGCCTGGCCTGGCAGACAGCGTTTATGCCCTGGCT  8102
           |||| || ||| ||||| |||| |||| |||| || ||||| | |||| || |||||||  ||||
Db   8040  TTCGACAGTAGCATAACTGAAGGAGGACGTGGTGGCTGGGGTTTGGAGACAGAGCTATACCGCTCTGCC  8099

Qy   8103  TCAGACCATCCAGAATGGGTGCGTGCGCCGTGCGCGGCCACTGGGCACACCATGGTC  8162
           || ||||||| |||||||||| | |||||| || ||| |||||||||||||||| ||
Db   8100  TCTGACCATCCAGAATGGGTGCGCGGCCACTGGGCACACCATGGTC  8159

Qy   8163  ACCCCGAGGGGTGCCAGTGCCAGTATTGTAGAGGTATTGTAGATCCTTGACCACC  8222
           |||||||||||| ||||  |||||||||||||| || |||||||||||| |||||
Db   8160  ACCCGGAGGGGTGCCCGTCGCCCGTCGTGAGAGGTATTGCAGATCCTGTCCTAACACT  8219

Qy   8223  AGTGGCGCAACTGCTTGACTTGCTCTATATCAGGTGAAAGCCGGCCCTGTGAGAGGGTGGGG  8282
           || ||||||||||||||||| | |||||| ||||| |||||||||||||||||| ||||||
Db   8220  TGCTCGCAGAGCCCTTCCCCGATGGGCACAGTGGCACTGTGATCTGTGATCTGTGAAGGGGTGCACCCC  8282
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Qy    9363 GGTAAGAGCTCGGCCCAAGGCCGGGTTCTACT 9395
           ||  |||||||||||||| |||||||||||||||
Db    9360 GGGAAGAGCTCGGCCCGAAGGCCGGSTTCTACT 9392
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CC    Of the twelve clones isolated, eight contained essentially the same
CC    insert. One was the same as these eight, except for a 3 nucleotide
CC    insert. Two of the 12 clones were unique long clones and one was a
CC    unique chimera. Analysis of the position of the K1-2-3a sequence
CC    w.r.t. the sequence of the negative strand of HGV indicated that it
CC    is contained within a 100 amino acid ORF that is located in the
XX    negative strand of the NS3 gene of HGV.
SQ    Sequence 9391 BP; 1694 A; 2551 C; 2998 G; 2148 T; 0 other;
```

```
RESULT 8
AAT15656
ID    AAT15656 standard; DNA; 9391 BP.
XX
AC    AAT15656;
XX
DT    16-SEP-1996 (first entry)
XX
DE    HGV-PNF 2161 polyprotein coding region.
XX
KW    Hepatitis G virus; HGV; hepatitis C virus; HCV; antigen; Y10;
KW    reverse open reading frame; Clone 470-20-1; serum PNF 2161;
KW    detection; vaccine; K3; ds.
XX
OS    Hepatitis G virus.
XX
FH    Key            Location/Qualifiers
FT    CDS            459..9080
FT                   /*tag= a
FT                   /product= HGV polyprotein
XX
PN    WO9532292-A2.
XX
PD    30-NOV-1995.
XX
PF    17-MAY-1995; 95WO-US06266.
XX
PR    15-FEB-1995; 95US-0389886.
PR    03-AUG-1994; 94US-0246985.
PR    26-OCT-1994; 94US-0285551.
PR    23-NOV-1994; 94US-0329729.
PR    16-DEC-1994; 94US-0344271.
PR                 94US-0357509.
XX
PA    (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI    Fry KE, Kim JP, Linnen JM, Murphy FA, Wages J;
PI    Young LM;
XX
DR    WPI; 1996-097371/10.
DR    P-PSDB; AAR90796.
XX
PT    Antigen encoded by reverse frame of positive strand RNA virus -
PT    used to determine infection by the virus and to vaccinate against
PT    e.g. hepatitis.
XX
PS    Disclosure; Page 119-136; 303pp; English.
XX
CC    This sequence represents the sense strand polyprotein coding region
CC    derived from hepatitis G virus (HGV). The reverse frame corresponding
CC    to this sequence encodes antigenic proteins which may be used in the
CC    detection of HGV infection, and also in the production of vaccines.
CC    Three distinct immunogenic regions have been isolated from three
CC    different HGV-epitope libraries. All three epitopic regions, K1-2-3a,
CC    K3 and Y10-13, are encoded by the negative strand of HGV. The antigenic
CC    regions encoded by the negative strand are all contained within
CC    relatively short and separate open reading frames. The Y10 series of
CC    clones was isolated from a cDNA library designated env which was
CC    generated by PCR amplification. Sequence independent single primer
CC    amplified (SISPA) PNF 2161 serum DNA was used as template. The primers
CC    given in AAT15652-55 amplify a fragment of the negative strand of HGV
CC    which contains a 139 amino acid ORF. The ORF has a methionine present
CC    at position 22, where the longest open reading frame is 117 amino acids.
CC    Both the cloned Y10 sequences, Y10-13-1 and Y10-13-2 start downstream of
CC    the Met codon. The primers given in AAT15630-37 amplify a fragment of
CC    HGV containing the C-terminal 31 amino acids of the E2 protein and the
CC    N-terminal 166 amino acids of NS2, which corresponds to the K3 clones.
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Qy    Best Local Similarity    84.9%;    Score 7971.8;    DB 17;    Length 9391;
      Matches 8509;  Conservative  0;  Mismatches  877;  Indels  1;  Gaps  1;
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Qy       3 ACGTGGGGGGGTTGATCCCCCCGGCACTGGGTGCAAGCCCCATAAACCGACGCCT 62
           |||||||||||||| || |||||||| ||||||||||||||||| ||||||||||
Db       1 ACGTGGGGGAGTTGATCCCCCCGGCACTGGGTGCAAGCCCCAGAAACCGACGCCT 60

Qy      63 ATCTAAGTAGACGCAATGACTCGGCGGCCGACCGGCCAAAAGGTGGTGGATGG 122
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ATCTAAGTAGACGCAATGACTCGGCGGCCGACCGGCCAAAAGGTGGTGGATGG 120

Qy     123 GTGGTGACAGGGTTGGTAGGTCGTAAATCCCGGTCATCCTGGTAGCCACTATAGGTGGGT 182
           ||| ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     121 GTGATGACAGGGTTGGTAGGTCGTAAATCCCGGTCACCTTGGTAGCCACTATAGGTGGGT 180

Qy     183 CTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTGCGGCCGGAGACCGCGCAGGTCCACAGGT 242
           ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db     181 CTTAAGAGAAGGTTAAGATTCCTCTGTGCCTGCGGCCGGAGACCGCGCAGGTCCACAGGT 240

Qy     243 GCTGGCCCTACCGGTGTGAATAAGGGCCCGACGTCAGGCTCGTGTTAAACCGAGCCCGT 302
           ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db     241 GTTGGCCCTACCGGTGGGAATAAGGGCCCGACGTCAGGCTCGTGTTAAACCGAGCCCGT 300

Qy     303 CACCCACCTGGGCAAACGACGCCCACGTACGGTCCACGTGGCCCTTCAATGTCTCTCTTG 362
           ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db     301 TACCCACCTGGGCAAACGACGCCCACGTACGGTCCACGTGGCCCTTCAATGTCTCTCTTG 360

Qy     363 ACCAATAGGTTTATCCGGAGTTGACAAGGACCAGTGGGGCCGGGGGTTATGGGAAG 422
           ||||||||||||| |||||||| |||| ||||| |||||||| ||||| | ||| ||||
Db     361 ACCAATAGGCGTAGCCGGCGAGTTGACAAGGACCAGTGGGGCCGGGGGCT-TGGAGAGG 419

Qy     423 GACCCCAAACCCTGCCCTTCCCGGTGGCCGGGAAATGCATGGGGCCACCCAGCTCCGCG 482
           || ||||  | |||||||  |||||||||||||||||||||||||||||||||||||||
Db     420 GACTCCAAGTCCCCTTCCCGTGGCCGGGAAATGCATGGGGCCACCCAGCTCCGCG 479

Qy     483 GCGGCCTGCAGCCGGGTAGCCCAAGAATCCTTCGGTGAGGCGGGGTGGCATTTCTTT 542
           |||||||||||||||||||||||||||||||||  | ||  | ||||||| ||||  ||
Db     480 GCGGCCTGCAGCCGGGTAGCCCAAGAATCCTTCGGGTGAGGCGGGGTGGCATTTCCTTT 539

Qy     543 TTCTATACCATCATGGCAGTCTTCGCTCCTTCTGCTCTTCTGGTTGAGGCGGGCCATTCTG 602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 TTCTATACCATCATGGCAGTCTTCGCTCCTTCTGCTCTTCTGGTTGAGGCGGGCCATTCTG 599

Qy     603 GCCCCGGCCACCCACCGTCTGTGCGAATGGCAATATTGCTGTGCC 662
           |||||| |||  |||||||||||||||||||||||||||||  |||||
Db     600 GCCCCGGCCACCCACCGTCTGTGCGAATGGCAATATTCCTCACAAATGTGTGCC 659

Qy     663 CCGGAAGACATCGGGTTCTGCCTGGAGGCCGATGCCTGGGGTGCCGTT 722
           |||  ||||||||||||| || |||  | || || |||||||||||||||
Db     660 CCGGAGGACACATCGGGTTCTGCCTGGAGGGTCGATGCCTGGGGTGCCACCATT 719

Qy     723 TGCACCGACCGGTTGCTGGCCACTGTATCAGGCGGTTTGGCTGTGCGGCCTGGCCAAGTCC 782
           || |||  ||||| ||| ||||||||||||||||||||| ||||||||||||||||||||||
Db     720 TGCACTGACCAATGCTGGCCACTGTATCAGGCGGGTTTGGCCTGCTGGCCTGGCCAAGTCC 779

Qy     783 GCGGGCCCAGCTCGTTGGGGAACTGGGAGCCTTGTACGGGCCCTTGCCGTCGGCGTTAC 842
           || ||||||||||||||||| ||||||||| |||||||||||||||||||||||||||||||
Db     780 GCGGGCCCAACTGGTGGGGGAGCTGGGTAGCCTATACGGGCCCCCCTGTCGGCGTCGGCCTAT 839

Qy     843 GTAGCCGGATCCTGGGTCTGGGCGAGGTTTACTCCGGGTCCTGACAGTTGGTGTTGCG 902
           ||||||||||| |||||||||||||| |||||||||| |||||||||||||||||||||||
Db     840 GTGGCTGGGATCCTGGGTCTGGGCGAGGTGTACTCGGGTGTCTTCAACGGTGGGAGTCGCG 899
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Qy   903 TTGAGGCGCCGGGTCTTACCTGATGCCCAACCTGAAGTGTGCCAGTAGAATGTGACGTTAAG 962
         || |||||||| || ||||||||||||| |||||||  |  |||| ||  ||  ||| ||||
Db   900 TTGACGCGCCCGGTCTTACCCGGTGCCTAACCTGACGTGTGCCGTGTGAGCGTGAGCTAAAG 959

Qy   963 TGGGGAAGTGAGTTTTGGAGATGGACTGAGCAGTTGGCCTCCAATTACTGGATTTTGGAA 1022
         |||||||||||||||||||||||||||||| || |||||||||| |||||||| ||||||
Db   960 TGGGGAAGTGAGTTTTGGAGATGGACTGAACAGCTGGCCTCCAACTACTGGATTCTGGAA 1019

Qy  1023 TACCTTTGGAAAGTCCATTTGAATTTTGGAGAGGAGTGATGAGCCTGACCCCTGTTG 1082
         |||| | |||| |||| |||||| || |||||| ||| || ||||||||||| ||||
Db  1020 TACCCTGGGAAGTCCCCATTTGATTTCTGAGAGGCGTGATAAGCCTGACCCCCTGTTG 1079

Qy  1083 GTTTGGGTGGCCGCATTGCTTTTGCTTGGTGGAGCAACGGATTGTCATGTTTTCCTGCTGGTG 1142
         |||| || || ||  || ||||||||||| ||||| ||||| |||| ||| ||| ||||| ||
Db  1080 GTTTGCGTGGCCGCATTGCTGCTGCTTGAGCAACGTTACGCGTTGGGAACGTTGCATGGTGGTGTG 1139

Qy  1143 ACGATGCGGGGATGTTGCAAGGCGGCCCTCCGTTTGGGGTGGGGTCCCGCCCCTTGAC 1202
         ||||||| ||||||||||||||||||| ||||||||||||| ||||||| ||||||||
Db  1140 ACGATGCGCCGGATGTTGCAAGGCGGCCCTCCGTTTGGGGTCACGCCCCTTGAC 1199

Qy  1203 TACGGGTTGAACGTGGCAGTCATGCTCTTGTGTGACTGCGGGTCGCGTATTCCCACTGGG 1262
         |||||||||||| |||| ||||| ||| || |||||||| || ||||||||| ||||||
Db  1200 TACGGGTTGACTTGGCAGAACCTGCTCTTGCAGAGGGTCAACGTTCGCGTTTTTTCGACTGGG 1259

Qy  1263 GAGAGGGTGTGGATCGAGGGAATGTTCACGCTCTTGTGTGACTGCGCCAACGGCCCCTGG 1322
         |||||||| ||||| |||||||||||||| ||| || ||||||| ||| ||||||||||
Db  1260 GAGAAGGTGTGGGAACGTTACGCGTTGGGAACGTTCAGTGCGTCAGTGACTGCGCCAACGGCCCCTGG 1319

Qy  1323 GTTTGGGTTCCCGGCCCTTTGCCAGTGGGTTGGCGGGGTGGTGGGCCGCACCCCATCACCCCATTGGAGC 1382
         || |||| ||||||||| || ||||| || || ||||| | || ||| |||||||| |||| ||| |||
Db  1320 GTGTGTGTTGCCTGTACTTTTAGATGTTGGGACCCCCAACCGTGATGTTCCTCGTTCCTCGTTGG 1379

Qy  1383 CACGGACAAAACCAGTGGCCCCTATCATGTCTATGGGTCTGTGTCCGTA 1442
         |||||| |||| ||||| || |||| ||||| ||||||||| || |||
Db  1380 AAGCGGTTGCTGATGTGGGAGCTTCGCCTGGGTCTTTGATGGGATTTCGGCGACCCCGGG 1439

Qy  1443 ACGTGCGTGTGGGGTTCCGTGTTGTTTGCCTCCACCGGCCGGTCGTGATTCGAAGATC 1502
         || |||| ||| || || ||||| || |||||||||||||| ||||| |||||| ||
Db  1440 ACTTTGCGTGTGGGGTTCCATTCCATCCGTTCGTTTGCCTCCACCAGTGGTCGTCGCGAAGATA 1499

Qy  1503 GATGTGCGGGAGTTTGTGCCCGTTGACTCGCCAGCTGCCACTGCACCTGGGTCTAGGGTCA 1562
         ||||| || |||||||||||| ||||| ||||| |||||||||||| |||| |||| ||
Db  1500 GATGTGCGGAGTTTAGTGCCCGTTGGTCAGTGTGGTGCCCATTAGCCGCACTTGGATCA 1559

Qy  1563 TCGGATCGGACACGGTTGTTGCCGCCTGTTGAGCTCTCCGAGTGGGAGTCCCGTGCGTAACGTGTATT 1622
         ||| |||| |||||||||| || ||||| || |||||||| | |||| | |||||||||| ||| |||
Db  1560 TCGGATCGGACACGGTTGTTGCCGCCTGTTGGAGAATCGGTGTCGGTGACGTGTGTT 1619

Qy  1623 CTGGACCGTGTGCCTGCTTCATGTGCGGCACCTGTGTCGGCCCCGAAACCGGG 1682
         |||||| ||||||||||| || || || ||||| ||||| ||||||||||||||
Db  1620 CTGGACTCGGCCTCCTCGGCGGGCAACCTGTGTCGGCTGGCCCCGAGACCCGGG 1679

Qy  1683 TCGGTTAGATTCCCTTTCCATCCGTCGGCACGGGCGCCTCGGGCCTGGGGCCTTGACAAAGGACTTGGAA 1742
         |||| |||| ||||| || || ||||| ||||||| ||||||| ||||| || |||||||||| ||||||
Db  1680 TCGGTTAGGTTCCCATTCCATCCGTCGCTCGGCACGGGCGCCTCGGCCTGGGGCCTTCGGCCTGGGGCCTTCCGGCCTGGACAAAGGACTTGGAA 1739

Qy  1743 GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATAAGGGGCCCCTGGGCAACCAG 1802
         ||||||||||| || |||||||||||| |||| || ||| ||||||||| |||||||||
Db  1740 GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGCCCCTGGGCAACCAG 1799

Qy  1803 GGGAGAGGCAACCGGTGCGCCTGCTTGTGTGGCCCGAACCATGACCAAGATC 1862
         || |||||||| |||| || || ||||||||| || ||||| |||||||||
Db  1800 GGCCGGAGGCAACCCGGTGCGCGTGCCTGCTCTCGGGTCCCATGACCATGACCAGGATC 1859

Qy  1863 CGGGTTCCCTGCATTGGTGAAATGCCCACAGCCATAGAGCCTCCGACTGAACG 1922
         || ||||||| ||||||| ||| || |||||| |||||||| ||||| |||
Db  1860 CGAGATACCCTACATCGGTGTGAGTCCCGCCACCATTGAGCCTCCCACCGGGACG 1919

Qy  1923 TTCGGGTTCTTCCCCGGAGTCCCGGGAGCTCTAGGCCACGGAAGTG 1982
         || ||||||||| ||||| || |||| || |||| |||||| |||
Db  1920 TTTGGGTTCTTCCCCGGGGTCTTGTTTCAACAACTGCATGCTGTTCGGGCACGGAAGTG 1979

Qy  1983 TCTGAGGCGGATTGGGCGGAGCTGGGCTTACGGGGGGGTTCTACGAGGCCTCTGGTTCGCAGG 2042
         | | |||||||||||||| |   |||||||||||||||| ||| ||| ||  ||||| |||||
Db  1980 TCCGAGGCGACTTGGGGCGGGCTTGGGCTTCTATGGAACCCCGGTGTGTGCGCAGG 2039

Qy  2043 TGTTCGGAGCTGATGGGACGGCCGAAATCCGGTTTGCCGGGGTACGCATGGCGTGTCTCCT 2102
         ||||||| || ||||| ||| | ||||||| ||||| ||||||| ||| |||| |||| ||
Db  2040 TGTTCGGAGCTGATGGGAGGGCCGAAATCCGGTTTGTTGCCGGGGTTGCGGAGCGCTTCTTCG 2099

Qy  2103 GGTAGAACCTGACGGGTTCATACGGTCCAGGGCCACCTGCAGGGGTGGATGCGGGCAAC 2162
         |||| || |||||| |||||  || || || |||||| ||||| |||||| ||| ||||
Db  2100 GGCAGGCCTGATGGTTTATACAGTGTCCAGGGTCACTGCGATCGCAGGAGGTGGATGCAGCAGGCAAC 2159

Qy  2163 TTCATCCCTCCTCCACGCTGGTTGCTCTTGGATTTTGTATTTGTCCTGCTCTATCTGATGC 2222
         ||||| | |||| ||  |||||||||| ||| || ||||||| || | ||| ||| ||||
Db  2160 TTCATCCCGCCCCCGCCGGTTGCTCTTGGACTTTGTATTTGTCCTGTTATACCTGATGC 2219

Qy  2223 AAGCTGGCTGAGGCACGGTTGGTGCCCGTTGGCCCCCTTGAGTCTTGCTTGTTCTCTGTGTGGTGGTGAAC 2282
         ||| ||||||| ||||||||||| ||||| ||| |||||| || |||| ||  | |||| ||| |||||||
Db  2220 AAGCTGGCTGAGGCACGGTTGGTGCCCGTATCTTGCTCTGTCAGTATGATGATGTGCTGTGTGGTGGTGTGGGTGAAC 2279

Qy  2283 CAGTTGGCGGTTCTAGGACTGGCCTTTGGGCCTGCGGTGATTTTTTCGG 2342
         ||| ||||||| ||||||||||||||| ||||||| |||| ||||||||
Db  2280 CAGCTGGCAGTCCTGCTGGCCTGCGGTGCCCACCCTCAGCTTGGGTGTTTCCTGTTGTTGGG 2339

Qy  2343 GGCCTGCTTGTCATGGTGTTTGGGCTCGGGGCCGAGTTCTCGTCAGTATGATACTAGCA 2402
         |||||||| || || | |||| |||| ||||| ||||||| | ||||| || || || |
Db  2340 GGCCTGCTCCCGTCCCGTCCTGCTCGGGGACTCCCCGTCGTCAGTATGATGATTGGGTTTGGCA 2399

Qy  2403 AACCTGTGTGTTGTTTGGTTGGATGGGCCCTCAGCGGCCTCATGTTCCTCGTGTGTTGTGG 2462
         |||||||| || |||| ||| ||||| |||||||||||| || ||| | ||| |||||||
Db  2400 AACCTGGTGCTGTTTTAGATGTTGGGACCTGGCCTCAGCGTGTCCTCGTGTGTTGTGG 2459

Qy  2463 AAGCTCGCTCGGGGAGCTTCCCGCCGCACTTTTGATGGGATTTCGGCGACACCCCGGG 2522
         |||||||| |||||||| | ||||| ||||||||||||||||||| |||||||||||
Db  2460 AAGCTTGCTCGGGGAGCTTTTTCCGCTGGCCTGCTCTTGATGGGGATTTCGGCGACCCCGGGG 2519

Qy  2523 CGCACCTCTGTGTCTGGGGCCGAGTTCTCGTCACATTGACGTGGACACTTCG 2582
         ||| || | |||| |||||| ||||||||||||  |||||| ||||| |||
Db  2520 CGCACCTCAGTGTCCGGGGCCGAGTTCTCGTCATCGCTGGTCTACATTCGGAGGTGGACACTTCG 2579

Qy  2583 GTGTTGGCTGGTGGTGGTGCCCAGCGGCTTGGCTTGGGCCATAGCGGCTCCTGAGCTCAATG 2642
         |||||||| || || || ||||| ||| || ||| ||||| ||||| || |||||||||||
Db  2580 GTGTTGGGCTGGTGGTGGTGCCCAGTGGCTTGGGTGTGCGCTCCTCGAGCTCGATG 2639

Qy  2643 AGCGCAGGGGGTGGAAGCACAAGGCCGTGATCTATCGAGAGGACCGTGTGTGTAAAGGGTACCAG 2702
         ||||||||| || ||| ||||||||||| | ||||| ||| || |||||| ||| ||||||||||
Db  2640 AGCGCAGGGGGTGGAGGCACAAAGCGTGATCTATAGGACGTGGTGTTAAGGGTACCAG 2699

Qy  2703 GCTGTGCCCAGAGGGTGGTGCGAGCCCTCGGGGAGGGGCGTGTTGAGTGTCTCCACCAAGCTTCTG 2762
         | |||||| ||||||| ||| |||||| | |||||||| |||| ||||| ||||||||||||||
Db  2700 GCAATCGGTCAAAGGGTGGTGAGGAGCCCCTGCCGTGGTTGCCAAACCCCTGCTGCTCCACCAAGCTTCTG 2759

Qy  2763 ACGTTCGCCTGGTCGCTTGGCCTCATACATCTGGACGGATGCTGATGATGTGGTGGTG 2822
         || ||| |||||||| || |||| || | || || ||| ||||| |||| |||| |||
Db  2760 ACCTTTGCCTGGTCGCTTGGCCTCTGTACATCTGCCAGATGCTGTGATGTGATGTGTTGT 2819

Qy  2823 GCCTGGTGCCCGTTGCGACTGGACTGGGCCCTCGGAGAGCTCCTGG 2882
         |||| || |||||| || ||||||||| ||||||||| ||| ||||
Db  2820 GCCTTGGTGCCTGTTGTTGCTGGCCGGTTGGATTGGGCCTTGGAGGAGATCTTG 2879

Qy  2883 GTCTCCCGGCCCCTCGTTACGGCCACGGGTGTGTCGGTTCTGTTGAGTGCTGTGATGGCGGGC 2942
         |||| ||| ||||| ||| ||| || ||||| || |||| |||| |||| || ||||| |||
Db  2880 GTGTCCCGGCCCCTGGTCCGTCGGGAATCGGTGTTGCCGTGGTCGGTGGTTGGTGAATGGCGGGT 2939

Qy  2943 GAGAAGGCCACCACCATCCGACTGGTCGCCAAGAGGGCCTACCTGTT 3002
         || |||||||| ||||||| ||| | | || |||||| ||||| |||
Db  2940 GAGAAGGCCACCAACCGTCCGGCTCCCAAGAGTGTGCCGAGAGAGCTTATTTGTTC 2999

Qy  3003 GACCACGTGGCTCTTCTCCGCCGTCAATGCCATGCGTCTAGGCACGCGGACGCGGC 3062
         ||  |   || || | |||| |||| |||||||| || || ||||| |||||| ||
Db  3000 GATCATATGGGCTCTTTTTCGTCGTCAAGGAGCCCCTGTTCAAGGAGGACGCAGCT 3059

Qy  3063 TTGGGTTCTTCCCCGGAGTCGGGACGACGCTGCCGATCATCAGAGATCCCGCAGGACC 3122
         |   || |||||||| || |||| ||||| ||||| ||| ||||| |||||||||||
Db  3060 TTTGGGTTCTTCCCCGGGGTCTTGTTCAACAACTGCATGCTGTTCAACGTGCGCTTGGGCACGGAAGTG 3119
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Db  4140 ATTGGGAGAGTCCGGAGCTGGCCGTCGGGGTGCGGGGTGCGGGGTCGAACTAGTGCTCTACGGCCACC 4199
              ||||    ||||||||||| |||  |||||||  ||| ||||| ||||||||||||
Qy  4203 GCCACCCCTCCGGATCCCGATGACCCCAGCACCACCCATCCCATCATTGAGACAAAACTGGAC 4262
         ||||||||||  |||||||||||||  ||  ||||||||  |||||||   |||||||
Db  4200 GCTACACCTTCCGGATCCCGATCCCCTATGACGCAGCACACCCTTCCATAATTGAGACAAAATTGGAC 4259

Qy  4263 GTGGGAGAGATCCCTTCTATGGCCATGGCATACCTCTTGAGCGGATGCGGACCGGGAAGG 4322
         ||||| |||| |||||||  |||||||||  |||  ||||||||||||
Db  4260 GTGGGCGAGATTCCCTTTTATGGGGCATGGGAATACCCCTGCAGCCGGATGCGGAACCGGAAGG 4319

Qy  4323 CATTCGTATTCTGCCACTCCAAGCTGAGTGCGAGCGCCTGGCGGGCCAGTTTTCGGCT 4382
         |||||| ||| |||||||||  ||||  || ||||||  ||||||||||||
Db  4320 CACCTTCGTGTTCTGCCATTCTAAGGCTGAGTGCGAGCGCCTTGCTGGCCAGTTCTCCGCT 4379

Qy  4383 AGGGGGGTAAATGCCATCGCCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATGGA 4442
         ||||||| |||||| ||||||||||||||| ||||  |||||||
Db  4380 AGGGGGGGTCAATGCCATTGCCTATTATAGGGGTAAAGACAGTTCTATCATCAAGGATGGG 4439

Qy  4443 GACCTGGTGTGTGCTACAGACGCCACTATCCCACTGGGTACACTGGAACTTCGATTCT 4502
         ||||||||||| |||||||  |||||||  ||||||||  |||||||| ||
Db  4440 GACCTGGTGTCTGTGCTACAGACGCGCTTTCCCACTGGGTACACTGGGAAATTTCGACTCC 4499

Qy  4503 GTCACCGATTGTGGTTAGTGTGGAGGAGGTCGTTCGAGGTGACCCTGACCTCACCATT 4562
         |||||||||||||| ||||||  |||||||||||||||||||||||||
Db  4500 GTCACCGACTGTGGATTAGTGGTGGAGGAGGTCGTTGAGGTGACCCTTGATCCCACCATT 4559

Qy  4563 ACCATCTCCCTGCCACGGTGCCCGTGGCTGGCTGGATCGTCGAGCTGCGGGGTCGCGGG 4622
         |||||||||||||| ||||||||| ||||| |||||| ||||||||||||||
Db  4560 ACCATCTCCCTGCCGACAGTGCCTCTGCGTGGCTGGATCGTCGAGACGAGGACGC 4619

Qy  4623 ACGGGTAGGGCAGGTCTGGGCGGCTTGGTGGTGCCATGGCTTGAGCAAGGGGGACAAGGTT 4682
         |||||||||||||||| ||||| |||||||||| ||||| ||||||||||
Db  4620 ACGGGTAGGGGCAGGTCTGGGCGGCTACTACTACTACGGCGGGTCGCGGGT 4679

Qy  4683 GTGGTGCGCTCAGGTCCTGTTCGGTCGGCGGCGAGACTTTACGACAACTGCCCTTACACCGCAGCC 4742
         |||||||||||||||||||||||  ||||||||||||||||||
Db  4680 GTGGTGCGCTCAGGTCCTGTTCGGTCGGCGGCGAGAGTTGACCTGGAAGCTGGAAAGGGGGT 4739

Qy  4743 GAACCTGACCTGACAGCAAACCTACTGAGACTTTACGGCTGCCCTTACACCGCAGCC 4802
         |||||||||||||||||||||||||||||||||||||
Db  4740 GAACCTGACTTGACAGCTGAACTACTACTGAGACTTTACGGCTGCCCTTACACCGCAGCC 4799

Qy  4803 GTCGCAGCTGACATTGGGAGCATTGGGAAGCCCGTGTTCTTTTCGGGGCTTGCCCCCGTTGAGGATG 4862
         |||||||||||||  |||||| ||||||||||||||||||
Db  4800 GTCGCGGCTGACATCGGAGAAGCGCGGTGTTGTTCTTCTCTGGGCTCGCCCCATTGAGGATG 4859

Qy  4863 CATCCCGATGTTAGCTGGCAAAAGTTCGCGGCGTCAACTGGCCCTTCGGTGGTGGTGTT 4922
         |||||||| ||||||||||||||||||||||||||||||
Db  4860 CACCCTGATGTGCAGCTGGCAAAAGTTCGCGGCGTCAACTGGCCCTCGGTGGTGGTGTT 4919

Qy  4923 CAGCGGACCATGTGCCCGGAAACACTCGTCTCCCGGCCATCGGATGACCCCAGTGGGCA 4982
         |||||||||||||||||||||||||||  ||||||||||||
Db  4920 CAGCGGACCACATGTGTCGGGAAACACTGTCTCCCGGCCATCGGATGACCCCAATGGGCA 4979

Qy  4983 GGTCTGAAGGGCCCGAATCCTGTCCCACTCGTGCTGAGTGGGCAATGATTTACCATCT 5042
         ||||||||||||||||||||||||||||||  ||||||||||||||
Db  4980 GGTCTGAAGGGCCCCAAATCCTGTCCCACTCCGTGCTGGATGAGTGGGCAATGATTTACCATCT 5039

Qy  5043 AAAGTGGCCCGGCCATCACATCGTGACGACCTGGTCCGGGGTGGGCCGAGGGT 5102
         ||||||||||||||||||||| ||||||||||||||||||
Db  5040 AAAGTGGCCCGGCCATCACATCGTGACGACCTGGTCCGGGGATGTGAAGGGGGT 5099

Qy  5103 TACGTCCGGTCGGATGGCGGGACCCATCTTGATGGTGGGGCCTCGCTATTGCGGGGGCATG 5162
         |||||||||| ||||||||||||||||||||||||||||
Db  5100 TACGTCCGTGCGACGCTGGGCCGATCTTGAATGATCGGTCTAGCTTATCCGCGGGGGGGGAATG 5159

Qy  5163 ATCTATGCTCATACACCGGGTCTCTCGTTGGTTACAGACTGGGATGTGAAGGGGGT 5222
         |||| ||||||||||||||||||||||||||||||  |||||
Db  5160 ATCTACGCGTCATACACCGGGTCGCTCGGTGACGACTGGGATGTGAAGGGGGT 5219

Qy  5223 GGCAGCCCCCTTTATCGGCAGTGCCCGGTTGTGTCAGGTCCCC 5282
         ||  ||||||||||||||||||||||||||||||||||||
Db  5220 GGCGCCCCCCTTTATCGGCAGTGCCCGGTTGTGTCAGGTTCCT 5279
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Db  3060                 | |||    |||||||||||||||||||||||||||||||||||||||||
         CTTGAACCTCTGTCATTCACTAGGACGGACGCTGTGCATCACTACGGGATGCCGGCGAGGACT 3119

Qy  3123 CTGTCCTGCGGGACAGTGCGCTCATGGGTTTACCCGGTGGTAGCACCGGCGCCGCGGTGATGAGGTT 3182
         ||||||||||| ||||||||||||||||| || || |||||||||||||||
Db  3120 TTGTTCCTGCGGGGGCAGTGCGCTCATGGGTTTTACCCGGTGGTTGCGCCGGCGCCGGGTGATGAGGTT 3179

Qy  3183 CTCATCGGGCTCTTTCAGGATGTGAATCATTGCCTCCCGGGTTGTCCCGACTGCACCA 3242
         |||||||||| |||| |||||||  ||||||||||||||||||
Db  3180 CTCATCGGGCGTCTTCCAGGATGTGAATCATTGCCTCCCGGGTTGTCCCGACCGCGCCT 3239

Qy  3243 GTTGTCATCCGTGCGGGAAAGGGCCTTCCTCGGGGTCACGAAGGCAGCCTTGACAGGT 3302
         ||||||||||||||||||||||||||  |||||||||||||||||
Db  3240 GTTGTCATCCGACGGTGCGGGAAAGGGCTTCTTGGGGTCACAAAGGCTGCCCTTGACAGGT 3299

Qy  3303 AGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTTGGGGACGGCTACGTCACGAAGC 3362
         |||||||  |||||||||||||||||||||||  ||||||||||||||
Db  3300 CGGGATCCTGACTTACATCCAGGGAACGTCATGTGTTGGGGACGGCTACGTCGCGAAGC 3359

Qy  3363 ATGGGCACATGTCTGAATGGCCTGCTGTTCACAACTTTCCATGGGCTTCATCCCGAACC 3422
         |||||||||||||||||||| ||||||||||||||||||||||
Db  3360 ATGGGAACATGCTGAACGCCTGTCTGTTCACGACCTTCCATGGGCTTCATCCCGAACC 3419

Qy  3423 ATCCCCACCGTGGGGGCCCTAATCCAGGTGGTGTCAGCCAGTGATGACGTCACG 3482
         ||||||| |||||||||||||||||||||||| ||||||||||||
Db  3420 ATCGCCACACCGTGGGGCCCTTAATCCAGGATGGTGCTCAGCCAGTGATGATGTCACG 3479

Qy  3483 GTGTACCCGCTTCAGATGGGCAACTTCGTTGACGCCCTGCCAGGCCGGAGTCC 3542
         ||||||||||||| ||||| |||||| |||||||||||||||||
Db  3480 GTGTATCCACTCCCGGATGGGTCACTTCGTTAACACCTTGTACTTGCCAGGCTGAGTCC 3539

Qy  3543 TGTTGGGTTATTAGCATCCGACGGGGCTTTGTGCCATGGCAAGGGGGACAAGGTT 3602
         ||||||| |||||  ||||| |||||||||||||||||||||
Db  3540 TGTTGGGTCATCAGATCCCACGGGGCCCATGCCATGGCAAGGGGACAAGGTG 3599

Qy  3603 GAGCTGGATGTGGCCACGCACGCAGTGAAGATGCTCGTGTCAGTGCTTCCACTCTGCGGGCAGGGTT 3662
         |||||||||||||||||||||||| |||| ||||||||||||||
Db  3600 GAGCTGGATGTGGCCACGCACGCAGTGAAGATGCTCGTGTCGGTGCTCGGCCTCACCGGTCCTA 3659

Qy  3663 TGCGACAAAGGGCACGCAGTAAGAATGCTCGTGTCAGTGCTCCACTCTGCGGGCCAGGGTT 3722
         ||||||||||||  |||||||||||||||||| || |||||||||||||
Db  3660 TGTGACGAAAGGGCACGCAGTAAGAATGCTCGTGTTTCGGCTTCCACTCCCGGTGGTAGGGTC 3719

Qy  3723 ACTGCGGCCGCCGATTCACTCAGCCGTGGACTCAAGTGTGGCCAAGACTACCACA 3782
         |||||||||||||||||| ||||| |||||||||||||||||||
Db  3720 ACCGCGGCCGCACGGTCTCCTTCACTAGGCCGTGGACCGCCCAAGATGCCAAAACCACTACT 3779

Qy  3783 GAACCCCTTCCGGTTGCCGGCCGCAAAAGGAGTTTCAAGGAGGCCCCGTTTGTTTATGCCTACG 3842
         |||||||||||||||||||||||||||||| ||||||||||||||
Db  3780 GAACCCCTTCCGGTGCCGGCCGCCAAAGGAGTTTTCAAAGAGGCCCCGTTTGTTTATGCCTACG 3839

Qy  3843 GGGCGGGAAAGAGCACCCCGTACCGGGAAGTTTTTTGGCCGTACGGCCAACATGGGCTCTTG 3902
         |||||||||||||| |||||||||||||||||||||||||
Db  3840 GGAGCGGGAAAGAGCACACCTCGGTTTTTTTGGCCGTTACGGCCAACATGGGCTCTTA 3899

Qy  3903 ATCTTTGAACCGTCGATCATTGGTCGTGTGGCCATGGCCCATACATGAGCCGTGGCG 3962
         |||| |||||||||||||||||||||||||| |||||||||||
Db  3900 ATCTTTGAACCGTCATATCGTGTGGCCGGCCATGTGGGCCCATACATGAGCCGTGGCG 3959

Qy  3963 GGGAAACACCCCAGTATTACTGTGGCCATGACCACCACTGCTTTCACAAGGATCACTGAC 4022
         |||||||||||| |||| || |||||||||||||| ||||||||||
Db  3960 GGTAAACATTCCAAGTATACTGTGGGCATGACATGATCAACTGCTTTCACAAGGATCACTGAC 4019

Qy  4023 TCGCCCCTTACGTATTCCACTTACGGAAGGTTTTTGGGCTCCAACCCTAGGCCAGATGCTGAGG 4082
         ||||||||  ||||||||||||||||||||||| || |||||||||
Db  4020 TCCCCCCTGACGTATTCAAACCTATGGAGGTTTTTGGGCTCCAACCCTAGGCCAGATGCTACGG 4079

Qy  4083 GGTGTCGGTGGTCATTTGTGACGAGTGCCAGAGTCATGACTTCAACTTGTGTTGTTGGGC 4142
         ||||||||| |||||||||| |||  ||  ||| ||||||||||||||||
Db  4080 GGCGTTTCGGTGGTCATTTGTGATGAGTGCCACAGTCATGACTTCAACCCTGCTGTTAGGC 4139

Qy  4143 ATTGGGGCGTGTCAGGGAGCTGGCCGGAGGTGTTGCAATTGGTGCTCTACGGCCACT 4202
         ||||| | ||| || ||||| ||||||||||||
Db  4140 
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Qy  5283  CCGGTAGACCATCGGCCGGGGGAGAGTCTGCGCCATCGGATCGCAACACAGTGACAGAT  5342
          ||||||||||||||||||||||||||||||| | |||||| ||||| |||||||||||||
Db  5280  CCGGTAGACCATCGGCCGGGGGGTGAATCAGCAGCACCATCGGATCGCAAGACAGTGACAGAT  5339

Qy  5343  GCGGTGGGGCCCATCCAGTTGGATTGCCGATTGGTCAGTCATGACCCTGTCGATCGGGGAA  5402
          ||||| |||||||||||||||||||||| ||||||| ||| ||| |||||||||||||||||
Db  5340  GCGGTGGGCAGCCATCCAGTTGGACTGCCGATTCAGTCATGACTCTGTCGATCGGAGAA  5399

Qy  5403  GTGTGTCCTTGGCCCAGGCTAACGCGCCGAGGCCTACGCGCTACCACCAAGTGGCTT  5462
          ||| |||||||||||||| |||||||||||||| ||| ||||||||||||||||||||
Db  5400  GTGTGTCCTTGGCCTCAGGCTAAGACGCGGCCGCTAAGACGCGGCCGCTACCACGTGGCTC  5459

Qy  5463  GCTGGCTGCTACACGGGGACGCGCGGCCGTCCCCACTGTTTCAATTGTTGACAAGCTCTTC  5522
          ||||||||| |||||||||||||||||||| |||||||||||| ||||||||||||||||
Db  5460  GCTGGCTGCTATACGGGGACGCGCGGCCGTTCCCACTGTATCCATTGTTGACAAGCTCTTC  5519

Qy  5523  GCCGGGGCTGGGGCGCGTGGTAGGCGTGGTAATAGCTGCGCCAGTGGCG  5582
          ||||||| || ||||||||||  ||||||| |||| |||||||||||||||
Db  5520  GCCGGAGGTGGGGCGGTGTGGTGGGCGTGGCGTGGGCCATTGCTGCGCCAGTGGGC  5579

Qy  5583  GCCTATATGGGGCTTCTAGGAGCCCTTCCATTGGCTGCTCGCGCCTTCCTACCTCATGGGGTTG  5642
          ||||||||||||||||||||||||||||||||| ||||||| |||||||||||||||||||||
Db  5580  GCCTACGGGGCTTCAAGGAGCCCCGTTGGCAGCGCCGTTCCTACCTGATGGGGTTG  5639

Qy  5643  GGCGTCGGAGGCAACGCGCCAAAACCCGCTTAGCCTCGTCTCCTACTAGGGGCCGCTGGG  5702
          |||||||||||||||||  ||| || || |||||||| |||||| || ||||||||||||
Db  5640  GGCGTTGGAGGCAACGCGCTCAGACGCTTGCCTCGTCTGCCTCGTCTGGGGGCTGCTGGA  5699

Qy  5703  ACCGGCTTGGCCACGCGTCGTGGGGTTAACCATGGCGCGGCCGCCGTTCATGGGGAAGTGCT  5762
          |||||| || ||||||||| ||||||| |||||||||| |||| |||||||||| ||||  ||
Db  5700  ACCGGGCTTGGGCACTCCTGTCGTGGGGCTTGACCAGTGCCGTTCATGGGGGGGGCC  5759

Qy  5763  AGGGTCTCCCCCTCCTTGGTCACCATTTTTACTGGGGGGCCCGTGGGGGGCGTGGAGGGCGTG  5822
          || ||||||||||||||||||||||||||| ||||||| |||| ||||||||||||||
Db  5760  AGTGTTTTTGATTCACCATTTATTGGGGGGCCCGTGGGGGTTGGGAGGCGTT  5819

Qy  5823  GTGAATGCCGCTAGCCTTGTCTTCGACTTTATGCGGGAAACTATCATCAGAAGATCTG  5882
          ||||||||||| |||| ||||||| |||| || ||||| ||||||||||||||||||||
Db  5820  GTCAACGCGGCGAGCCTAGTCTTTGACTTCATGCGGGAAACTTCATCAGAAGATCTG  5879

Qy  5883  TGGTATGCCATCCCAGTGCTAACGCTGGGGGCAGGACTTCGCGGGGATCGCCCTCGGG  5942
          |||||||| |||||||| |||| ||||| | ||||||||||||||||||| ||||||||
Db  5880  TGGTATGCCATCCCAGTGCTACTGACCACCGGGGCCGGGGGCTTGCGGGGATCGCTTCGGG  5939

Qy  5943  TTGGTGTTGTACTCAGCTAACAACTCTGGCACTACCACCTGGTTGAACCGTCTGCTGACT  6002
          ||||||| |||||||||||||| || |||||||||||||||||||||||| |||||||||
Db  5940  TTGGTTTTGTATTCAGCTAACAACTCTGGCACTACCACCTGGTTGAACCGTCTGCTGACT  5999

Qy  6003  ACATTGCCAAGGTCCTCATCATGCAGTTACTTCGACAGTTACTTTCAGCAGGCCGATTACTGTGAC  6062
          ||||| || |||| |||||||||| |||||||| || |||||||||| |||| ||||||||||||
Db  6000  ACGTTACCAAGGTCTTCATCATGCAGTTACTTTCGGCAGGCCGATTACTGTGAC  6059

Qy  6063  AAGGTCTCAGCTGCTGTCGAGCCTGAGCCTGTGGTTGCCCTGGTCAAC  6122
          ||||||||||| |||||||| |||||||| ||||||||||||||||||
Db  6060  AAGGTCTCAGCTGCTGTCGACCCTGAGCCTGTGGTTGCCCTGGTCAAC  6119

Qy  6123  AGGGAGGCCACTCGCGGAGGGGTGGGGGTCCGGAGTTCAGGTGGGGTACGTGGGGACTGGATC  6182
          ||||||||||| ||||||||||||||||| ||||| ||||| |||| |||||||||||||||
Db  6120  AGGGAGGCCTAAGGTGGATGGAGGGGTGGGGGTCCGGAGTTCACCGCCAGGTGGGGTACGTGGGGACTGGATC  6179

Qy  6183  ACATTGCCAAGGTGCCATGGTGAATGGCCAGACTTCGGGGAGCTGCGACTTCAGCCGGGTCAGGTGTCATTA  6242
          |||| ||||||||||||| ||||||||| |||||||||||||||| ||||||||| |||||||||||||
Db  6180  ATGCGCCAAGGTCTGGGCGTGAATGGCCAGACTTTCGGGGAGCTGCGACTTCAGCCGGGTCACTA  6239

Qy  6243  AGGGAGGCCTTAAGGTGGCACTCGCGGAGGGGTGGGGGTGTCCGGAGATTCAGGTTCAGGTGGGGATC  6302
          ||| ||| ||||||||||| |||||||||||||||||||| ||||||||||||| ||||||||||||
Db  6240  CCCTTGGTGCCATTGGCGGAGGGGTGGGGGTGTCCGGGGAATGTTGCCTTGACCGGTCATGTTGGGGATC  6299

Qy  6303  AGTCGTTGTCTTTGTGTCGTGATCACCGGTGTGTCGATGTTTGAATGGCAACTCAAAGAT  6362
          ||||||| || ||||| |||||||||||||| |||||||||||||||| ||||||||||||
Db  6300  AGTCGTTGTGCCTCTGTGCCTCTGTGCCTCGTGATCACTGGTGTGTCGATGTTTGAATGGGCAACTCAAAGAA  6359
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Qy  6363  CCAGTTTACTTCACCAAGCTGTGTCAGGCAGTATTGGATGGGGACAGTCCCTGTGAACATG  6422
          ||||||||||||||||||||||||||  |||| ||||||||||||| ||||||||||||||
Db  6360  CCAGTTTACTTCACCAAGCTGTGCCGGCACTGTTGGATGGGGACTGTCCCTGTGAACATG  6419

Qy  6423  CTGGGCTATGGCGAGACGTGCGCCTTTGCTCGCCTCCTCGCCTCCGCCGGAGGTGTACCATTC  6482
          |||||| ||||||||||||||||||||| || | ||||||||| |||||||||||||||||||
Db  6420  CTGGGGTACGGTGAAACGTGCGGGCTGCTGGGCTCCGCCGGAGGTGTGCCCTTTC  6479

Qy  6483  GGGACGTCTGGTGGGCTGAGTGGTGGTGACCCTACCCACGTTGTGATCGATCAGGCGGAACA  6542
          ||||||||||||||||||||||||||| ||||| |||||| ||||||||||||||||||||
Db  6480  GGGACGTCTGCGTGGGCTGAGTGGTGACCACTACCACGTGGTAATCAGGAGGACC  6539

Qy  6543  TCCGCCTACAAACTGCTGCGCCAGCAAATCTGCTGCGTCTGTTGCTGCGAGCCCTATTAC  6602
          ||||| ||| || || |||| |||| ||||| || || || ||||||||||| ||||||||
Db  6540  TCCGCCTATAAGCTGCTGCGCCAGCAAATCCTATCGGCTGTGCTAGCTGCGAGCCCTACTAC  6599

Qy  6603  GTCGACGGCATACCCGTCTCATGGACGCGGACGCGCCGAGCCGCGCCTGCGCCTGGTCTATGGC  6662
          ||||| |||||| ||||||||||||||||| ||||| |||||||||| |||||||||||||||
Db  6600  GTCGACGGCCATTCCGGTCTCATGGGACGGGACGCGCTCGTGCGCCCCCATCCTCATGGTCTATGGC  6659

Qy  6663  CCTGGGCAAAGTGTCACCATTGACCGGGACGCGCTACACCCTTCCGCCATCAACTGCGGCTT  6722
          ||||| |||||||||||| ||||||||| ||||||| |||||| ||| |||||||||||||
Db  6660  CCTGGGCAAAGTGTTACCATTGACCGGGACGCGGCTACACCCTTGCCTCATCAACTGCGAGGCTC  6719

Qy  6723  AGGAATGTGGCGCCCTCTGAGGTGTCATTGACAGTGTCATTGACATTGGGACGGGAGACT  6782
          |||||||||||| ||||||| |||| ||||||| ||||||||||||||| ||||||||||
Db  6720  AGGAATGTGGCACCCTCTGAGGTTTCATTGCAGTGTCATTGACATTGGGACGGGAGACT  6779

Qy  6783  GAAGACTCAGAACTGACTGAGGCCAACCTGCCGGCGGACCTGCAGCCCCTTCAGGCTATC  6842
          ||||||||||| |||||||| ||||| ||||||||||||||||||| || |||||||||||
Db  6780  GAAGACTCAGAACTGACTGAGGCCGATCCTGCGGCGGACCTGCTGCTCTCCAAGGCGATC  6839

Qy  6843  GAGAATGCTGCCGAGAATTCTGAACCTCACATAGAGTCATCATGGAAGATTGCAGTAGTACA  6902
          |||||||||||||||||| |||||| || || ||||||||||| ||||||||||| ||||||
Db  6840  GAGAATGCTGCCGAGAATTCTTGAACCGACACATTGATGTCATCATGGGACTGCAGTAGTACA  6899

Qy  6903  CCCTCTTCTTTGTGGGAGTAGCCGAGATGCCGTGTGTGGGAGAAGCAGCATACCCCCACT  6962
          ||||||||||||| ||||||||||| |||||| |||||||||||||||||||| ||||||
Db  6900  CCCTCTTCTTTGTGGTGGTAGCCGAGATGCCGTGTATGGGAGAAGCAGCACATCCCCCTACT  6959

Qy  6963  CCATCGCCAGCACTTATCTCGGTTACTGGCAGCCAGATGAGAAGAGACCCCGTCGGTG  7022
          |||| ||||||||| |||| ||||| |||| |||||| ||||||||||||||||||||
Db  6960  CCATCGCCAGCACTTATCTCCGTTACTCGTAGCTGCAGATGAGAAGAGACCCCGTCGGTG  7019

Qy  7023  TCTTCTCGCAGGAGGATACCCCGTTCATTCCTGACTCATTGACGAGTCATTGACGAGTCCGAG  7082
          | |||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||
Db  7020  TCCTCCTCGCAGGAGGATACCCCGTTCTTTCTCTGACTCATTGGGTTCAATTGTCAGCGCTGGTCAGAGTCCGAG  7079

Qy  7083  ACAGCCGAAGGGGAGGAAAGCGTCTTCAACGTGGCTCTTTCCGTACTAAAAGCCTTGTTT  7142
          |||||||||||||||||||||||| |||| |||| |||||||| |||||| ||||| ||||
Db  7080  ACAGCCGAAGGGGAGGAAAGTGTCTTCAACGTGGCTCTTTCCCGTTCCGTTTATTTAAAAGCCTTATTT  7139

Qy  7143  CCACAGAGCGATGCCACAGAAAGCTTACCGTTAAGATGTCATGCTGTGTTGTCGCTGAAGAGC  7202
          |||||||| ||| ||||||||| ||| ||| ||||| |||||| ||| ||| || ||||||||
Db  7140  CCACAGAGCGACGCGGACCAGGTGACACCGAAGCGCTGATGTCGTGCTGTGTTCAAGATGAGAGC  7199

Qy  7203  GTAACACGCTTCTTTCATTGGATTGACGCGTCGCTGGCAAGCCTGCCTGGAGATG  7262
          || || || ||| ||||||| ||| |||||||| ||||||| ||| |||||||||
Db  7200  GTCACGCGCGCTTTTTCTCATTGGGTTTGACGCGTGGCGATGTTGCAAGTGTGACAAGTGTAGGCAAGAA  7259

Qy  7263  GAAATCAGAACCATCAGCTATTGGTCTCCGCTTACATTTGGTCTCCGCCTTGAATTGCAGGTT  7322
          |||| |||||||||| || ||||| ||||| ||||| ||||| |||| || ||||||||| ||
Db  7260  GAAATCCAGAACCATCAGCCTATTGGTCTCCGCTTACATTTGGTCTCCGCCTTGAATTGCAGGTT  7319

Qy  7323  GGGTGCTTGGCAATGAACTTACCTTTGAATGTGACAAGTGTAGGCGGCAAGAGC  7382
          |||||||||||||||||||| || ||||| ||||||||||||| ||||||||||
Db  7320  GGGTGCTTGGGCAATGAACTTACCTTTGAATGTGACAAGTGTAGGCGGCAAGAA  7379

Qy  7383  ACCTTGGCTTCCTCTTCTTTACATTGGTCTCGGGTCGACTGGCCACTCCGGCC  7442
          ||||||||||||| || || ||||| ||||| |||||||||||||| ||||||
Db  7380  ACCTTTGGCTCCTCTTCTTTACATTGGTCTCGGAGTGCTTGACTAGGGGCCACGCCGCCGCCC  7439

Qy  7443  AAGCCCCCCTGTTGGTGAGGCCCGGTTGCTGGTCGTGCTCCTTGCCGACACCACCAAGGTGTAT  7502
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Db   7440  ||||| || |||||||||||||||||||||||| || |||||||||||
            AAGCCTTCCGTGCTGAGCCGGTTGGCTCTTTGTTAGTGGCCGACACTACTTAAGGTGTAT  7499

Qy   7503  GTCACCCAACCCGACAAATGTTCGGAGAAGAGTTGACAAGGTTACTTCTGGCTGCCCCT   7562
            ||||||| |||||| || ||||||||||  ||| || ||||||| ||| || ||||||||
Db   7500  GTTACCCAATCCAGACAAATGTGGGACGGAGGGTGGGACAAGGTGACCTTCTGGCGTGCTCCT  7559

Qy   7563  AGGGTTCATGACAAATTCCTCGTGACTCCATAGAGCGCGTCTAAGAGGGCAGCTCAAGCC  7622
            |||||||||||| |||||||||||||||||| |||||||||||||  |||||||||||||
Db   7560  AGGGTTCATGATAAGTACCTCCTGGACTCTATTGAGCGCGTCTAAGAGGGCCCTCAAGCC  7619

Qy   7623  TGCCTAAGCAATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCCACATGCTGCC  7682
            |||||||||||||||||| |||||||||||||||| |||||||||||||||||||||||||
Db   7620  TGCCTAAGCAATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACACATGCTGCC  7679

Qy   7683  ATGGGCTGGGATCTAAGGTCGGTCAAGGACCTCCCACCCTCGCGGGAAGGATGGCT  7742
            |||||||||||| |||||||||||||||||| | ||||||| || ||||||||||
Db   7680  ATGGGCTGGGATCTAAGGTCGGTTAAGGACTTAGCCACCCACCCCGGGGAAGGATGGCC  7739

Qy   7743  GTCCATGACCGGCTCCAGGAGATACTTGAAGGGACCGCCAGTCCCTTACTTCTTACTGTG  7802
            |||||||||||||||||||||||||||| |||||||||| ||||||||||| | ||||||
Db   7740  GTCCATGACCGGCTTCAGGAGATACTTGAAGGGACTCGGTCCCGTCCCTTTACTTCTTACTGTG  7799

Qy   7803  AAAAAGGAAGTGTTCTTCAAAGACCGAAAGAGAAGAGGCCCCCGCCCTCATTGTGTTC  7862
            ||||||||||||||||||||||||| ||| | |||||||||||||||||||||||||||
Db   7800  AAAAAGGAGGTGTTCTTCAAAGACCGAA  GAGGAGAAGGCGGGCCCCGCCCGCTTCATTGTGTTC  7859

Qy   7863  CCCCCCTGGACTTCCGATAGCTGAAAAGCTTATTCTGGGAGACCCTGGACGGGTAGCC  7922
            ||||||||||| || ||||||| || ||| ||||| | ||||||||| | ||||||||
Db   7860  CCCCCCTGGACTTCCGATAGCTGAAAAGCTCATCTTGGGAGACCCCAGGCGCGGGTAGCC  7919

Qy   7923  AAGGCCGGTGTTGGGGGGGCCTTCCAGTACACCCCAAAATCAGCGAATCAGGGAG  7982
            |||||||||||||||||||| ||||||| || |||| || ||||| |||||||||
Db   7920  AAGGCCGGTGTTGGGGGGGCCTTCCAGTACACCCCAAAATCAGCGAGTCAAGGAG  7979

Qy   7983  ATGCTCAAACTGTGGGAATCAAAGAGAACACACCATGCGCCATCTGTGTGGACGCCACATGC  8042
            ||||||||||| || ||||||| ||| ||||||||| ||||| || |||||||| ||||
Db   7980  ATGCTCAAGCTATGGGAGTCTAAGAGACCCTTGCGCCATCTGTGTGGACGCCACCTGC  8039

Qy   8043  TTCGACAGTAGCATAACTGAAGAGACGTGGCGCTGGAGACAGAGCTTTATGCCCTGGCT  8102
            ||||| ||||||||| || ||||| ||||||||| | |||||||| ||| |||||||||
Db   8040  TTCGACAGTAGCATAACTGAAGAGACGTGGCGCTGTTTGGACAGAGCTATACGCCCTGGCC  8099

Qy   8103  TCAGACCATCCAGAATGGGTCGCGTGGGGGGCCCTGGGGAAATATATGCCTCTGGCACAATGGTA  8162
            || | |||||||||||||||| || || |||| || || |||| ||||| |||||||||| ||
Db   8100  TCTGACCATCCAGAATGGGTCGCGGGACCACTTGGGAAATATATGCCTCCAGGCCACCATGGTC  8159

Qy   8163  ACCCCGAGGGGTGCCAGTGGGTGAGAGGTATTGTAGATCCTCAGGGGTCTTGACCACC  8222
            |||||| || || ||||||||||| || ||||||||||||| |||||| || |||||
Db   8160  ACCCCGAGGGGTGCCACTGGGTGAGAGGTATTGTAGATCCTCAGGGGTCTTAACAACT  8219

Qy   8223  AGTGCGAGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCCCGCTGTGTGAGAGGGTGGGG  8282
            ||||||||||||||||||| |||| ||||||||||||| ||||| ||||||||| |||||
Db   8220  AGCGCGAGCAACTGCTTGACCTGCTACATCAAGGTGAAAGCTGCCTGTGTGAGAGTGGGG  8279

Qy   8283  CTGAAAAATGTCTCGCGTCCCTCATCGCGGCGATGACGTGTTGATCATATGCCGAAGCAGCGCGGCCT  8342
            ||||| |||||||||||||||| ||||| |||||||| | |||||||||| ||||||||||
Db   8280  CTGAAAAATGTCTCTCGTCTTTCTCATAGCCGATGAGTGACGCTGAATCATATGTGAGCGGCCA  8339

Qy   8343  GTGTGCGGATCCGACGACGCTTTGGGCAGAGCCCTTGGCGAGCTACGGGTACGCATGCGAG  8402
            |||||||||| || ||||||||||||||||||||| |||||| ||||||||||||||||||
Db   8340  GTGTGCGGACCCAAGCCAAGCGACGCTTTGGGCAGAGCCCTAGGGTACGCCGTGCGAG  8399

Qy   8403  CCTTCGTATCATCACTGACACGGCCCCCTTCTGCTCGGCTTGGCTAGCTGAGTGC  8462
            || |||||| || ||||||| ||||||||||||| | |||||||||||||||||||
Db   8400  CCCTCATATCATCATTGGACACGGCCCCCCTTCTGCTCCACTTGGCTGCTGAGTGC  8459

Qy   8463  AATGCAGATGGGAAAGCCCATTTTCTTCCTGACCACGGACTTTCGGAGGCCCCCTCGCGC  8522
            |||||| ||||||||| ||||||||||||| ||||||||||| |||||||||||||||||
Db   8460  AATGCAGATGGGAAGCCGCCATTTTCTTCCTGACCACCACGGACTTCCGGAGGCCGCTCGCTCGC  8519

Qy   8523  ATGTCGAGCGAGTACACAGTGACCCAATGCTTCGGCCATCGGTTACATCCTCCTATACCCT  8582
            |||||||| |||||| ||||| ||||||||||| |||||||||||||| | |||
```

```
Db   8520  ATCTCGAGTGAGTAGTGACCCGATGGCTTCGGCGTACGTCGGTACATCCTCCTTTATCCT  8579

Qy   8583  TGGCATCCTATCACACGTGGGTCATCATCCTCACGTGCTTCACCTGCCGCGTTAGGGGT  8642
            |||||| |||||| |||||||||||||||||||||||||||| |||||||| ||||||||
Db   8580  TGGCACCCATCCATCATCCTCATGTGCTAACGTGCCGCATTCAGGGGT  8639

Qy   8643  GGTGGCACCCGCTGATCTCGTGTGCCAGTACATGGTAATTACTACAAGTTTCCA  8702
            ||||||||||||| |||||||||||||||||||||||| || ||||| ||||||||||
Db   8640  GGAGGCACACCGTCTGATCCGGTTTGGTGCCAGGTGCATGGTAACTACTACAAGTTTCCA  8699

Qy   8703  CTGGACAAACTGCCTAACATCATGTCGCCTCCACGGACCAGCGTTGAGGGGTTACC  8762
            ||||| |||||||||||||||||||| |||||||| |||||||||||||||||||||
Db   8700  CTGGACAAACTGCCTAACATCATGTCGCCTCCACGGACCAGCGTTGAGGGGTTACC  8759

Qy   8763  GCAGACAACAACTAAGACAAAAATGGAGCGTCAGATGGCT GCTGAGGCACCTCAAGCTCCCT  8822
            |||||||||||||||| ||| ||||||||| ||||| |||||| ||||||||||||||||||
Db   8760  GCAGACAACAACTAAAACAAAGATGGAGGCTGTAAGGTTCTGAGCGACCTCAAGCTCCCT  8819

Qy   8823  GGCCTAGCAGTCCACCGGAAGAAGGCCCGGGCCATTGCCAACGCTATGCTCCGGTCCGC  8882
            |||||||||||||| |||||||||||||| || ||||||| |||| |||| |||| |||||
Db   8820  GGCTTAGCAGTCCACCAAAAGAAGGCCGGGGCCTTGCCGAACACGCATGCTCCGCTCCGCGC  8879

Qy   8883  GGTTGGGCTGAGTTGGCTAGGGGGCTGTTGTGGCGTCAGAAGTTCTTGGTCCCCCCTCCG  8942
            ||||||||||||||||||| |||||||||||||||| ||||||||||||||||||||||
Db   8880  GGTTGGGCTGAGTTGGCTAGGGGGCTGTTGTGCATCCAGGCCTACCGGCGCTTCTCTCCCCCT  8939

Qy   8943  GAGATTGCTGGTATCCCCGGGGGTTTCCCCCCTTATATGGGGTGGTTCAT  9002
            |||||||||||||||||||||||| ||||| | | |||||||| ||| |||
Db   8940  GAGATTGCTGGTATCCCCGGGGGTTTCCCCTCTCTCCCCCTATATGGGGTGGTACAT  8999

Qy   9003  CAATTGGATTTCACAAGCCAGAGGAGTCGCTGCGCGGTGGTTCTTAGCCCTGCTC  9062
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9000  CAATTGGATTTCACAAGCCAGAGGAGTCGCTGCGCGGTGGTTCTTAGCCCTGCTC  9059

Qy   9063  ATCGTAGCCCTTCGGGTGAACTAAAATTCATCTGTGCGGACTGATC  9122
            |||||||||||||||||||||||||||||||||||||||||||||||
Db   9060  ATCGTAGCCCTTCGGGTGAACTAAAATTCATCTGTGCGGACTGATC  9119

Qy   9123  ATCACTGGAGAGGTTCCGGCGCCTCCCGCCTCCCCCGCTGGGTAAAAAGGG  9182
            ||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   9120  ATCACCGGAGAGGTTCCGGCGCCTCCCGCCTCCCCCGCTGGGTAAAAAGGG  9179

Qy   9183  CCCGGCCTTGGGAGGCGATGGGTGGTTACTAACCCCGTCAAAGCCTGATGTGC  9242
            ||||||||||||||||||||||| || |||||| ||| |||||||||||||||
Db   9180  CCCGGCCTTGGGAGGCGATGGGTGGTTACTAACCCCTGCAGGGTCAAAGCCTGATGTGC  9239

Qy   9243  TAATGCACTGCCACTTCGGTCGCGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC  9302
            ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   9240  TAATGCACTGCCACTTCGGTCGCGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC  9299

Qy   9303  TGCTCGCAGAGCCCTCCGGATGGGGCACAGTGCACTGTGATCTGAAGGGGGTGCACCCC  9362
            ||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||||
Db   9300  TGCTCGCAGAGCCCTCCGGATGGGGCACAGTGCACTGTGATCTGAAGGGGGTGCACCCC  9359

Qy   9363  GGTAAGAGCTCGGCCCAAAGGCCGGGT  9389
            |||||||||||||||||| |||||||| |
Db   9360  GGGAAGAGCTCGGCCCGAAGGCCGGTT  9386
```

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RESULT 9
AAT94168
ID   AAT94168 standard; cDNA; 9391 BP.
XX
AC   AAT94168;
XX
DT   01-MAY-1998  (first entry)
XX
DE   Hepatitis G virus PNF-2161 genome.
XX
KW   HGV; protease; fusion protein; diagnosis; treatment; infection;
KW   protease; PNF-2161 genome; ds.
XX
OS   Hepatitis G virus.
```

```
XX
FH   Key             Location/Qualifiers
FT   CDS             459..9080
FT                   /*tag= a
XX
PN   WO9740168-A1.
XX
PD   30-OCT-1997.
XX
PF   24-APR-1997; 97WO-US06944.
XX
PR   24-APR-1996; 96US-0638911.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Belyaev AS, Chong SM;
XX
DR   WPI; 1997-535852/49.
DR   P-PSDB; AAW34983.
XX
PT   Hepatitis G virus protease - useful to develop products to study,
PT   diagnose and treat hepatitis G virus infection
XX
PS   Example 1; Pages 26-38; 115pp; English.
XX
CC   The present sequence was used in the development of a composition
CC   comprising, or a polynucleotide encoding an isolated hepatitis G
CC   virus (HGV) protease, or a fusion protein comprising a suitable
CC   fusion partner fused to a proteolytic polypeptide derived from HGV.
CC   The products can be used to diagnose and treat HGV infection.
XX
SQ   Sequence 9391 BP; 1694 A; 2551 C; 2998 G; 2148 T; 0 other;

Query Match             84.9%;  Score 7971.8;  DB 18;  Length 9391;
Best Local Similarity   90.6%;  Pred. No. 0;
Matches 8509;  Conservative 0;  Mismatches 877;  Indels 1;  Gaps 1;

Qy      3 ACGTGGGGGGTTGATCCCCCCCCCGGCACTGGGTGCAAGCCCCATAAACCGACGCCT    62
          | |||||| |||||| |||||||||||||||||||||||| || |||||||||||||
Db      1 ACGTGGGGGAGTTGATCCCCCCCCCGGCACTGGGTGCAAGCCCCAGAAACCGACGCCT   60

Qy     63 ATCTAAGTAGACGCCAATGACTCGGCGGCCGCCGACTCGGCGGCCGCCAAAAGGTGTGGATGG  122
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     61 ATCTAAGTAGACGACCAATGACTCGGCGGCCGCCGACTCGGCGGCCGCCAAAAGGTGTGGATGG  120

Qy    123 GTGGTGACAGGGTTGGTAGTCGTAAATCCCGGTCATCCTGGTAGCCACTATAGGTGGT  182
          || |||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    121 GTGATGACAGGGTTGGTAGTCGTAAATCCCGGTCAACCTGGTAGCCACTATAGGTGGT  180

Qy    183 CTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTGCGGCGGAGACCGCGCACAGGT  242
          ||||||||||||| ||| |||||||||||||||||||||||||||||||||||||
Db    181 CTTAAGAGAAGGTTAAGATTCCTCTTGTGCCTGCGGCGGAGACCGCGCACAGGT  240

Qy    243 GCTGGCGCCCTACCGGTGTGAATAAGGGCCCGACGTCAGGCTCGTCGTTAAACCCGAGCCCGT  302
          | ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTTGGCGCCCTACCGGTGGGAATAAGGGCCCGACGTCAGGCTCGTCGTTAAACCCGAGCCCGT  300

Qy    303 CACCCACCTGGGCAAACGACGCCCACGTACGGTCCACGTGCGCCCTTCAATGTCTCTCTTG  362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TACCCACCTGGGCAAACGACGCCCACGTACGGTCCACGTGCGCCCTTCAATGTCTCTCTTG  360

Qy    363 ACCAATAGGTTATCCGGCGAGTTGACAAGGACCAGTGGGGGCCGGGGGTTATGGGGAAG  422
          ||||||||| || ||||||||||||||||||||||||||||||||||||| | |||| | ||
Db    361 ACCAATAGGCGTAGCCGGCGAGTTGACAAGGACCAGTGGGGGCCGGGGGCT-TGGGAGAGG  419

Qy    423 GACCCCAAACCCTGCCCTTCCCGGTGGCCGGGAAATGCATGGGGCCACCCAGCTCCCCG  482
          ||| ||||| || ||||||||||||||||||||||||||||||||||||||||||||| |
Db    420 GACTCCAAGTCCCGCCCCTTCCCGGTGGCCGGGAAATGCATGGGGCCACCCAGCTGATCA  479

Qy    483 GCGGCCTGCAGCCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGGCATTTCTCTT  542
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    480 GCGGCCTGCAGCCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGGCATTTCCTT   539

Qy    543 TTCTATACCATGGCAGTCCTTCTGCTCCTTCGTGGTTGAGGCCGGGCCATTCTG  602
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 TTCTATACCATGGCAGTCCTTCTGCTCCTTCGTGGTTGAGGCCGGGCCATTCTG  599

Qy    603 GCCCCGGCCACCCACGCTTGTCGCGACGCGAATGGCAATATTCCTCACAAATTGCTGTGCC  662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    600 GCCCCGGCCACCCACGCTTGTCGCGACGCGAATGGCAATATTCCTCACAAATTGTGTGCC   659

Qy    663 CCGGAAGACATCGGGTTCTGCCTGAAGCGGCGATGCCTGGTGGCCCTGGGGTGCACGGTT  722
          |||||| ||||||||||||||||||| | ||||||| ||||||||||||||||||||||||
Db    660 CCGGAGGACATCGGGTTCTGCCTGGAGGGTGGATCCTGGTGGCCCTGGGGTGCACGGTT   719

Qy    723 TGCACCGACCGTGCTGGCCACTGTATCAGGCGGTTTGGCTGTCGCGGCCAAGTCC  782
          ||||| ||||  |||||||||||||||||||||||||||||||||||||||||||||
Db    720 TGCACTGACCAATGCTGGCCACTGTATCAGGCGGTTTGGCTGTCGCGGCCAAGTCC  779

Qy    783 GCGGCCCAGCTCGTTGGGAACTGGGAGCCTGGGGCCTGTACGGGCCTTGTCGGTCTCGGCTTAC  842
          |||||| || |  |||||| ||||  ||||  | ||| |||| || || | |||||||| || |
Db    780 GCGGCCAACTGGTGGGGAGCTGGGTGAGTTGTACTCGGGTGTCCTAACGGTGGGAGTGCGCGCAT  839

Qy    843 GTAGGCGCCGGGTCTACCTGATGCCCAACCTGAAGTGCAGTAGAATGTGACGTTAAG  902
          || |||||||||||||||||| ||||||||| ||||||||| |||| |||||||||||
Db    840 GTGCGCTGGGATCCTGGGCCTGGGAGTGTACTCGGGTGTCCTAACGGTGGGAGTGCGCG  899

Qy    903 TTGAGGCGCCGGGTCTACCTGATGCCCAACCTGAAGTGCAGTAGAATGTGACGTTAAG  962
          ||| |||| ||||  | ||||||| ||| |||| |||||||||||| | | ||| |||
Db    900 TTGACGCGGCGGGTTACCCGTGCCTAACCCGTGCCGTGCCAGTGCCGTGTGAGTGAGCTAAAG  959

Qy    963 TGGGAAGTGAGTTTTGGAGATGGACGCAGTTGGCCTCCAATTACTGGATTTTGGAA  1022
          |||||||||||||||||||| ||||||| |||| ||||||||||||||| |||| ||||
Db    960 TGGGAAGTGAGTTTTGGAGATGGACGCAGTGAACAGCTGCCTCCAACTACTGGATTCTGGAA  1019

Qy   1023 TACCTTGGAAAGTCCCATTTGAATTTGCTTTGCTGGAGCAAGCTGATGAGCCTGACCCCTGTTG  1082
          ||| | ||||||| |||||||||||||| ||||||||| ||||| ||| | ||||||||| ||||
Db   1020 TACCTCTGGAAGGTCCCATTTGATTTCTGTGCTGGAGCAACGCGGTGATAAGCCTGACCCCTGTTG  1079

Qy   1083 GTTTGGTGGCCGCATTGCTTTTGCTGGAGCAACCGATTGTCATGTTTTCTGCTGCTG  1142
          |||| ||||||||||||| | |||||||| |||||||||||| |||  | ||||| ||||
Db   1080 GTTTGCGTGGCCGCATTGCTGCTGCTGGAGCAACGCGGTGATGTCATGTCATGTCTCCTGTTGGTG  1139

Qy   1143 ACGATGGCGGGGGATGTTGCAAGGCGGCCCGGACCGGCCAAAAGGTGTGGATGG  1202
          ||| ||||| ||||| |||||||||| ||||  ||||||||||||||||||||| |||
Db   1140 ACGATGGCCGGGGATGTCGCAAGGCGCCCGGACCGGCCAAAAGGTGTGGATGG  1199

Qy   1203 TACGGGTTGAAGTGGCAGTCATGCTCCTGCAGGGTCAACGGGTCGCGTATTCCCACTGGG  1262
          ||||| ||||||||  || ||||| |||| | | ||||||||||| |  | || ||||||||
Db   1200 TACGGGTTGACTTGGCAGACCTGCGCTCCTTGCGAGGGCCAACGGTTCGCGTTTTCGACTGGG  1259

Qy   1263 GAGAGGTGTGGATCGAGGGGAATGCACGGTCCTTGTGACTGCCCCAACGGCCCCTGG  1322
          |||||| |||||| |  |||||| ||| || | |||| ||||  || || |||||||||
Db   1260 GAGAAGGTGTGGACGTGGGAACGTTACCGTCCAGTGTGACTGCGCTACGGCCCCATTGGAGC  1319

Qy   1323 GTTTGGTCCGGCCTTTGCCAGCTTTGCCAAGCAATCGCCCCCATCACCCATTGGTCTGTCCGTA  1382
          |||| | ||||||||| || | | |||| || ||| || |  | | || || | ||||| ||||
Db   1320 GTGTGTTGCCAGCCTTTGTTGCCAAGCAATCGCTGGGTGACCCCATCACCACTGTTGGTCGTCTACAGTC  1379

Qy   1383 CACGGACAAAACCGTGGCCCCTATCATGCGGTCCCGTCGTTCGTGTCCGTA  1442
          ||||| ||||| || |||||| |  |||| || || | |  |||  | ||||
Db   1380 CACGGCAAAATCAGTGGCCCTTTCATGCCGTCCCAGTGGTCTCATTATTGGAGC  1439

Qy   1443 ACGTGCGTGTGGGGGTTCCGGTTGTCTTTGGTTTCGCGCGGTCGTGATTCGAAGATC  1502
          ||| |  ||| |||| ||||  | || |||| ||| | | || |  ||||| | | ||
Db   1440 ACTTGCGTGTGGGGTTCCGGTTCTGGTTCCTTCCACCAGTGTCCGGACTCGGAAGATA  1499

Qy   1503 GATGTGTGGAGTTGTCGGCCGGTGGGGGAATGCATGGGGCCACCCAGCTCTAGGGGTCA  1562
          ||||| ||||| ||||| ||||||| | ||| |||| ||| |||||||| || |||| |
Db   1500 GATGTGTGGAGTTTTAGTCCCAGTTGCCCACCAGTGCTCTGCCACCACTTGATCA  1559

Qy   1563 TCGGATCGCGACACGGTGTTGAGCTCCGAGTCGGTGGAGTCCCGTGCGTAACGTGTATT  1622
          ||||| | |  ||||| |||  |||   |||| |||| || |||| |||  | |||| | |
Db   1560 TCGGATCGGCACACGGTGCCTGGGCTCTCCGAGTGGGGAATCCCGTGCGTGCGTGACGTGTGTT  1619

Qy   1623 CTGGACCGTCTCGCCCTTCCATGTGCCACCTGTGTCGCACTGTGTCGCCCCGAAACCGGG  1682
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Left column:

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Db  1620  ||||||||||||| || |||||||||  |||||||||||||||||||  1679
          CTGGACCGTGCGCCTTCGGCCACCTGTGTGAGGGACTGCTGGCCCGAGACCGGG

Qy  1683  TCGGTTAGAATTCCCTTCCATCGGTGCGGAACCGTGCGGCCTCGGCCTGACAAAGGACTTGGAA  1742
          |||||  ||||  |||  ||| ||||||  ||||||||||||||||||
Db  1680  TCGGTTAGGTTCCCATTCCATCGGTGCGGAAGCCGTGCGGCCTCGGCCTGACAAAGGACTTGGAA  1739

Qy  1743  GCTGTGGCCCTTCGTCAACAGGACAACTCCCTTCACCATAGGGGCCCCTGGGCAACCAG  1802
          |||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  1740  GCTGTGGCCCTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGCCCCTGGGCAACCAG  1799

Qy  1803  GGGAGAGGCAACCCGTGCGCGTGGGCTCGCCGCCCGGTGTTTGGGTTCCTACCATGACCAAGATC  1862
          | ||||||||||||||||||||||  |||||||||  ||||||||||| || |||||||||
Db  1800  GGCCGAGGCAACCCGTGCGCGTGGGCTGGCCGCCCGGTGTTTGGGTTCCTACCATGACCAGGATC  1859

Qy  1863  CGGGATTCCCTGCATTGGTGAAATGTCCCACCAGCCATAGAGCCTCCGACTGGAACG  1922
          ||||| ||  ||| || ||||||||||||||||||||||||||||||||  ||||||
Db  1860  CGAGATACCCTACATCTGGTGAGTGTCCCACCAGCCATTGAGCCTCCACCGGGACG  1919

Qy  1923  TTCGGGGTTCTTCCCCCGGAGTCCCGGCCATTAACAACTGCACATGCCCGCTAGGCACGGAAGTG  1982
          |||||||||| | |||||||||||  ||  |||||||||||||||||||||||
Db  1920  TTTGGGGTTCTTCCCCCGGACGCCGCCTCTCAACAACTGCACATGCCTTGGGCACGGAAGTG  1979

Qy  1983  TCTGAGGCATTGGGCGGAGCTGGGCTTACGGCGTTCTACGAGCCTTCGGTTCCGCAGG  2042
          ||||||||||||| ||||||| | |||||||||||||||||||||||||||||
Db  1980  TCCGAGGCACTTGGGCGGAGCTGGGCTTACGGCGTTCTATGAACCCCTGGTGCGCCAGG  2039

Qy  2043  TGTTCCGGAGCTGATGGGACCGCCGGAAATCCGGTTTGCCCGGGGTACGCATGGCTGTCCTCT  2102
          |||| ||||  |||| |||||||||||||||  ||  ||| |||||| ||||||||||  |||
Db  2040  TGTTCGAAGCTGATGGGAAGCCGCCGGAAATCCGGTTTGTCCGGGGTTTGCATGGCTGTCCTTCG  2099

Qy  2103  GGTAGACCTGACGGGTTCATCACGTTCCAGGGGCACTGCCGGCGTCGAGGTGGATGCGGCAAC  2162
          |||||||| ||| |||||||||||||||| ||||||||||||||||||||||||||||||||
Db  2100  GGCAGGCCTGATGGGTTTATACATGTGCCAGGGTCACTTGCAGGAGGTGGATGCGGCAAC  2159

Qy  2163  TTCATCCCTCCTCCACGCTGGTGCTTGGGATTTTTGTATTTGTCCTCTATCCTGATGC  2222
          |||||||| ||||||||| |||||||| ||||||||||||||||||| ||||||||
Db  2160  TTCATCCCGCCCCCGCGCCGCTGGTGTTGGGGACTCCCGTCTATGGGTGTCCTATACCTGATG  2219

Qy  2223  AAGCTGGTGAGGCACGGTTGGTCTGTGGTCCCGTTGCTTCTTGCTGGTGGTGGTGGTGAAC  2282
          |||||| |||||||||||||||| ||| ||||||||||||||||  || ||||||||||
Db  2220  AAGCTGGTGAGGCACGGTTGGTCCGTGTTGGTCCCGTCTATGCTGGTGGTGGTGGTGAAC  2279

Qy  2283  CAGTTGGGGCGTTCTAGGGACTGCCGGGCTGCCGTGAGAGTTTTTTGCG  2342
          || ||||||||||||||||||||||||||||||||||| |||||| || ||
Db  2280  CAGCTGGCAGTTCTCCTAGGGCTGCCGTGAAGCCGCCGCCAGGTGGGCTCTTCGCG  2339

Qy  2343  GGCCCTTGCCTTGTCATGGTGTTTGGGCCTTCCCACTGTCAGTATGATGATAGGTCTAGCA  2402
          ||||||||||||| |  ||| |||||||||| |  || | |||||||||| |||||
Db  2340  GGCCCCTTGTCCTGGACTCCCGGTCGTCGTCAGTATGATGATATTGGGTTTGGCA  2399

Qy  2403  AACCTTGTGTATTTCGGTGGATGGGCCCTCAGCGCCTCATGTTCCTGCGTGTTGTGG  2462
          |||||| |  || ||||||| ||| |||||||||||||  ||||| ||||||||| |||
Db  2400  AACCTTGTGTATTTTAGATAGTTTGGGACCCCAACGCGTCTGATGTTCCTGTGTTGTGTG  2459

Qy  2463  AAGCGCAGGGGGTGGAAGCCACAAGCACCGACCCCGGG  2522
          ||||||||||||||||||||||| ||||||||| |||||||
Db  2460  AAGCGCAGGGGGTGGAGGCCACAAAGCACCGACCCCGGG  2519

Qy  2523  CGCACCTCTGTGCTGCTCGGGGGCCGAGTTCTGCTTCGCGATGTCAGTATAGGTCACAGCA  2582
          |||||||||||| |  ||||||||||||| | || |||  ||||| || |||||
Db  2520  CGCACCTCAGTTGCTGCTCGGGGGCCGAGTTCTGCTACATTCGGAATGCTACACCGGTCCTA  2579

Qy  2583  GTGTTGGGCTGGGTGTACTTTCGGTGGATGGGCCCTCAGCGCCTCGTGTTCCTGCGTGTTGTGG  2642
          ||||| ||||||||| |||||||||||  | |||||||||||||||||| ||| || |||||
Db  2580  GTGTTGGGCTGGGTGTGGCCCGTGGGCCGTTGGGCCCTCAGCTCTGGCCTTCGATG  2639

Qy  2643  AGCGCAGGGGGTGGAAGCACCAAAGCCGTGGTTATAGGACGTGGTAAGGGTACCAG  2702
          ||||||||||| ||||  | ||||||||| |||||||||||||| |||||||
Db  2640  ACCGCGGGGCACGGTGATATCGATCTAGTCGTGTAAGGGTACCAG  2699

Qy  2703  GCTGTGCGCCAGAGGGTGGTGCGGAGCCCCTCGGGGAGGGGG ||| |||| |||  2762
          || |  || |||||||||||  ||||| |||||||||||||
Db  2762
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Right column:

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Db  2700  GCAATCGTCAAAGGTGGTGAGGAGCCCCTCGGGGAGGCGGCCTGCCAAACCCTG  2759

Qy  2763  ACGTTCCCTGTGCTGCTTGGCCTCCATACATCTGCCGCCGATGCGTGATGATGGTGGTGGTG  2822
          ||  |||||||||||||||||||||||| ||||||||||||| ||||||||||||| |||||
Db  2760  ACCTTTGCCTGTGCTTGGCCTGTCGTACATCTGCCAGCGTGTGATGATGGTGGTGGTT  2819

Qy  2823  GCCTTGGTCCTCCTCTTCGGCCTTCGACGCGTTGGACCGCCGTTGGCGCCCTGGAGGAGCTCCTG  2882
          |||||||||||||||| |||||  ||||||||||||||||||||||||||||||||| || ||||
Db  2820  GCCTTGGTCCTTCTCTTTGTCCTTCGACGCGTTGGATTGGGCCGTTGGAGGAGATCTTG  2879

Qy  2883  GTCTCCCGGCCCTCGTTACGGCGACTGGCACGGCGTGTTGAGTGCTGTGTGATGGCGGGC  2942
          |||||||||||||||||| || || |||||||||||||||||||| |||||||||||||
Db  2880  GTGTCCCGGCCCTCGTTGCGGCGGTTGGCACGGCGTGTTGAGTGCTGTGTGATGGCGGGT  2939

Qy  2943  GAGAAGGCCACCACCATCCGACTGGTCGTCCCAAGATGTGCCAAGAGGGGCCTACCTGTTT  3002
          ||||| |||||||  ||  ||||  |  |||||||||||||||  || ||||| |||| ||
Db  2940  GAGAAGGCCAACAACCGTCCGGCTGGTCTCCAGATGTGCGGAGAGGAGCTTATTGTTC  2999

Qy  3003  GACCACATGGCTCTTTCTCGCGCGTCGTGTCAAGGAGCGCTTGTGAATGGGACCGCGGCT  3062
          ||  || || |||| ||| || ||||||||||||||||| |||||||||||| ||||||||
Db  3000  GATCATATGGGCTCTTTTCTGCGTCGTGTCAAGGAGCGCGTTGGAATGGGAGGCCAGCT  3059

Qy  3063  TTGGAGCCCTTGTCATTCACTAGGACGGACTGTCGCATCATCAGAGATGCCCGGAGGACC  3122
          ||| ||||||||||||| || |||||||||||||||||||||| |||
Db  3060  CTTGAACCTCTGTCATTCACTAGGACGGACTGTCGCATCATACGGGATGCGCGGAGGACT  3119

Qy  3123  CTGTCCTGGACAGTCGTCATGGGTTTACCCTGTAGCACGCGCGGTGATGAGGTT  3182
          ||| |||||||||||| |||||||||||||||||| |||||||||||||||||
Db  3120  TTGTCCTGCGGCAGTCGTCATGGGTTTACCCGTGTGCGCGTGGTGATGAGGTT  3179

Qy  3183  CTCATCGGCGTCTTTCAGGATGTGAATCATTGCTTCCCGGGGTTGCTCCCGACTGCGACCA  3242
          |||||||||||||||||||||||| ||||||||||||||||||||| |||||||||||||
Db  3180  CTCATCGGCGTCTTCCAGGATGTGAATCATTTGCTTCCCGGGGTTGTTCCCGACCGGCCT  3239

Qy  3243  GTTGTCATCGGTGCGGTGGCGGGAAAGGGCTTCCTGGGGTCACGAAGGCAGCCTTGACAGGT  3302
          ||||| || |||| |||  |||  ||||||||||||||| |||||||||||| ||||||||
Db  3240  GTTGTCATCGACGCGTGCGGGAAAGGGCTTCTTGGGGGTCACAAAGGCAGCCTTGACAGGT  3299

Qy  3303  AGGATCCTGACTTACATCCAGGGAACGCCATGGTGTTGGGACGCGGCTACGTCGACGAAGC  3362
          ||||||||||||  |||||||| |||||||||||||||| || || ||||||||| |||||
Db  3300  CGGGATCCTGACTTCGTCATCCCAGGAGTGTGGGACGTGCTCGCGAAGC  3359

Qy  3363  ATGGGCGCACATGTCTGAATGCCGTGCTCTTCCATGGGGCTTCATCCCGAACC  3422
          ||| ||| |||||||| |||| ||||||||| |||||||| ||||||||||||
Db  3360  ATGGGAACATGCTTGAACGGCGTGCTCGTTCCATGGGCTTCATCCCGAACC  3419

Qy  3423  ATCGCCACGCGCCGGGGGCGGGCCCCTTAATCCCAGCTGGTCGTCAGCTGATGACGTCACG  3482
          ||||||||||| | |||||| ||||||||||||| |||||||||||||||||||| ||||||
Db  3420  ATCGCCACCACCCCGTGGGGGCGGGCCCCTTAATCCCAGATGGTGGTCAGCTGGTCACG  3479

Qy  3483  GTGTACCCGGTTCCAGATGGGGCAACTTCGTTGACGCGCCGGAGTCC  3542
          |||| |||||||| ||||| ||||||||||  ||| || ||||| ||||
Db  3480  GTGTATCCCGGTTGCTCGTTTGTACTTCGTTGTACTTCGGTAGGGTCC  3539

Qy  3543  TGTTGGGTTATTAGATCCGACGGGGGCTTGTGTGCCATGGCTTGAGCAAGGGGGACAAGGTT  3602
          |||||||| | |||| |||||||||||| | ||||||||  |||| ||||||||||||
Db  3540  TGTTGGGTTCATCAGATCCGACGGGGGCCCTATGGCTTGACAAGGGGACAAGGTG  3599

Qy  3603  GAGCTGATGTGGCCATGGAGGTTCCGGTTCACCGGTCCTT  3662
          |||||||||||||||||||||||||||||||||||||| ||
Db  3600  GAGCTGATGTGGCCATGGAGGTCTCGTGGCTCGTCGTCACCGGTCCTA  3659

Qy  3663  TGCGACAAAGGGCACGCAGCCAGTAGAAATGCCGTGTCAGTTGCCACTCTGGCCGCAGGGTT  3722
          ||||  || |||||| ||||| |||||||||||||  ||  |||  ||||||||| ||||||
Db  3660  TGTGACGAAGGGCACCGCAGTTAGGAATGCTCGTGTCGTCGGTTCACTCCGGTTAGGGTC  3719

Qy  3723  ACTGCGCGGCGATTCACTAGGACGTGGACTCAAGTACCAAGATGCCAAGATACCACCACA  3782
          || |||| ||| |||||||||| || |||  ||||||||| | ||  || |||  |||||
Db  3720  ACCGGCGGCACCGTTCACTAGGACGTGGTCAACAGATGCCAAGATATGCCAAAACCACTACT  3779

Qy  3783  GAACCCCTCCGGTGCCGGCAAAAGAGTTTTCAAGGAGGTTTTATGCCTACG  3842
          ||| |||||||||||||||||| || ||||||||  || |||| ||||||||
Db  3780  GAACCCCTCCGGTGCCGGCCAAAGGAGTTTTCAAAGAGGTTTTAAGCCTACG  3839
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Qy  3843  GGGGCGGGAAAGAGACACCCGCTACCGTTGAGTACGCAACAAGGTCTTG           3902
          || |||||||||||||  |||| |  || |||||||||||||||||||
Db  3840  GGAGCGGGAAAGAGCACTCGCGTCCCGTTGGAGTACGCAACAATAACATGGGCACAAGGTCTTA  3899

Qy  3903  ATCTTGAACCCGTCGGTAGCTACGTGCGAGGCCATGGCCCATCACATGGACGAGGCGGCTGGCG   3962
          ||||||||| |||  ||| || |||||| |||||||||||||||||||| ||||||||||||||
Db  3900  ATCTTGAACCCCAGTGCCACTGTGCGGCACTGTGCGGCCCATCGGCCCGTACATGGAGCGGCTGGCG 3959

Qy  3963  GGGAAACACCCCAGTATTTACTGTGGCCATGACACCACTGCTTTCACAAGGATCACTGAC       4022
          ||||| | |||||||  ||  |||||||| || || || || ||| ||||||||||||||
Db  3960  GGTAAACATCCAAGTATATACGTGGGCATGATAACAACTGCTTTCACAAGGATCACTGAC       4019

Qy  4023  TCGCCCCTTACGTATTCCACTTACGGAAGGTTTTGGCCAACCCTAGGCAGATGCTGAGG       4082
          || |||||||||||   |  ||||||||| |||||||||||||||||||| | |||  |
Db  4020  TCCCCCCTGACGTATTCAACCCATGGAAGGTTTTGGCCAACCCTAGGCAGATGCTACGG       4079

Qy  4083  GGTGTGTGGTGGTCATTGTGACGAGTGCCACAGTCATGACTCAACTGTGTGTTGGGC         4142
          || | || |||| |||| ||| |||||||||||| ||  |||| |||  |||||| ||
Db  4080  GGCGTTTCGGTGGTCATTGTGATGAGTGCCACAGTGCAACTGTTCAACTGTCTGTTAGGC      4139

Qy  4143  ATTGGGCGTGTCAGGGAGCTGGCGCGAGGATGTGGAGTGCAATTGGTGCTCTTACGCCACT     4202
          |||||||||| |||  ||||||||||||||| || || |||| |||||||||||||||||
Db  4140  ATTGGGAGAGTTCCGGGAGCTGGCTGGGGTGTGCCGAGCTGGTGCAACTAGTGCTCTACGCCACC    4199

Qy  4203  GCCACCCCTCCCGGATCCCCAGCACACCCATCAAATCATTGAGACAAAACTGGAC          4262
          || ||||| |||||||||| |||||||||| | | |   || || ||||| ||||
Db  4200  GCTACACCCCCCGGATCCCCTATGTGGCCTGCCCTTCCATAATTGAGACAAAATTGGAC       4259

Qy  4263  GTGGGAGAGATCCCCTTCTATGGGCATGGCATAGCGATACCTCTTGAGCGGATCGGACCGGAAGG  4322
          |||||||||| ||||| |   ||||||||| || ||   ||||||||||||| ||||||||||||
Db  4260  GTGGGGCCAGATTCCCTTTTATGGGCATGGCATGGAATACCCCTTGAGCGGATCGGACCGGAAGG   4319

Qy  4323  CATCTCGTATTCTGCCACTCCCAAGGCTGAGTCGAGGCCTGCGGCCCAGTTTTCGCT         4382
          ||||||||| || |||||||| ||||| || ||||||||| |   ||||| |||| |
Db  4320  CACCTCGTGTTCTGCCATTCTAAGGCTGAGTCGAGGCCTGCGGCCCAGTTCTCCGCT         4379

Qy  4383  AGGGGGGTGTAAATGCCATCGCCTATTACAGGGGAAACAGTTCTATCATCAAAGATGGA       4442
          ||||||| |||||||| ||| |  || || ||  ||||||||||||||||||| |||||
Db  4380  AGGGGGGTCAAATGCCATTGCCTATTATAGGGGTAAACAGTTCTATCATCAAGGATGGG       4439

Qy  4443  GACCTGTGGTGTGCTACAGACCGACCACTATCCACTGGTACACTGGGAACTTCGATTCT      4502
          |||||||||||||||||| ||||   ||||||| | |||||||   |||||||| | |
Db  4440  GACCTGTGGTGTGCTCTGCTACAGACGCGCTTCCCACTGGTACACTGGGAAATTTCGACTCC     4499

Qy  4503  GTCACCGATTGTGGGTTAGTGTGGGAAGCCGGTCGTCGAGGTGTCGAGGTGTCGTCATCCACCATT 4562
          |||||||| ||| |||||| | || |||||||| ||| |||| || ||| |||| ||||||||||
Db  4500  GTCACCGACTGTGGGTTAGTGTGGGAAGCTGGTCGTTGAGGTCGTTGAGGTGACCCCTTGATCCCACCATT 4559

Qy  4563  ACCATCTCCCTGCCACACGGTCGCGGCTGCTCGCGCTGACTGTCGATGCAGCGGCGAGGACGC    4622
          |||||||||||||||||||||| |||||| || |||||| ||| || |||||| |||||| |
Db  4560  ACCATCTCCCTGCCACACGGTCGCGGCTGCTCGCGCTGACTGTCGATGCAAAGACGAGGACGC   4619

Qy  4623  ACGGGTAGGGGCCAGGTCTGGGCCGTCTGGGGGGTCGGCAAGGCCCCTGCTGGT          4682
          ||||| || |||||||| |||| ||||| ||||||||||||||| |||||| |
Db  4620  ACGGGTAGGGGCCAGGTCTGGGCACGCTCTACTACGCGGGGGTGGGCAAAGCCCCTGCCAGCC   4679

Qy  4683  GTGGTGCGTCAGGTGTCTGTGGTTAGTGTGGGAAGCCGGTGTGACCTGTACGGAATG          4742
          |||||||||||||||| || ||  ||| ||||||||||||| || ||||||||||||
Db  4680  GTGGTGCGGTCAGGTGTCTGTCGTTGAGTGTGGGAAGCTGGAAGCTGACCTGGTACGGAATG    4739

Qy  4743  GAACCTGACCTGACAGCAAACTACTGACATTTACGACAACTGCCCTTACGACCGCAGCC      4802
          |||||||||| |||  |||| ||||||| ||| ||||||||||||| ||||||||||||
Db  4740  GAACCTGACTTGACAGCTTAACTACTGACACTTTACGACAACTGCCCTTTTACACCGCAGCC    4799

Qy  4803  GTCGCAGCTGACATTGGGAAGCCCGGTGTCTTTTCGGGGCTTGCCCGTTGAGGATG          4862
          ||||||| ||| |||| |||| |||||||| |||| ||||| ||||  || |||||
Db  4800  GTCGCGGCTGATATCGGAATCTTCCTCGGGGTGTCTCCTGGCTGTCTCGTGGGGGTGTT      4859

Qy  4863  CATCCCCGATGTGTTAGCTGGGCAAAAGTTCGCGGCGTCCAACTGCCTTCCTGGTGGGTGTT     4922
          ||||||||| ||||||||||||||||| ||||||||||||||||  | ||||||||||||||
Db  4860  CACCCTCGATGTGTCAGCTGGGCAAAAGTTCGCGGCGTCCAACTCCGCGCCCTTCTTGGTGGGTGTT  4919
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Qy  4923  CAGCGGACCATGTGCCGGGAAACACTGTCTCCGGCCATCCTGCTCCGGCCCAGTGGGCA      4982
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  4920  CAGCGGACCATGTGCCGGGAAACACTGTCGCCCATCCTGCTCCGGCCCAATGGGCA         4979

Qy  4983  GGTCTGAAGGGCCCGAATCCTGTCCCACTCCTGCTGAGGTGGGCCAATGATTTACCATCT      5042
          ||||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||||
Db  4980  GGTCTGAAGGGCCCAAATCCTGTCCCACTCCTGCTGAGGTGGGCCAATGATTTACCATCT      5039

Qy  5043  AAAGTGCGCCGGCCCATCACATCGTGACGACCTGGTCCGTCGGGCTCCGTCGGCTGGCGAGGGT   5102
          |||||||| ||||||||| |||||||||||||||||||||||| |||||||||||||| |||||
Db  5040  AAAGTGGCCGCGGCCCATCACATCGTGACGACCTGGTCCGTCGGACTCGGTGTGGCGAGGGT      5099

Qy  5103  TACGTCCGTGCGATGCGGGACCCATCTTGATGGTGGGCCTCGCTATTGCGGGGGGCATG        5162
          |||||||||||||||| ||||||| | |||||||||| |||||||||||||||||||||
Db  5100  TACGTCCGTGCGACGTCTGCCGATCTTGATGATGCGGTCTAGCTTATCGCGGGGGGGAATG     5159

Qy  5163  ATCTATGCTCATACACCGGTCTCTCGTGGTGTGTTACAGACTGGGATGTGAAGGGGGGGT      5222
          ||||||| |||||||||||||| |||||| || || ||| |||||| ||||||||||||
Db  5160  ATCTACGCGTCATACACCGGTCGCTCGTAGTGTTGATGACACTGGTGATGTGAAGGGGGGT     5219

Qy  5223  GGCAGCCCCCCTTATCGGCATGGACCACCCCCACCGCCCGCAGCCGGTGTGCAGTGCCCC       5282
          |||||| ||||| |||| ||||| |  |||||| |||||| |||| || ||||| ||||
Db  5220  GGCGCCCCCCTTTATCGGCATGGACCAGCCCTCAGCCGCCTCAGCCGGTGTGCAGTTCCT      5279

Qy  5283  CCGGTAGACCATCGCCCGCGGGGGGAGAGTCTGCGCCGCCATCGCGACCACAGTGACAGAT     5342
          ||| |||||||||||||| ||||| || |||| ||||| || ||||||||||||||||||
Db  5280  CCGGTAGACGATCGCCCGCGGGGGTGAATCAGCAGCCATCAGCAGCCAAGCAGTGACAGAT     5339

Qy  5343  GCGGTGGCGGCCATCCAGTGGATTGCGATTGCAGTTGGTCAGTGTGATGACCCGATCGGGGAA    5402
          | |||||||| || |||||||| ||  ||||||||||||||||| |||||||||||||||||
Db  5340  GCGGGTGGGCGGCAGCCATCCAGTGGACTGCGATTGCAGTTGGACTCGTCGTCGATCGGAGAGA   5399

Qy  5403  GTGCTGTCTTCTGCCCCAGCTGAGACGGCCTAAGAGACGCCAGTTACCACCAAGTGGCTT      5462
          |||||| ||||||||||||| ||| || |||||||||||||| ||||||||||||||||
Db  5400  GTGTTGTCCTTGGCCTCAAGGCTGAGACGGCCTAAGAGACGCCGAGCCAGCCCAAGTGGCTC    5459

Qy  5463  GCTGCTGTACACGGGACGCGGCCGTCCCACTGTTCAATTGTTGACAAGCTCTTC          5522
          |||||||| ||||| ||||||||||||||| ||||||||| ||||| |||||||
Db  5460  GCTGCTGTCTATACGGGGACGCGGCCGTCCCACTGTATCCATTGTTGACAAGCTCTTC       5519

Qy  5523  GCCGGGGCCTCGGCACGCGCTGGCCGTGGTAGGCCAGTGTAATAGCTGCCGCAGTGGCG       5582
          |||||| || ||||| |||||||||| ||||| | |||||||| ||||||||||||||
Db  5520  GCCGAGGGCGTGGGCCGGCGCTGGCCGTGGTGGCCATTGCCATTGCCACAGCGGGGCC      5579

Qy  5583  GCCTATGGGCGCTTCTAGGAGCCCTCCATTGGCTGCGCCTTCTACTTCATGGGGTTG         5642
          |||||||| | ||||||||||| |||||||||||| |||||||| |||||| ||||||
Db  5580  GCCTACGGGCGCTTCAAGGAGCCCGTTGGCAGCCGCGGCTTCCTCCTACCTGATGGGGTTG     5639

Qy  5643  GGCGGAGGCAACGCCAAACCCGCTTAGCCTCCTCCTTACTAGGGGCGCCGCTGGG          5702
          |||| ||||||||||||| || |||||||||||||||| ||||||| ||||||||
Db  5640  GGCGTTGGAGGCAACGCCTAGAGGCTCCTGGCGTCTGCCCTCCTATTGGGGGCTGCTGGA     5699

Qy  5703  ACCGCTCGTGCAGCTGCACGCGCTCGTGTGGGGGTTAACCATGCGGGCGGTTCATGGGAAGTGCT  5762
          |||||||| ||||||| || ||||||||||||| ||||||||||| || ||||||||||| |||
Db  5700  ACCGGCTCCTGTGCAGCTCAACCGCGCTCGTGTGGCGTGTTGACCATGCAGCGGTTCATCATCAGAAGTCTG 5759

Qy  5763  AGGCTCCCCCCTCCTGGTCACCATTTACTGGGGGCTGGACGGTG             5822
          || |||||||||||||||||||||||||  ||||| ||||| ||
Db  5760  AGTGTCTCCCCCTCCTGGTCACCATTTATTGGGGGCCTGGACGGTTG         5819

Qy  5823  GTGAATGCGGCTAGCCTTGTCTTCTGACTTTATGGCGGGAAACTATCATCAGAGATCTG       5882
          || || ||||| ||||| ||||||||| ||| || ||||| ||||||||||| ||||||
Db  5820  GTCAACGCGGAGCCAGTCTTTGACTTGATCATCATCAGGGAAAACTTTCATCAGAAGATCTG   5879

Qy  5883  TGGTATGCCATCCCAGTGCTAACCAGTCCGGGGGGACTTGCGGGGATCGCCCTCGGG         5942
          |||||||| |||  |||| |||||||||||| ||||||||||||||| ||||||||||
Db  5880  TGGTATGCCATCCCAGTACTCGGTACTGACCAGCCGCCCGGGGGGATCGCTTCATCCTCTCGGG   5939

Qy  5943  TTGGTGTTGACTTGACTTCAGGTTTGAACCGTTGGTGTTGAACCTCTGCTGACT          6002
          | ||||||  |||||||| | ||||| |||||||||||||||||||||||||||
Db  5940  TTGGTTTTGTTATTCAGCTAACAACTCTGGTGCTACCACTTGTTGAACCGTCGTCGCTGACT     5999

Qy  6003  ACATTGCCAAGGTCCTCATGCATCCCTGACGTCATCCCTGACGTCACTGTGAC             6062
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Db  6000  || ||||||||| ||||| |||||| ||||||||||||||  |  | ||  |||||  ||| ||   6059
          ACGTTACCAAGGTCTTCATGTATCCGGACAGTTACTTTCAGCAAGTTGACTATTGCGAC

Qy  6063  AAGGTCTCAGCTGTGCTCCGACGCTTGAGCCTCACTGCACCGTGGTTGCCCTGGTCAAC  6122
          |||||||||||||| || |||||||||||||| || |||||||||||||||||||||||
Db  6060  AAGGTCTCAGCCGGTCTCCGCCGACGCTCCGAGCCTCACCGCACAGTGGTTGCCCTGGTCAAC  6119

Qy  6123  AGGGAGCCTAAGGTGATGAGGTTCAGGTGGGGTACGTCTGGGGTATGTCTGGGAGTTGGGATC  6182
Db  6120  AGGGAGCCTAAGGTGATGAGGTACAGGTGGGGTATGTCTGGGAGCCTGTGGGAGTTGGGATC  6179

Qy  6183  ATGGTCAAGTGCGCATGGTGATGCCGACTTCGGGCCCTCGCCCGTGGTGTCATTA  6242
Db  6180  ATGGCCAAGTGCGCGTGGTCATGGCCAGACTCAGGGCCCTCGCCCGTGGTGTCACTA  6239

Qy  6243  CCCTTATGGCACTGCGCGGGAGGGGTGGTCCGGAGAATGTTGTTGGACGGCCATGTTGAG  6302
Db  6240  CCCTTGTGGCCATTGCCGGGGGGGTGGGGTTGGTCCGGGAATGTTGCTTGACGTCATGTTGAG  6299

Qy  6303  AGTCGTTGTCTTTGGTTGGCTGTCGGATGATCGGTGATGTTTTGAATGGGCAACTCAAAGAT  6362
Db  6300  AGTCGCTGCCCTCTGGTGCGGTGATCACTGGTGATCACTGGTGAATGGGCAACTCAAAGAA  6359

Qy  6363  CCAGTTTACTTCACCAAGCTGTGCAGGCATTATTGGATGGGACAGTCCCTGTGAACATG  6422
Db  6360  CCAGTTTACTTCACCAAGCTGTGCGGGCACTATTGGATGGGACTGTCCCTGTGAACATG  6419

Qy  6423  CTGGGCTATGGCGGAGACGTCGCCTTTGCTCGCGCCCAGACACCCCGAAGGTGTACCATTC  6482
Db  6420  CTGGGTTACCGGTGAAACGTGCGCCTCTCCTCCCGAAGGTGTGCCCCTTC  6479

Qy  6483  GGGACGTCTGGGTGGCTGAGGTGGTGACCCCTACCCCACGTTGTGATCAGGCGAACA  6542
Db  6480  GGGACGTCTGGGTGGCTGAGGTGGTGACCACTACCCACGTGGTAATCAGGAGGACC  6539

Qy  6543  TCCGCTACAAACTGCTGCGCGCAGCAAATCCTGTCGGCTGCTGCTGTCTGAGCCCTATTAC  6602
Db  6540  TCCGCTATAAGCTGCTGCCGCGCAGCAAATCCTATCGGCTGCTGTAGCTGAGCCCTACTAC  6599

Qy  6603  ATGGGCGGCATAACCGGTCGTCATGGGACGCGAGCCGCCTGCCCATGGTCTATGCGC  6662
Db  6600  ATGGGGGTACGGTCATTCCGGATCCCGCCCATGGTCTGCCCCGTCTATGGC  6659

Qy  6663  CCTGGGCAAAGTGCCACCATTGACCGGGAACGCTACACCCTTCCCATCAACTGCGGCTT  6722
Db  6660  CCTGGGCAAAGTGCTACACCCTTCCCATCAACTCTCATCAACTCAACGGCTC  6719

Qy  6723  AGGAATGTGGGCCCCTCTGAGGTGTCATTGCCGAGGTGTCCATTGACATTGGACGGAGACT  6782
Db  6720  AGGAATGTGCACCCTCTGAGGTTTCATTGCCGAGGTGTCCATTGACATTGGGACGGAGACT  6779

Qy  6783  GAAGACTCAGAACTGACTGAGGGCGACCTGCCCGCGGCCCTTGCAGCCCTTCAGGCTATC  6842
Db  6780  GAAGACTCAGAACTGACTGAGGGCGACCTGCGCCCGGCCCTTGCAGCCCTTCAGGCTATGC  6839

Qy  6843  GAGAGTGCTGCGAGAATTCTTGAACCTCACATACATGGAAGTCATCATCATGGAAGATTGCAGTACA  6902
Db  6840  GAGAGTGCTGCGAGAATTCTTGAACCTCACATGGAAGTCATCATCATGGAAGATTAAGGAG  6899

Qy  6903  CCCTTCTTTGTGGAGTTAGCCGAGAGATGCGTGTGTGGGAGAGACATACACCCCGCACT  6962
Db  6900  CCCTTCTTTGTGGTAGTAGCCGAGAGATGCGTGTGTATGGGGAGAGACATCCCCGTACT  6959

Qy  6963  CCATCGCCCAGCACTTATCTCGGTTACTGAGACCCAGATGAGAAGAGACACCCCGGTG  7022
Db  6960  CCATCGCCCAGCAGCTTATCTCGGTTACTGAGAGCAGAGATGAGAAGAACCCCGGTG  7019

Qy  7023  TCTTCCTGCGAGGATACCCCGTCTTCTGACTCATTGAAGGTCATCCAAGAGTACCGAG  7082
Db  7020  TCTTCCTGCGAGGATACCCCGTCTTCTGACTCATTCATCCGAGGTCATCCAAGAGTCCGAG  7079

Qy  7083  ACAGCCGAAGGGGAGGGAAAGCGTCTTCAACGTGGCTCTTCCGTACTAAAAGCCTTGTTT  7142
Db  7080  ACAGCCGAAGGGGAGGGAAAGTGTCTTCAACGTGGCTCTTCCGTATTAAAAGCCTTTATTT  7139
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Qy  7143  CCACAGAGCGATGCCACAGAAAGCTTACCGTTAAGATGTCATGCGTGTTGAGAAGAGC  7202
Db  7140  CCACAGAGCGACGCGACCCAGAGAAGCTTACCGTCAAGATGTCGTGCGTCGCGTTGAAAAGAGC  7199

Qy  7203  GTAACACGCTTCTTTCATTGGAATTGACGGTCGCTGACGTGGCAAGCCTTGTGTGAGATG  7262
Db  7200  GTCACGCGCTTTTTTCATTGGGGTTGACGGTCGCTGATGTGTCTAGCCTGTGTGAGATG  7259

Qy  7263  GAAATCCAGAACCATACAGCCTATTGTGACAACAAGTGCGCACTCCGCTTGAATTGCAGGTT  7322
Db  7260  GAAATCCAGAACCATACAGCCTATTGTGACCAGGTGCGCCACTCCGCTTGAATTGCAGGTT  7319

Qy  7323  GGGTGCTTGGTGGCAATGAACTACCTTTGAATGTGACAAGTGTAGGCAAGAG  7382
Db  7320  GGGTGCTTGGTGTGGCAATGAACTACCTTTGAATGTGACAAGTGTAGGCAAGAA  7379

Qy  7383  ACCTTGGCTCTCCTTCTCTTACATTGGTCTGGGGTGCCACTGACGAGGGCACTCCGCC  7442
Db  7380  ACCTTGCCCTCTTCCTCTTCTTACATTGGTCTGGGGTGCCACTAGGGCCACCGCCGC  7439

Qy  7443  AAGCCCCCTGTGGTGAGGCCCGTTGGCCTCCTTGCTCGTCGGTCGCGACCACCAAGGTGTAT  7502
Db  7440  AAGCCCTCCCGTGGTGAGGCCCGGTTGCCGTGGCTCTTTGTTGTGCCGACACTACTAAGGTGTAT  7499

Qy  7503  GTCACCAACCCGACAATGTTGGGAGAAGAGTTGACAAGTTACCTTCTGGCGTGCCCCT  7562
Db  7500  GTTACCAATCCAGACAATGTTGGGACGGTGGGACAAGGTGACCTTCTGGCCGTGCTCCT  7559

Qy  7563  AGGGTTCATGACAAATTCCTCGTGGACTCCATAGAGGGCGCTAAGAGGGCAGCTCAAGCC  7622
Db  7560  AGGGTTCATGATAAGTACCTCGTGGACTCTATTGAGCGGCGTAAGAGGGCCCGCTCAAGCC  7619

Qy  7623  TGCCTAAGCATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACCATGCTGCC  7682
Db  7620  TGCCTAAGCATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACCATGCTGCC  7679

Qy  7683  ATGGGCTGGGATCTAAGGTCGGTCGGTCGGTTCAGGAGATGGCT  7742
Db  7680  ATGGGCGTGGGGATCTAAGGTGTCGGTTAAGGACTTAGCCACCCCGCGGGGAAGATGGCC  7739

Qy  7743  GTCCATGACCGGCTCCAGGAGTACTTGAACGGGACCCAGTCCCCTTTACTCTTACTGTG  7802
Db  7740  GTCCATGACCGGCTCCAGGAGTACTTGAAGGGGACTCCGGTCTCCCTTTACTCTTACTGTG  7799

Qy  7803  AAAAAGGAAGTGTTCTTCAAAGACCGAAAGAGAAGAGAGGCCCCCCGCCCCCATTGTTC  7862
Db  7800  AAAAAGGAGGTGTTCTTCAAAGACCGAAAGAGAGGAGAAGCCCCCCGCCCCCATTGTTTC  7859

Qy  7863  CCCCCCCTGGACTTCCGGATAGCTGAAAGCTTATTCTGGGAGACCCTGACGGGTAGCC  7922
Db  7860  CCCCCCCTGGACTTCGGGATAGCTGAAAGCTCATCTTGGAGACCAGGCGGGTAGCC  7919

Qy  7923  AAGGCCGGTGTTGGGGGGGTGCGCCTCTACGCCTTCCAGTACACCCCAAATCAGGAATTAGGGAG  7982
Db  7920  AAGGCCGGTGTTGGGGGGGTGCCGCCACTTGGGAAATACTATGCCTTCCCAGTACCCCCAAATCAGAGTTAAGGAG  7979

Qy  7983  ATGTCAAACTGTGGAATCAAAGAAGACACCATGCGCCATCTGTGTGGACGCCCACATGC  8042
Db  7980  ATGCTCAAGTCATGGCTATGCAGTGGTCTAAGAAGACACCATTCGCGCCATCTGTGTGGACGCCCACCTGC  8039

Qy  8043  TTCGACAGTAGCATAACTGAGAAGAAGGACTCCCTGTCGGTG  8102
Db  8040  TTCGACAGTAGCATAACTGAGAGGAGGACTGGGTATACGCGTCGGCC  8099

Qy  8103  TCAGACCATCCAGAATGGGTGCGTCGGAAATACTTCCTCTGGCACAATGGTA  8162
Db  8100  TCTGACCATCCAGAATGGGTGCGGGCACTTGGAAATACTATGCCTTCAGGCACCACCATGGTC  8159

Qy  8163  ACCCCGGAGGGGGTGCCAGTGGGTCGGTGAGAGGTATTGTAGATCCTCAGGGGTCTTGACCACC  8222
Db  8160  ACCCCGGAAGGGGTGCCCGTCGGGTGAGAGGTATTGCAGATCCTCCGGGGTGTCCTAACAACT  8219
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Qy  9303  TGCTCGCAGAGCCCTCCCCGATGGGCGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC  9362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9300  TGCTCGCAGAGCCCTCCCCGATGGGCGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC  9359

Qy  9363  GGTAAGAGCTCGGCCCAAAGGCCGGGT  9389
          ||||||||||||||| ||||||||||
Db  9360  GGGAGAGCTCGGCCCGAAGGCCGGTT  9386
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RESULT 10
AAV66279
ID AAV66279 standard; cDNA; 9327 BP.
XX
AC AAV66279;
XX
DT 23-DEC-1998 (first entry)
XX
DE Recombinant HGV sequence designated 3z-HGV94-6.
XX
KW PNF2161 sera; antigen; immunoreaction screening;
KW Non-A Non-B Non-C Non-D Non-E Hepatitis virus; HGV;
KW anti-HGV antibody; vaccine; 3z-HGV9461; ds.
XX
OS Synthetic.
OS Hepatitis G virus.
XX
PN US5824507-A.
XX
PD 20-OCT-1998.
XX
PF 19-MAY-1995; 95US-0444733.
XX
PR 19-MAY-1995; 95US-0444733.
PR 20-MAY-1994; 94US-0246985.
PR 03-AUG-1994; 94US-0285543.
PR 03-AUG-1994; 94US-0285561.
PR 26-OCT-1994; 94US-0329729.
PR 23-NOV-1994; 94US-0344271.
PR 16-DEC-1994; 94US-0357509.
PR 15-FEB-1995; 95US-0389986.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fry KE, Kim JP, Linnen JM, Wages J, Young LM;
XX
DR WPI; 1998-582553/49.
XX
PT Polypeptide antigens hepatitis G virus - useful as vaccines against
PT the virus and raising antibodies for use in immuno-testing for the
PT virus
XX
PS Example 18; Columns 337-346; 206pp; English.
XX
CC The present sequence represents a recombinant Hepatitis G virus (HGV)
CC sequence, derived from PNF2161, and designated 3z-HGV9461. The
CC specification describes HGV antigen clones isolated from PNF2161
CC sera. This sera is obtained from a patient suffering from Non-A Non-B
CC Non-C Non-D Non-E Hepatitis Virus, also known as Hepatitis G virus (HGV).
CC HGV antigens can be used in immunoreaction screening for presence of
CC anti-HGV specific antibodies, especially in patient sera, e.g. enzyme
CC linked immunoassay (ELISA). They can also be used as vaccines, and to
CC raise the polyclonal and monoclonal antibodies.
XX
SQ Sequence 9327 BP; 1682 A; 2532 C; 2984 G; 2129 T; 0 other;

Query Match   83.9%; Score 7885.6; DB 19; Length 9327;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;

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Qy  8223  AGTGTGGAGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCCGCCTGTGAGAGGGTGGGG  8282
          || |||||||||||||||||| ||||| |||||||||||||| |||||||||||| |||||
Db  8220  AGCGGCGAGCAACTGCTTGACCTGCTACATCAAGGTGAAAGCTGCCTGTGAGAGGAGTGGGG  8279

Qy  8283  CTGAAAAATGTCTCGCTCCTCATCGCTGGCGATGACTGTTGATCATATGGCGAACACGGCCT  8342
          |||||||||||||||| || ||||||||||||||||||| |||||||||||||||||||||
Db  8280  CTGAAAAATGTCTCATCTTCTCATAGCCGGCGATGACTGCTTGATCATATGGCGAACACGGCCA  8339

Qy  8343  GTGTGCGATCCTAGCGACGCTTTGGGCAGAGCCCTGGCGAGCTACGGGTACGCATGGCGAG  8402
          |||||| ||| |||||||||||| ||||||||| |||||||||||||| ||||||| ||||
Db  8340  GTGTGCGACCCAAGCGACGCGCTTTGGGCAGCAGCCCTGGCGAGCTATGGGTACGCCTGGCGAG  8399

Qy  8403  CCTTCGTATCATGCATCACTGACACGGCCCCCTTCTGCTCCACTTGGCTAGCTGAGTGC  8462
          |||| |||||||| ||||||||||||| ||||| |||||| |||| ||||||||||||
Db  8400  CCCTCATATCATGCATCATTGGACACGCCCCCCTTCTGTCCCACTTGGCTTGCTGAGTGC  8459

Qy  8463  AATGCAGATGGCGAAAACCCATTTCTTCCGACCACGGACTTTCGGAGGCCCCTGCCTCGC  8522
          ||||||||||||||| ||||||||| || |||||||||||| || ||||||| |||||||
Db  8460  AATGCAGATGGGAAGCCGCCATTTCTTCCTGACCACGGACTTCCGGAGGCCCCGCCGTCGC  8519

Qy  8523  ATGTGGAGCGAGTACAGTGACCCAATGCTTCGGCCATCGGTTACATCCTCCTATACCCT  8582
          |||||||| |||| |||||||||||||| ||| |||||||||||||||||||||| | ||
Db  8520  ATGTGGAGCGAGTATAGTGACCCGATGGCTTCGGCCATCGGTTACATCCTCCTTTATCCT  8579

Qy  8583  TGGCATCCTATCACACGGTGGGTCATCATCCCTCACGTGCTCACCTGCCGTGGTTAGGGGT  8642
          |||||| || |||||||||| |||||||| |||||| |||| ||| |||| || ||||||
Db  8580  TGGCACCCCATCACACGGTGGGTCATCATCCCTCACGTGCTCAACGTGCTCAATCGTCGCATTCAGGGGT  8639

Qy  8643  GGTGGCACACCGTCTGATCCTGTGTGTGCCAGGTACATGGTAATTACTACAGTTCCA  8702
          ||||||||||||| |||||||| ||| |||||||||||||||||||||||||||||
Db  8640  GGAGGCACACCGTCTGATCCGGTTGGTGCCAGGTGCATGGTAACTACTACAGTTTCA  8699

Qy  8703  CTGGACAAACTGCCTAACATCATCGTGCCCTCCACGCGGACCAGCAGCGTTGAGGGTTACC  8762
          |||||||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||
Db  8700  CTGGACAAACTGCCTAACATCATCGTGCCCTCCACCGCGGACCAGCAGCGTTGAGGGTTACC  8759

Qy  8763  GCAGACACAACAACTAAGACAAAAATGGAGGCTGCTGAGCGACCTCAAGCTCCCT  8822
          |||||||||||| |||| | |||| ||||||| || ||||||| ||||||| || 
Db  8760  GCAGACACAACAACTAAAACAAAGATGGAGGCTGTGAAGGTTCTGAGCGACCTCAAGCTCCCT  8819

Qy  8823  GGCCTAGCAGTCCACCGGAAGAAGAGGCCGGGCATTGCGAACCGCGTATGCTCCGGTCGCGGC  8882
          ||||||| ||||||||||||||||| |||||||| ||| ||||||||  ||||||||||||||
Db  8820  GGCTTAGCAGTCCACCGGAAGAAGAGGCCGGGCGTTGCGAACACGCATGCTCCGGTCGCGGC  8879

Qy  8883  GGTTGGCTGAGTGGCTAGGGGGTCGTGTGGCGTTCCCCCCGGTTCTCCCCCTCCG  8942
          ||||||||||||| |||||| ||| ||||||||||| ||| || |||| ||||| 
Db  8880  GGTTGGGCTGAGTTGGCTTGTTGTGTGGCGTTGGGGGGTTCCCCCCTTCTCCCCCCT  8939

Qy  8943  GAGATTGCTGGTATCCCCGGGGGTTTCCCCCTTCCCCCCCTATATGGGGTGGTTCAT  9002
          ||||||||||||||||||||||||| |||||| ||||||||||||| |||||||||| 
Db  8940  GAGATTGCTGGTATCCCCGGGGGGTTCCCCCTTCTCCCCCCTATATGGGGTGGTACAT  8999

Qy  9003  CAATTGGATTCACAACGGCCAGGAGTCGCTCGGCGGTGGTTCTTAGCCCTGCTC  9062
          |||||||||||||||||||||||||||| |||||||||||| |||||||||||| 
Db  9000  CAATTGGATTCACAAGCGGCCAGGAGTCGCTGGGCGGTGGTTGGTTCTTAGCCCTGCTC  9059

Qy  9063  ATCCTAGCCCCTTCGGGTGAACTAAATTCATCTGTTGCGGCCAAGGTCCGGTGACTGATC  9122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9060  ATCCTAGCCCCTTCGGGTGAACTAAATTCATCTGTTGCGGCCAAGGTCTCGGTGACTGATC  9119

Qy  9123  ATCACTGAGGAGGAGTTCCCCGCCTCCCCGGGTCTCCCCGCTGGGTAAAAAGGG  9182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9120  ATCACCGGAGGAGGAGTTCCCCGCCTCCCCGGGTCTCCCCGCTGGGTAAAAAGGG  9179

Qy  9183  CCCGGCCTTGGGAGGCATGGTGGTTACTCAACCCCTGGTCAGGGTCAAAGCCTGATGGTGC  9242
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9180  CCCGGCTTTGGGAGGCATGGTGGTTACTTAACCCCCTGCCAGGGTCAAAGCCTGATGGTGC  9239

Qy  9243  TAATGCAACTGCCACTTCGGTGGCGGTCGCTACCTTATAGCCGTAATCCGTGACTACGGGC  9302
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  9240  TAATGCAACTGCCACTTCGGTGGCGGTCGCTACCTTATAGCCGTAATCCGTGACTACGGGC  9299

Qy  40  GCAAGCCCCATAAACCGACCCCTATCTAAGTAGACGCAATGACTCGGCGGCCGACTCGGCG  99
         ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  GCAAGCCCCAGAAACCGACCCCTATCTAAGTAGACGCAATGACTCGGCGGCCGACTCGGCG  60
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Qy   100  ACCGGCCAAAAGGTGGTGGATGGGTGGTGACAGGTTGGTGGTAGTCGTAAATCCCGTCAT  159
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    61  ACCGGCCAAAAGGTGGTGGATGGGTGATGACAGGTTGGTGGTAGTCGTAAATCCCGTCAC  120

Qy   160  CCTGTAGCCACTATAGGTGGTCTTAAGAGAAGTCAAGACTCCTCTTGTGCCTGCGGC    219
          | |||||||||||||||||||||||||||||||| |||| ||||||||||||||||||
Db   121  CTTGGTAGCCACTATAGGTGGTCTTAAGAGAAGTTAAGATTCCTCTTGTGCCTGCGGC    180

Qy   220  GAGACCGGCCGACGGTCCACAGTGCTGGCCCTACCGGTGTGAATAAGGGCCGACGTCAG   279
          ||||||||||||||||||||||||  |||||||||||| |||||||||||||||||||
Db   181  GAGACCGCGCGACGGTCCACAGGTGTTGGCCCTACCGGTGAATAAGGGCCGACGTCAG    240

Qy   280  GCTCGTCGTTAAACCGAGCCCGTCACCCACTTGGGCAAACGACGCCCACGTACGGTCCAC  339
          ||||| ||||||||||||||||||||||||||||| ||||  |||||||||||||||||
Db   241  GCTCGTCGTTAAACCGAGCCCGTCACCCACTTGGGCAAACGACGCCCACGTACGGTCCAC  300

Qy   340  GTCGCCCTTCAATGTCTCTCTTGACCAATAGGTTTATCCCGGCGAGTTGACAAGGACCAGT  399
          |||||| |||| |||||||||||||||||  ||||||||||||||||||||||||||||
Db   301  GTCGCCCTTCAATGTCTCTCTTGACCAATAGGGTAGCCGGCCGAGTTGACAAGGACCAGT   360

Qy   400  GGGGCCGGGGGTATGGGAAGGACCCCAAACCTGCCCTTCCCGGTGGGCCGGGAAAT      459
          ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   361  GGGGCCGGGGGT-TGGAGGAGGACCCCAAACCTCCCGCCCTTCCCGGTGGGCCGGGAAAT  419

Qy   460  GCATGGGCCACCCAGCTCCGGCGGCCTGCAGCGCGGGTAGCCCAAGATCCTTCGGG     519
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   420  GCATGGGCCACCCAGCTCCGGCGGCCTGCAGCGCGGGTAGCCCAAGAATCCTTCGGG    479

Qy   520  TGAGGCGGTGGCATTTCTTTCTATACCATCATGGCAGTCTTTGCTCCTCTCTCG      579
          ||||||||||||||||| ||||||||||||||||||||||| ||||||||||||
Db   480  TGAGGCGGTGGCATTTCCTTTCTATACCATCATGGCAGTCTCGAGTCCTCTCTCG     539

Qy   580  TGGTTGAGGGCGGCGGCCATTCTGGCCGCCCCGCCACCCACGCGGGCCAAT        639
          ||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   540  TGGTTGAGGGCGGCGGCCATTCTCGGCCGCCCACCCACGCGGGCCAAT          599

Qy   640  ATTTCCTCACAAATGCTGTGCCCCGGAAGACATCGGTTCTGCCTGGAAGGCGGATGCC    699
          |||||||||||||| ||||||||||||||||||||||||||||||||||| |||||||
Db   600  ATTTCCTCACAAATTGTGCCCCGGAAGACATCGGTTCTGCCTGGGAGGTGTACTCGG    659

Qy   700  TGGTGCCCTGTGGGGTGCACGGTTTGCACCGACCGTTGCTGGCCACTGTATCAGGCGGGT  759
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   660  TGGTGCCCTGTGGGGTGCACGGTTGCACCGACCGTTGCTGGCCACTGTATCAGGCGGGTT  719

Qy   760  TGGCTGTGCCTGGCGAAGTCGCGCGCCAGCTCGTTGGGGAACTGGGGAGCCTGTACG     819
          ||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db   720  TGGCTGTGCCTGGCGAAGTCGCGCGCCCAACTGGTGGGGAGCTGGGTAGCCTATACG    779

Qy   820  GGCCCTTGTCGGTTCGCCGGGCTTACGTGGCGTCTGGGCGGATCCGGGTTTACTCCG    879
          ||||| ||||||||||||||||| ||||||||||||||||| |||||||||||||||
Db   780  GGCCCCTGTCGGTTCTCCGGGCTTACGTGGCCGGATCCGGGTGAGGTGTACTCGG     839

Qy   880  GGGTTCCTGACAGTTGGTGTTGCGTTGAGGGCCCGGGTTACCCTGATGCCCAACCTGAAGT  939
          |||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   840  GGTCCCTAACGGTGGGAGTCGCGTTGACGGCCGCCGTACCCGTGCCTAACCTGACGT    899

Qy   940  GTGCAGTAGAATGTGACGTTAAGTCACGTTAAAGTGGGAAGTGGGAAGTGAGTTTTGGAGAGGAG  999
          |||||||||||||||||| | |||| ||||||| ||||||||||||||| |||||||||||||
Db   900  GTGCAGTGGCTGTGTGAGTTAAAGTGAGTTAAAGTGGGAAGTGAGTTTTTGGAGAGGAGG  959

Qy  1000  CCTCCAATTACTGGATTTTGGAATACCTTGGAAAGTCCCATTTGAATTTGCTGTTGGAGAGGA  1059
          |||| |||||||||||||||| |||||||||||||||||||||||| ||||||||||||||
Db   960  CCTCCAACTACTGGATTCTGGAAATACCTTGGAAGGCTCCGAAGTCTCGGAAGGAGAGGCG  1019

Qy  1060  TGATGAGCCTGACCCCTCTGTTTGGTTGGCCGCATTGCTTTTGCTGGAGCAACCGA     1119
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  1020  TGATAAGCCTGACCCCTCTGTTTGTGTTGCGTTGGCCGCCGCCATTGCTTGCTGGAGCAACGGG  1079

Qy  1120  TGTTCATGGTTTCCTGCTGGTGACGATGCGGGAGATGTTGCAAGGCGCCCGCCTCCG     1179
          ||||||||||| | |||||||||||||||||||||||||||| ||||||||||||||
Db  1080  GTGTTCATGGTCTTCCTGTGTGGTGACGATGCGGGAGATGTTGCAAGGCGCCCGCCTCCG    1139

Qy  1180  TTTTGGGGTCCCGCCCCCTTTGACTACGGGTTGAAGTGGCAGTACGGGTTCCTGGAGGGCTA  1239
          | ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
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Db  1140  TTTTGGGGTCCACGCGCCTTTGACTACGGGTTGACTGGCAGACCGGTTGACTGGGGGCCCA   1199
          |||||||||||| |||||| |||||||||||||||||| ||||| |||||||||||||||

Qy  1240  ACGGGTCGCGTATTCCACTGGGGAGAGGGTGTGGGATCGGAGGTGGGAATGTCACGCTCTGT  1299
          ||| ||||||| |||||||| |||||||||| |||||||||||||||| ||||| ||||||
Db  1200  ACGGGTTCGCGTTTTCGACTGGGGAGAAGGTGTGGGAACCGTGGGAACGTTACGGTTCAGT  1259

Qy  1300  GTGACTGCCCCAACGGCCCTGGGTTTGGGTCCGGCCTTTTGCCAGGCGGTTGGGTGGGG  1359
          |||||||||||||||| ||||||||||||||||||||||||||||||||| |||||||
Db  1260  GTGACTGCCTCAACGGCCCCTGGGTGGTGTCCAGCCTTTGCCAAGCAATCGGCGTGGG   1319

Qy  1360  GCGACCCCATCACCCATTGGAGCGACCACGGACAAAAACCAGTGGCCCCTATCATGCCCCCAAT  1419
          |||||||||||||||| ||||||||||||||| ||||||||||||||||||||||||||||
Db  1320  GTGACCCCATCACTTATTGGAGCCACGGACAAATCAGTGGCCCCTTCATGCCCCCAGT   1379

Qy  1420  ATGTCTATGGGTCTGTCCGTAACGTGCGTGTGGGTTCCGTGTCTTGGTTGGCCTCGA  1479
          |||||||||||||||||||||| ||||||||||||||||||||||||| |||||||
Db  1380  ATGTCTATGGGTCTGTACAGTCACTTGCCTGTGGGTTCCGTGTCTTGGTTATGCCTCCA   1439

Qy  1480  CCGGGCGGTCGATTCGAAGATCGATGTGTGGAGTTGGTGTCCGACACGCGGTTGAGTCTGCCAGCT  1539
          |||||||||| ||||||||||| || ||||| |||||||||||||||||||||||||||||
Db   1440  CCAGTGTCGGCGACTCGAAGATAGATGTGTGGAGTTAGTGCCAGTGGCCTCTGGGCACGTGGCTGCCACCT  1499

Qy  1540  GCACCATAGCCGCTCTAGGGTCATCGGATCGCGACACGCGGTGGTTGAGCGTCTCCGAGTGGG  1599
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  1500  GCACCATAGCCGCCACTCGGATCATCGGATCGCGACACGCGGTGGTTAGTGCCTCTGGGCGAGTGGG  1559

Qy  1600  GAGTCCCGTGCGTAACGTGTATTCTGGACCGTCGGGCCTGCTTCATGTGGCACCTGTGTGC  1659
          |   |||||||||||  ||||||| ||||||||||||||||||||||||||||||||||
Db  1560  GAATCCCGTGCGTGACGTGTGTTCTGGACCGTCGGGCCTGCTTCATCGGCACCTGTGTGA   1619

Qy  1660  GGGACTGCTGGCCCGAAAGCGGTCGGTTAGATTCCCTTCCATCGGTGGCGGCGGCCACGGGGC  1719
          |||||||||||||||||| ||||| |||| || ||||||||||| |||||||||||| |||
Db  1620  GGGACTGCTGGCCCGAGATCCCGAGACCCGGTTCCCATTCCATCGTGGCGTGGCGTGGGGC  1679

Qy  1720  CTCGGCTGACAAAAGGACTTGGAAGCTGTGCCCTTCGTCAACAGGAGCAACAACTCCCTTCACCA  1779
          |||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db  1680  CTCGGCTGACAAAAGGACTTGGAAGCTGTGCCCTTCGTCAATAGGACAACAACTCCCTTCACCA  1739

Qy  1780  TAAGGGCCCCCCCTGGGTTGCTCGAGGTGTCAACCAGGGGAGAGCCAACCCGGTGCGGTCGCCCCCCGGGTTTG  1839
          | |||| |||||| |||||| ||||||||| |||||||||||||||||||||||||||||||||||| ||||||
Db  1740  TTAGGGGCCCCCCTTGGGTTTCTTCGAGGTGTTGGGCCAGCCAACCCGGTCGCGCGGTCGCCCCTTGGGTTTTG  1799

Qy  1840  GGTCTACCACCATGACCAAGATCCGGGATTCCGATGTTGTGAAATGTCCCACCACCAG   1899
          ||||||||||| ||||||||||||||| ||| |||| || ||||||||||| ||||||
Db  1800  GGTCCTACCACGCCCATGACCATGACCAGATCCGAGATACCCGTGGGAGTGTCCCACCACCAG  1859

Qy  1900  CCATAGAGCCCGACTGGAACCTTCGGGTTCTCCCCGAGGTCCGCCGCCCCTCAACAACT  1959
          |||| ||||||||| |||| | |||||||| |||||||| ||||  |||||| |||||
Db  1860  CCATCGAGCCTCCACCGGACGCTTCTTCCCCGGACGCGCCGATGGTTTATACAGTCCAGGGCGCT  1919

Qy  1960  GCATGGGAGGTGGATGCGGGCAACTTCATCCCTCGAGGCGGGGGGT    2019
          |||| ||||||| |||| |||||||||||||| ||||||||||||||
Db  1920  GCATGGGAGGTGGATGCAGCAGGCAACTTCATCATCCCCGGCGGGCTGGGGCGGAGCTGGGGGGGT  1979

Qy  2020  TCTACCAGCCTCTGTTTCGCAGGTGTTCGAGGCTGATGGGCTCGATGGACGGTTTGCC   2079
          |||| ||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  1980  TCTATGAACCCCGGTGTCCTGGTGCGTGTTCGGCGCGTGTTCGGAGGCCGAAATCCGGTTTGTC  2039

Qy  2080  CGGGGTACGGACCATGGCTGTCCCTCGGTAGACCTGAGCGGTTCATCACGTCAGGGGCACC  2139
          ||||| |||||| ||||||| | || |||  |||||||||| || ||||| ||||||||||
Db  2040  CGGGGTTGCATGGCTTTCTCTTGCGACGTTTGGGTTTATACATGGTTATACAGTCCAGGGTCACT  2099

Qy  2140  TGCAGGAGGTGGATGCGGGCAACTTCATCCCTCCTCCGCGGTTGCTTCTTCTGGATTTTG  2199
          |||||||||| |||||||||||||||||| ||| || |||| |||| |||||||| |||
Db  2100  TGCAGGAGGTGGATGCAGCAGGCAACTTCATCATCCCCGGCGGCTGGGCGGAGCTGGGACTTTTG  2159

Qy  2200  TATTTGTCCTGCTCATCTGATGAGCTGCCCGGTTGGTCCGTTGATCTTGC     2259
          |||||||||| | ||||| |||||| || ||| |||| |||||||||||||
Db  2160  TATTTGTCCTGTTATACCTGTTATACCTGATGAGCTGATGAGCTGCCCGGTTGTCCGCTGATCTTGC  2219

Qy  2260  TTCTGCTGTGGTGGGTGAACCAGTTGCGCCGGGTTCTAGGACTGCTGTGGACGCTG   2319
          | |||| ||||||||||||||||| ||  ||| ||||||| |  ||||||
Db  2220  TTCTGCTGTGGTGGGTGAACCAGTTGCGCCGGGTTCTAGGACTGCGTGGACTCTTTG  2259
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Qy   2320  CCGTGCGGGTGAAGTTTTGCCGGGCCCTGTTGTCATGGTGTTTGGGCTTCCCACTG  2379
           |||||||| |||||  | ||| ||||||||||| ||||  ||| ||||||||||||
Db   2280  CCGTGCGGGTGAGGTCTGTTGTCATGGTGTTGGGACTCCCGGTCG  2339

Qy   2380  TCAGTATGATACTAGGTCTAGCAAAACCTGGTTCTTGTACTTTCGGTCGGATGGCCCTCAGC  2439
           ||||||| | ||||  ||| |||||||||||||  ||||  || ||
Db   2340  TCAGTATGATATTGGGTTTGGCAAAACCTGGTTGCTACTTTAGATGGTTGGGACCCCAAC  2399

Qy   2440  GCCTCATGTTCCTCGTGTTGTGGAAGCTCGCTCGGGGAGCTTTCCCCTGGCACTTTTGA  2499
           | ||||||||||||| |||||||||||||||| || ||||||||||||||||||||||||
Db   2400  GCCTGATGTTCCTCGTGTTGTGGAAGCTTGCTCGGGGAGCTTTCCCCGGCCCTCTTGA  2459

Qy   2500  TGGGGATTTCGGCGACCGCGGGGCGCACCCTGTGCTGTCGGGGCGCGAGTTCTGCTTCGATG  2559
           |||||||||||||||||||| |||||  |||||||||||||||||||  ||||||||||||
Db   2460  TGGGGATTTCGGCGACCGCGGGGTGTAAGGGCGCACCGGTGCTGTCGGGCGCGAGTTCTGCTTCGATG  2519

Qy   2560  TCACATTCGAGGTGGACACTTCGGTGTTGGGCTGGTGGTGGCCAGCGTGGTGGCTTGGG  2619
           |||||||||||||||| || |||||||||| ||||||||||||  |||||||||||||
Db   2520  CTACATTCGAGGTGGACACTTCGGTGTTGGGCTGGTGGGCGCAATGTGGTAGCTTGGG  2579

Qy   2620  CCATAGCGCTCCTGAGCTCAATGAGCCAGGGGGTGGAAGCACAAGGCCGTGATCTATA  2679
           |||||||||||||||||||| ||| |||||||||||| ||||| ||||||| ||||||
Db   2580  CCATTGCGCTCCTGAGCTCGATGAGGCGCAGGGGGTGGAGGCGCACAAAGCCGTGATCTATA  2639

Qy   2680  GGACGTGGTGTAAAGGTACCAGGCGTGTGCGCCAGAGGGTGTGCGGACCCCTCGGGG  2739
           |||||||||||| |||||||||| |  |||| |||||||| ||||||||||||||||
Db   2640  GGACGTGGTGTAAGGGTACCAGGCAATCCGTCAAAGGTGTGAGGAGCCCCTCGGGG  2699

Qy   2740  AGGGGCCGCTCCTACCCAAGCTTCGACGTTCGCCTGCTTGGCCTCCATACATCTGGCCGG  2799
           |||||||| ||  ||||||| |||||||| ||||||||||||||||| |||||||||||
Db   2700  AGGGGCCGGCGGTCCAAAACCCCGCCTGCTTGGCCTCCGTACATCTGGCCAG  2759

Qy   2800  ATGCTGTGATGATGGGGCTACCTGTTGACCACATGGGCTCTTTCTCCGCCGTGTTCGAGCCGCACTGG  2859
           |||||||| ||||||||| || |||||||||  |  ||||||| |||||||||||  ||||||
Db   2760  ATGCTGTGATGATGGGGCTTATTGTTCGATCATATGGGCTCATTTCGGCCGTGTTCGCAGGAGC  2819

Qy   2860  ACTGGGCCCTGAGGAGCTCCTGTCTCCCGCCCTCGTTACGGCGACTGGCCACGGGTGG  2919
           | ||||||||||  |||||||| | | ||||||| |||||||||||||||||||||||
Db   2820  ATTGGGCCCTGGAATGGGAACGCGGCGGATCTGTGTCGCGGCGTTTGGCTGGTCGGGTGG  2879

Qy   2920  TTGAGTTGCTGTGTGATGGCGCGGCGAGAAGGCCACCACCATCCGACTGGCTCTCCAAGATGT  2979
           |||||||||||||||||||||||||||||||  |  ||  ||||||||||| |||||||||
Db   2880  TTGAGTTGCTGTGTGATGGCGGTGGCCACCACCCACAACCGCATCCGACTGGCTCTGGTCTCCAAGATGT  2939

Qy   2980  GCGCAAGAGGGGCCTACCTGTTGACCACATGGGCTCTTTCTTTGCCGCCTGTGTCAAGGAGC  3039
           | | ||||  || |||||| ||||||||||||  |  || ||||||||||||||||||||||
Db   2940  GTGCCGAGGAGGGTTATTGGTTCGATGGCTCATTTTCGCGCTGCCTGGTGTCAAGGAGC  2999

Qy   3040  GCTTGTTGGAATGGGACGCGGCTTTCGACCGCGTTCAGTCATTCACTAGGACGGACTGTCGCA  3099
           | |||||||||||||| || | | |||| ||||||||||||||||||||||||||||||||||
Db   3000  GCCTGTTGGAATGGGAACGGGCTCTGAACCTCTGTCATTCACTAGGACGGACTGTCGCA  3059

Qy   3100  TTGAGTTGCTGTGTGATGGCGCGGCGAGAGGCCGAGAAGCCACCACCATCCGTCTGCGGACAGACCCCTGG  3159
           ||| ||| ||  ||||| ||| |||||||||| || ||||||||||  |||||  ||||||||||||||||
Db   3060  TCATACGGATGCGCCCCGGATGCGCGGCGAGAGGACTTGGTCCGGGGTCATGGGTTTACCCGGTGG  3119

Qy   3160  TAGCACGGCGGCCGGTGATGAGGTTCTCATCGGCGTTTCAGGATGTGAATCATTGCCTC  3219
           | |||||||||||||||||||||||||||||| |||| |||||||| ||||||||| |||
Db   3120  GTGCGAGGAGCTTATTGTTCGATGCATATGGGGCTCATTTTGTGTCTGTCAAGGAGC  3179

Qy   3220  CCGGGTTGTGTCCCGGACTGTCACCAGTTCATCCGCCGCTCGGTGCGGAAAGGGCTTCCTGGGGG  3279
           |||||||||||  ||||||||||||| | |||||||||||||||||||||||||||||||||||
Db   3180  CCGGGTTGTTCCGACCGCGCCGGTGCAGCGGGTAATATGCGTCTGTCTTACGACGGGCGTCATGGTGT  3239

Qy   3280  TCACGAAGGCAGCCTTGACAGGTAGGGATCCTGACTTACATCCAGGGAACGTCATGGTGT  3339
           |||| ||| |  |||||||||  |||| || |||| ||||||| |||||||| ||||||||
Db   3240  TCACAAAGGCTGCCTTGGCCAGGTCGGGGATCGGTTTCGACTTACATCCAGGAACGTCATGGTGT  3299

Qy   3340  TGGGGACGGCTACGTCACGAAGCATGGCACATGGCCAATGGCCTGCTTGTCCACAACTT  3399
           |||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db   3300  TGGGGACGGCTACGTCCGGAAGCATGGGAACATGGGAACATGGGTTGAACGTCTGTTCACGACCT  3359
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Qy   3400  TCCATGTGGGCTTCATCCGGAACCATCGGCCACGCCGTGGGGCGCCCTTAATCCCAGGTGTGT  3459
           ||||||||||||||||||||||||||||||| || |||||||| |||||| ||||||||| ||
Db   3360  TCCATGTGGGCTTCATCCGGAACCATCGGGCTGCCGCACACCCGTGGGGCGCCCTTAATCCCAGGATGGT  3419

Qy   3460  GGTCAGCCAGTGATGATGACGTCACGTGGAGTCCTTGTTGTTATTAGATCCGACGGGCTTGTGCCATG  3519
           ||||||||||||||||||||||||||||||| ||||||||  ||||| |||| |||||||
Db   3420  GGTCAGCCAGTGATGATGATGTCAGGTGTATCCACGTGTATCCACTTCGTTCGTTAACCGC  3479

Qy   3520  CCTGCACTTGCCAGGCGGAGTCCTTGTTGTTGGGTTATTAGATCCGACTGGCTTGTGCCATG  3579
            | ||||||||||| |||||||||||||||| ||| ||||| ||||||||||||||||||||
Db   3480  CTTGTACTTGCCAGGTGGTCATCGAGTCCTTGTCATCATCAGATCGACAGTCATGCCATG  3539

Qy   3580  GCTTGAGCAAGGGGACAAGGTTGAGCTGCATTGGCCATGATGTGGCTCGTGACTTCCGTG  3639
           |||||||||||||| |||||| ||||||||||||||  |||| || |||| |||||||||
Db   3540  GCTTGAGCAAGGGGGACAAGGTGAGCCGGCATGTGGCCATGTGGCTCCCCGATTTCCGTG  3599

Qy   3640  GTTCGTCTGGTTCACCGGTCCTTGCGACAAGGCACCGCAGTAAGAATGCTCGTGTCAG  3699
           ||||||||||| |||||||| || ||| ||||||||| |||||||  ||| |||| | |
Db   3600  GCTCGTCTGGCTGGCCCCTATTGTGACGAGGGGCACCGGTAGGAGTGCTCGTGTCTG  3659

Qy   3700  TGCTCCACTCTGGCGGCAGGGTTACTGCGGCGGATTCACTAGGCCGTGACTCAAGTAC  3759
           |||||||||||||||| | | || |||||| ||| |||||||||| |||| |||||||
Db   3660  TGCTTCACTCCGGTGGTAGGGTTAGTCTTAGCCCTGCCCACTAGGCCGTGACCCAAGTGC  3719

Qy   3760  CAACAGATGCCAAGACTACCACAGAACCCCTCCGGTCGCGGCAAAAGGAGTTTTCAAGG  3819
           |||||||||||||| |||| ||  ||||||||| ||||||||| |||||||| |||||
Db   3720  CAACAGATGCCAAAACCACCACTGAACCCCTCCGGGTGCGGGCAAAGGAGTTTTCAAAG  3779

Qy   3820  AGGCCCCGTTGTTTATGCTGCTACGGGGCGGGGAAAAGAGCACCCGGCTACCGTAGCTACG  3879
           | |||||||| |||||||||||||||||||||||||||| ||||| |  ||||||| |||
Db   3780  AGGCCCCGTTGTTTATGCCTATCTACGGAGCGGGAAAGAGCACTCGCGTCCCGTGAGTACG  3839

Qy   3880  GCAACATGGGCCACAAGGTCTTGATCTTCGGTAGCTAGGCCGTGTACCGTCGGTAGTCTTGAGGCCATGG  3939
           |||||||||||| |||| || || |||  ||| || ||||| ||||| |||| ||||||||||||||||
Db   3840  GCAACATGGGCCACAAGGTTCTTGAACCCCCAGTTCTTGAACCCCCTCAGTGTCTTCGGGGCCATGG  3899

Qy   3940  ATGACTCAACATGTTGGGTTGGGCTGTCGGCGTGTTCAGGAGCGTGCGCGGAGATGTGGAG  3999
           || | || |||||  ||| |||||||  ||| ||||| |||| ||  ||| || ||||| |
Db   3900  ATGATCAACATGTTGGGTTGGGCTGGTCAAGCTGTTCAACATCCAAGTATATACTGTGGCATGATACAA  3959

Qy   4000  CTGCTTTCACAAGGATCACTGACTCGCCCCCTTACGCTCACTTACGGAAGGTTTTTGG  4059
           |||||| ||||||||| ||| |||| |||||||||  ||||||||| | ||||||||||
Db   3960  CTGCTTTCACAAGGATCACTGACTCCCCCCGTCGGTTATTCAACCTATGGGAGGTTTTTGG  4019

Qy   4060  CCAACCTAGGCAGATGCTGAGGGTGTCAGTGGGCGTTTCGGTTGTCAAGGAGC  4119
           |||| | ||||||||| ||||  |||||||||||||| ||||| ||||| |||
Db   4020  CCAACCTAGGCAGATGCTGAGGTGCAGGTGCAGGTGACGGCGTTTGTCAAGGAGC  4079

Qy   4120  ATGACTCAACATGTTGGGTTGGGCATTGGGCGTGTTCGGCGGGATGTGGGAG  4179
           || | || |||||  ||| ||||| ||||| |||||||||||| ||||||||
Db   4080  ATGATCAACATGTTGGGTTAGGCCATTGGGCGTGTTCGGGATGACCTGGGGAG  4139

Qy   4180  TGCAATTGGTGCTCTACGGCCACTGCCACCCTACCCCGGATCCCCGATGACCCAGCAGCCCAT  4239
            |||| | | ||||| ||||| ||||| || ||||||||||||| |||||| ||||||| |
Db   4140  TGCAACTAGTGCTCTACCCCCGCTGGTTCATGGGGTCCCCGATCCCCGATGACGCAGCAGCACCCTT  4199

Qy   4240  CAATCATTGAGACAAAACTGGACGTGGAGATCCCCTCCTATGGCATACCTC  4299
           |||| |||||||| |||  || ||||||||||  ||| |||||| |||||||
Db   4200  CCATAATTGAGACAAAATTGGACGTGGGCGGCAGATTGGACCCGAATACCCC  4259

Qy   4300  TTGAGCGGATGCGGACCCGGAAGGCATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGC  4359
            ||| ||| ||| |||||||||||| || ||||||||||  || ||| ||||| ||||||
Db   4260  TCGAGCGGATGCGGAACGGGCTAGGGGGTGCTGGGGTAAATGCCATCGCTTCTAAGGCTGAGTGAGTCGAGC  4319

Qy   4360  GCCTGCGGGGCCAGTTTCGGCTGGGGGTAAATGCCATTACACAGGGGGAAAG  4419
           ||||| ||| | |||||||||  | |  |||||||  |||||| ||||| |||
Db   4320  GCCTTGTCTGGCCAGTTCTCCGCTAGGGGGGTCAATGGCAATTGCCTATTATAGGGTAAAG  4379

Qy   4420  ACAGTTCTATCATCCAAAGATGGGAGCCATCGGCCACTGGTGTGTCTGACACTCCACTG  4479
           |||||||||||||||||||| |||||||||||||||| |||| | |||||||||||||||
Db   4380  ACAGTTCTATCATCCAAAGATGGGAACATGGGAACATGGGGTCTGTGGTCGTGTGTCCACAGCGCCTTTCCACTG  4439
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Qy  4480  GGTACACTGGGAACTTCGATTCTGTCACCGATTGTGGGTTAGTGTGTGGAGGAGGTCGTCG  4539
          ||||||||||| || |||| || || |||||||| ||||  |||||||||||||||| ||
Db  4440  GGTACACTGGGAAATTCGACTCCGTCACCGATTAGTGGTGGAGGAGGTCGTTG         4499

Qy  4540  AGGTGACCCTTGATCCACCATTACCATCTCCCTGCGCACGGTGCCCGCGTCGGCTGAAC   4599
          ||||||| ||  |||||||||||||||||||||||||||||||||||||||||||||||
Db  4500  AGGTGACCCCTTGATCCACCATTACCATCCCCCTGCGGCAGTGCCTGCTCGGCGGCTGAAC  4559

Qy  4600  TGTCCGATGCAGCGGCGGAGGACGCACGGTAGGGGCAGTCTGGGCGCTACTACTACGCGG    4659
          ||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||
Db  4560  TGTCCGATGCAAAGACCGAGGACGCACGGCAGGGGCAGTCTGGGCGCTACTACTACGCGG   4619

Qy  4660  GGGTCGCAAGGCCCCTGCTGGTGTGTGGCGCTCAGGTCTGCTGTCGCGGTGGAAG       4719
          ||| |||||||||||| |||||||||| |||||||||||||||||||||||||||||
Db  4620  GGGTCGCAAAGCCCCTGCGGGTGTGTGGCGCGTCGGTCTGCTGTCGCGGTGGAAG        4679

Qy  4720  CCGGTGTGCACCTGGTACGGAATGGAACCTGACCTGGGAAGCCGCGGTGTTCTTTT      4779
          || ||||||||| || |||||| ||||| ||||||||| || |||||||||||||
Db  4680  CTGGTGTGCACCTGGTACGGAATGGAACCTGACCTGGGAAGCCGCGGTGTTCTTCT      4739

Qy  4780  ACAACTGCCCTTACACCGCCAGCCGTGACAGTTGGGGAGCCGCGGCGTTCGCGGCGTCA   4839
          || || ||||||||||||||||| ||||||||  ||| ||| ||||||||||||||||
Db  4740  ACGACTGCCCTTACACCGCCAGCCGTGATATCGGAGATACCGGAGAGCCGCAAAGTCGCGGCGTCA  4799

Qy  4840  CGGGGCTTGCCCGTTGAGGATGCATCCCGATGTGAGCTGGCAAAGTTCGCGGCCGTCA   4899
          |||||||||||| ||||||||||||||||  || |||||||||||||||||||||||
Db  4800  CTGGGCTCGCCCATTGAGGATGCAGTCCGATGTGAGCTGGCAAAGTTCGCGGCCGTCA   4859

Qy  4900  ACTGGCCCTTCCTGGTGGTGTTCAGCGGACCACATGTGCCGGGAAACACTGTCTCCCGGCC   4959
          ||||||||| | |||||||||||||||| |||||||||||||||||||||||||||||||
Db  4860  ACTGGCCCTTCTGTGTGGTGTTCAGCGGACCACATGTGCCGGGAAACACTGTCTCCCGGCC  4919

Qy  4960  CATCCGGATGACCCCCAGTGGGCAGTCTGAAGGGCCGAATCTGTCCACTCGTCGTGA    5019
          |||||||||||||||||||||  |||||||||||||||||||||||||||||| ||
Db  4920  CATCGGATGACCCCCAATGGGCAGTCTGAAGGGCCCAAATCCTGTCCCACTCGTCGTGA   4979

Qy  5020  GGTGGGCAATGATTTACCATCTAAAGTGCCGGGCCATCACATCGGACGACCTGGTCC    5079
          ||||||||| ||||||||||||||||| |||||||||||||||||||||||||||||
Db  4980  GGTGGGCAATGATTTACCATCTAAAGTGGCCGGCCATCACCACCAGTGGACGACCTGGTCC  5039

Qy  5080  GTAGGCTCGGGGTGCCGAGGGTTACGTCCGCTGCGATGCGGACCCATCTTGATGGTGG   5139
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5040  GGAGACTCGGGGTGCCGAGGGTTACGCCCTGCGACCGCGGACCGGACCCAGTCTTGATGATCG  5099

Qy  5140  GCCTCGCTATTGCGGGGGGCCATGAATCATGCTCATACACACCGGGTCTCTCGCTGGTGTGGTTA   5199
          || || |||||| ||| |||||||| ||||||||||||||||||||||||||||||||
Db  5100  GTCTAGCTATCGCGGGGGAATGATGCCGTCTACACCGGGTCGCTAGTGGTGGTGA     5159

Qy  5200  CAGACTGGGATGTGCAGGGGTGAAAGGGGGGTGCAGCCCCTTTATCCGCATGGAGACCAGGCCACGC   5259
          |||||||||||| ||||| ||| |||||| ||||||||||||||||||||||||||||||||||
Db  5160  CAGACTGGGATGTGCAGGGGTGAAGGGGGTGCAGCCCCTTATCCGCATGGAGACCAGGCCACGC  5219

Qy  5260  CCCAGCCGGTTGTGACAGCTCTTCGCCGGGGGGGCGTAGAGAGTCCCCCGGGGGAGAGTCTGCGGCCAT   5319
          |||||||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||
Db  5220  CTCAGCCGGTGTGGACAGTCTTCGCCGGGGGGCGTAGAGAGTCCCGGGGGAGAGTCTGCGGCCAT  5279

Qy  5320  CGGATGCCAACACAGATGCAGAGATGCGGTGCGGCCATCCAGGTGCAGCCGATTGGTCAG    5379
          ||||||||||||||||||||| |||| || || ||||||||||| |||||| |||||||
Db  5280  CGGATGCCAAGACACAGATGCAGAGATGCGGTGCGGCCATCCAGGTGCAGCCGATTGGACTA  5339

Qy  5380  TCATGACCCTGTCGATCGGGGAAGTGCTGTCCCTTGGCCCCAGCCGGCCGAGGCCT      5439
          ||||||| |||||||| |||| ||||||  || || |||||||||||||| ||||
Db  5340  TCATGACTGTGTCGATCGGGGAAGTGGTTGTCCTGCTTGCCCCAGCCGGCCGAGGCCT   5399

Qy  5440  ACGCAGCTACCACCAAGTGCTTGGCTGCTACACGCGGGCGGCCGTCCCCACTG       5499
          || |||||||||||||||||  |||| |||| ||||||||||||||||||||
Db  5400  ACACAGCAGCCACCAAGTGCTTGTTTCCCTGCTATAACGGCGGGCCGTCCCACTG  5459

Qy  5500  TTTCAATTGTTGACAAGCTCTTCGCCGCTGGGCGGCGGTGTAGGCGATTGCCACA      5559
          || |||||| |||||| || |||||||||||| |||||||||||||||||||||||
Db  5460  TATCCATTGTTGACAAGCTCTTCGCCGGAGGGTGGGCGGCCATTGGCCATTGCCACA   5519

Qy  5560  GTGTAATAGCTGCGGCAGTGCGGCCTATGGGCGCCTATGGCGCCTTCTAGGAGCCCTGCTG   5619
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  5520  ACGTGATTGCTGCGGCGGTGGCGGCCTACCGGGCGTGCGGCCTACCGGGGGGCCTTCAAAGAGCCCGGCCGTTGGCAGCCG  5579

Qy  5620  CCGCTTCCTACCTCAGTGGGGTTGGGCGTGCGGCCCGTGGGCGTTGGGGTTGGGCTGCCG  5679
          ||||||||||||||||||||||||||| |||||||||||||| |||||| |||| ||||
Db  5580  CGGCTTCCTACCTCAGTGGGGTTGGGCGTTGGGCGTGCGGCCGCTCAGACGCGTCTGGCATCTG  5639

Qy  5680  CTCTCCTACTAGGGCCGTGGGGACCGTGGGCACGCGCTGTCGTGGGTTAACCATGG   5739
          | ||||||| ||| |||| |||||||||| |||||||| ||||||||| |||||||
Db  5640  CCCTCCTATTGGGCGGCTGCTGGAACCGCCCTGGGCACTCGTCGTGGGCTGACCATGG  5699

Qy  5740  CGGGGCCGTTCATGGGAGTGCTAGCGTCCTCCCCTCCTTGGTCACCATTTTACTGGGGG   5799
          | |||| |||||||||||||||| ||||||||| ||| |||||||||||||| |||||
Db  5700  CAGGTGCGTTCATGGGAGGGGCGCCCAGTGTCCTCCCCTCCTTGGTCACCATTTTATTGGGGG  5759

Qy  5800  CCGTGGGGGCTGGGAGGGCCGTGGTGAATGCGCGTAGCCTTGTCTTCGACTTTATGGCGG   5859
          ||||| |||||||||||| |||||||| ||| ||| |||| | ||| ||| ||||| |||
Db  5760  CCGTCGGAGGTTGGGAGGGCCGTGTGTCAACGCGGCGAGCCTAGTCTTTGACTTCATGGCGG  5819

Qy  5860  GGAAACTATCATCAGAAGATCTGTGTATGCCATCCCAGTGCTAACCAGTCCGGGGGGCAG  5919
          ||||||| ||||||||||||||| ||||| ||| ||||||||||||||| ||||||||||
Db  5820  GGAAACTTCATCAGAAGATCTGTGTATGCCATCTCCGGTACTGACCAGTCCCGGGGGCGG  5879

Qy  5920  GACTTGCGGGGATCGCCCTCCGGGTTGGTTGTTGTACTCAGCTACGATGCCTCGGCCACTACCA   5979
          |||||||||| |||||||| ||||||| ||| || |||||||| || ||||||||||||||||
Db  5880  GCCTTGCGGGGATCGCCTCTCGGGTTGGTTGTTTGTATTCAGCTACGATGCCTCGGCCACTACCA  5939

Qy  5980  CTTGGTTGAACCGTCTGCTGACTACATTGCCAAGGTCCTCCATGCATCCTGACAGTTACT   6039
          ||||||||||||||| |||||||||| ||||||||||| ||||  ||||| ||||||||
Db  5940  CTTGGTTGAACCGTCTGCTGACTACGTTGCCAAGGTCTTCATGCGTATCCCGACAGTTACT  5999

Qy  6040  TTCAGCAGGCCGATTACTGTTGACAAGGTCTTCAGCTGTCCGACGCTGTGCTCCACTC    6099
          ||||||| ||||||||| ||| |||||||||||||| |||||||||||| || |||||
Db  6000  TTCAGCAAGTTGACTATTGCTGGTCAACAGTCTTCAGCTCTTCAGCGGCCGTGGGCGCCTCCACCC  6059

Qy  6100  GCACCCTGGTTGCCCTGGTCAACAGGAGCAAGCCTAAGGTGAAGGTTCAGGTTGGGGTACG  6159
          |||||| |||||||||||||||||||||| || |||||||||||  ||| || |||||||
Db  6060  GCACAGTGGTTGCCCTGGTCAACAGGAGCCTAAGGTGGATGAGGTTACAGTGGGGTATG  6119

Qy  6160  TCTGGGACTTCTGGGAGTGGATCATGCGTCAAGTGCGCCATGTGGATGCTGATCGGG    6219
          | |||||||||||||||||| || |||||||||||||||||||||| |||||||||
Db  6120  TCTGGGACTGGTGGGAGTGGATCATGCGTCAAGTGGTGCTGCCCAGACTTCAGGG       6179

Qy  6220  CCCTCTGCCCCGTGTCATTACCCTTATGGCACTGCGGGGAGGGGTGTTCCGGAGAAT    6279
          ||||||||||| ||||| |||||||||||||| ||||||||||||||||||||||||
Db  6180  CCCTCTGCCCCGTGTCTCATTACCCTTGTGCACTGCGGGGAGGGGTGTTCCGGGGAAT  6239

Qy  6280  GGTTGTTGGACGGCCATGTTGAGACTGTCGTTGCTGTCTTTGTGATCACCGGTGATG   6339
          ||||||| ||||||||| || || ||| ||||||||||||||| ||||||||| |||
Db  6240  GGTTGCTTGACGGCCATGTTGAGAGTGTGAGGTCTGTGCGGCTGCGCCGATCATGTGGTGACG  6299

Qy  6340  TTTGAATGGCAACTCAAAGATCAAAGACATCAGTTCACTGGTTCAGGCATTATTGGA    6399
          || ||||||||||| ||||||| |||| |  ||||||||||||||||||||||||||
Db  6300  TTCTGAATGGGCAACTCAAAGAACCAGTTTTACTCTTACCAAGCTGTCGCGGCCACTATTGGA  6359

Qy  6400  TGGGGACAGTCCTGTGAACATGCTGGGCTATGGCGCAGCTCCGGCCAGACGTCGCCGTCAG   6459
          |||||| ||||||||||||| |||| ||||  ||||| ||||||||| |||||||  |||
Db  6360  TGGGGACTGTCCCCTGTGAACATGCTGGGTTACGGTTGAAACGTCGCCGCTCTCCTGGCCCCG  6419

Qy  6460  ACACCCGAAGGTGTTACCATTCGGACGTCTGGGCTGGCTGGCGTGAGGCGTGTGACCCCTA  6519
          ||||||||| ||| ||||| |||||||| |||||||||| |||||| |||||||| ||||
Db  6420  ACACCCGAAGGTTGTCCCCTTCGGGACGTCTGGGCTGGCTGGCGTGGAGGCGCCAGTGACCTA  6479

Qy  6520  CCCACGTTGTGATCAGGCGGAACATCCGCCTACAAAACTCCTGTCGG             6579
          |||||||||| |||| |||| || |||| ||||  ||| ||||||||
Db  6480  CCCACGTTGGTAATCAGGAGACCCCTCGCCCTATAAGCTGCTCCCATATCGG  6539

Qy  6580  CTGCTGTTGCTGAGCCTATTTACGTCCATGGGACCGCATGGCGCTCTCATGGACCGCGACGCGC   6639
          |||||||||||||| || ||||||||  || |||| ||||  ||||||  || ||||||||
Db  6540  CTGCTGTAGCTGACGTCTGAGCCGTCGACGCAGTTCCGGTCTCATGGGACCCACTGCGGCACGCTC  6599

Qy  6640  GAGCCGCTGCCAATGCTCTATGCGCCCTGGGCAAAGTCTCACCATTGCACCAGGAACGCTACA  6699
          |||||||||| || |||| ||||||||| |||||| |||||||||||||| || |||||||||
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Db   6600 GTGCGCCCGCCATGGTCTATGGCCCTGGGCAAAGTGTTACCATTGACGGGAGCGCTACA 6659

Qy   6700 CCCTTCCGCATCAACTGGGCTTAGGAATGTGCGCCCCTCTGAGGTGTCATCCGAGGTGT 6759
          |||| ||  |||||||||| ||||  |||||||||||  ||||||||||||| ||||||||
Db   6660 CCCTCCATCAACTGAGGCTTCAGGAATGTGCGCGCCCTCTGAGGTTTCATCCGAGGTGT 6719

Qy   6760 CCATTGACATTGGGACGGAGACTGAGAACTGACTGAGGCCGACCTGCGCCGCGG 6819
          |||||||| ||||||||||||||||||||||||||||||| |||||  ||||||
Db   6720 CCATTGACATTGGGACGGAGACTCAGGACTCGAGGACTCGAGGCCGATCTGCCGCCGG 6779

Qy   6820 CGGCTGCAGCCCTTCAGGCTGCTATCGAGAATGTGCGAGAATTCTTGAACCTCACATAGATG 6879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6780 CGGCTGCTCTCCAAGCGATCGAGAATGTGCGAGGATTCTGCAACCGCACCATTGATG 6839

Qy   6880 TCATCATGGAAGATTGCAGTACACCCCTCTTTGTGGGAGTAGCCGAGAGATGCCTGTGT 6939
          ||||||||||||   ||  ||||||||||| |||||||| ||  |||||||||||
Db   6840 CCATCATGGAAGACTGCAGTACGAGTACACCCCTCTTTGTGTAGTAGCCGAGAGATGCCTGTAT 6899

Qy   6940 GGGGAGAAGACATACCCCGCACTCCATCTCCGGTTACTGGTGATACCCCGTCTTCTGACTCAT 6999
          ||||||||||||||||||||||||||||  ||||||   |||  |||||||||||||||||||
Db   6900 GGGGAGAAGACACCCCCCGTCACTACTCCATCTCCGGTTACTGGTTACTGAGAGCAGCT 6959

Qy   7000 CAGATGAGAAGACCCCGTCGGTGTCTTCTCCGGAGGAGGAAAGCGTCTTCAACGTGGCTC 7059
          |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db   6960 CAGATGAGAAGACCCCGTCGGTGTCCTCTGCCAGGAGGATACCCCGTCCTCTGACTCAT 7019

Qy   7060 TCGAGGTCATCCAAGAGTCCGAGACAGCCGAAAGCGTCTTCAACGTTACCGTTAAGA 7119
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7020 TCGAGGTCATCCAAGAGTCCGAGACAGCCGAGAAAGCGTCTTCAACGTTACCGTGGCTC 7079

Qy   7120 TTTCCGTACTAAAAGCCTTGTTCCCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGA 7179
          |||||||  ||||  ||| |||||||||||||||||||||||||||||||||||||
Db   7080 TTTCCGTATTAGAAGCGTCATTCCCAGAGACCAGCAACAATCAGCCTATTGTGACAAGGTGC 7139

Qy   7180 TGTCATGCTGTGTTGAGAGAGCCTTCATTGGATTGACGGTCGCTG 7239
          |||||||||||||||||||||  |||| |||||||||||||  ||||||
Db   7140 TGTCGTGCTGCGGTGTTGAAAGAGCGTCACGCGCTTTTCTCATTGGGTTGGTTGGCTG 7199

Qy   7240 ACAAGTGTGAGGCTAGGCAAGAGACCTTGGCTTCCTTTACATTTGGTCTGGGGTGC 7299
          | |||||||||||  |||||| ||||||||||||||||||||||||||||||||
Db   7200 ATGTTGTAGGCCTGTGAGATGGAAATCCAGAACCATTACAGCCTATTGTGACAAGGTGC 7259

Qy   7300 GCACTCGCCGTTGAATTGCAGGTTGGTGCTTGGTGGCCAATGAACTTTACCTTTGAATGTG 7359
          ||||||||||||||||||||||||||||||| ||||   ||||||||||||||||||||
Db   7260 GCACTCCGTTGAATTGCAGGTTGGGTGCTTGGTGGGCAATGAACTTTACCTTTGAATGTG 7319

Qy   7360 ACAAGTGTGAGGCTAGGCAAGAGACCTTGGCTTCCTTTACATTTGGTCGGGGTGC 7419
          | |||||||||||  ||||||||||||||||||||||||||||||||||||||
Db   7320 ATGTTGTGAGGCTAGGCAAGAACCTTGGCTTGTCTTCTTTACCTTTGGTCTGGAGTGC 7379

Qy   7420 CACTGACGAGGGCCACTCGGCAAGAGACCCCTCGGGAGGCGTGGGCTCTCTTGCTGG 7479
          | |||||||||  |||||||||||||||||||| |||||| | |||||||||||
Db   7380 CGCTGACTAGGGCGACCACCGGCTCAAGCCTCCGGGAGGTGAGGGGTCTCTTTATTAG 7439

Qy   7480 TGGCCGACCACCAAGGTGTATGTCACCAACCCGGACAAGTTGGAGGAAGAGTTGACA 7539
          |||||||||||||||||| || ||||| |||||||||||||||| ||||||||||
Db   7440 TGGCCGACAACTACTAAGGTGTATGTTACCAATCCAGAACTTTCGTGGGACTGGTGACA 7499

Qy   7540 AGTTACCTTCTGCGGTGTCCCCTAGGGTTCATGACAAATTCCTCGTGGACTCCATAGAGC 7599
          |||| ||||||||||||  ||||||| |||| |||||  ||||||||||||||||||
Db   7500 AGGTCGACACTACTAAGGTGTATGTCCTAGGGTTCATGATGAATTCGTCGTGGACTCCATTAGC 7559

Qy   7600 GCGCTAAGAGGGCAGCTCAAGCGGTCAAGCGCTCAAGCCTTATGACTTATGAGGAGGCAATAA 7659
          ||||| |||||||||||||||||||  |||||||||||||||||||||||||||||||
Db   7560 GCGCTAAGAGGGCCGCTCAAGCGGTTCAAGCCTGCTAAGCATGGGTTACAACTTATGAGGAAGCAATAA 7619

Qy   7660 TGGCCGACGCGTTGAGCGGTCTGGGGATCGGGGATCTAAGGTCTCCGTGCCAAGGACCTTCG 7719
          |||||||||||||||| |||||||||||||||||||| | ||| |||||| ||||||
Db   7620 TGGCGACGTGTAAGGTGCCGACATGGGATCGGGATCTCCGGTTAAGGACTTAG 7679

Qy   7720 CCACCCCGGGGGAAGATGGCGTCCCATGACCGGCTCCATGCGGATACTTGAAGGGACGC 7779
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db   7680 CCACCCCGGGGAAGATGGCGTCCCATGACCGGCTCCATGCGGATACTTGAAGGGACTC 7739
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Qy   7780 CAGTCCCCTTTACTCTTACTGTGAAAAAGAAGGTGTTCTTCAAAGACCGAAAGGAAGAGA 7839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7740 CGGTCCCCTTTACTCTTACTGTGAAAAAGAAGGTGTTCTTCAAAGACCGGAAGGAGGAGG 7799

Qy   7840 AGGCCCCCGCCCTCATTGTGTTCCCCCCCCTGGACTTCCGGATAGCTGAAAAGTTATTC 7899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7800 AGGCCCCCGCCCTCATTGTGTTCCCCCCCTGGACTTCCGGATAGCTGAAAAGTCATCT 7859

Qy   7900 TGGGAGACCTGACGGGTAGCCAAGGCGGTGTTGGGGGGGGCCTACGCGTTCCAGTACA 7959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7860 TGGGAGACCCAGACCAGACCGGTAGCCAAGGCGGTGTTGGGGGGGCCTACGCGTTCCAGTACA 7919

Qy   7960 CCCAAATCAGCGAATTAGGGAGAGTGCTCAAACTGTGGGAATCAAAGAGACACCATGCG 8019
          ||||||||||||||||| ||||||| |||||||||||||| ||||||||||||||||
Db   7920 CCCAAATCAGCGAGTTAAGGAGAGTGCTCAAGCTCTAAGCCTATGGGAAGACCCCCTTGCGG 7979

Qy   8020 CCATCTGTGTGGCAGCCACATTGCCCTGGCTTCGACGTAGCATAACTGAGAGGACGTGGCGCTGG 8079
          |||||||||||||||||||| ||||||||||||||||||| ||||||||||||||||||
Db   7980 CCATCTGTGTGGACGCCGTCTGGCCCTCTGGCGACGTAGCATAACTGAGAGGACGTGGCTTTGG 8039

Qy   8080 AGACAGAGCTTATTGCCCTGGCTTCAGGACCATCCAGAATGGTGCGCGCCTGGGGAAAT 8139
          ||||||||||||  |||| ||||||||||||||||||||||||||||| ||||||||||
Db   8040 AGACAGAGCTGTACGGTCCTCTGACCAGTGGCACAACTGGTGGTGCGCGGCACTTGGAAAT 8099

Qy   8140 ACTATGCCTCTGGCACAATGGTAACCCCCGAGGGGGGTGCCAGTGGTGAGAGGTATTGTA 8199
          |||||||||||| || ||||||||  |||||||||||||||||||||||||| ||||
Db   8100 ACTATGCCTTCAGGCACCATGGTGCACCCCGAGGGGGTGCCCGTCCGTCGGAGAGGTATTGCA 8159

Qy   8200 GATCCTCAGGGGTCTTGACCACCAGTGCGGAGCAACTGCTTGACTTGCTATATCAAGGTGA 8259
          |||||||||| ||||  | || |||| |||||| ||||||||||| |||| |||||||
Db   8160 GATCCTCAGGGTGTCCTAACAACTAGCGCCGAGCAACTGCTTGAACCTGCTACACCAAGGTGA 8219

Qy   8260 AAGCCGCTGTGAGAGGTGGGGCTGAAAAATGTCTCGCTCCTCCATCGCTGGCGATGACT 8319
          ||||||||||||||||||||||  |||||||  |||||| |||||||||||||||||||
Db   8220 AAGCCGCTGTGAGAGGTGGGGCTGAAGAATGTCTCATATCATCCTGGACGCCGGCGATGACT 8279

Qy   8320 GTTGATCATATGGCGAACGGCCGCTTGTGCGATCCGTCTAGCGACGCTTTGGGCAGAGCCCTGG 8379
          ||||||||||||| |||||||||||||||| ||  || |||  ||||||||||||||||||
Db   8280 GCTTGATCATATGTGAGCGCGCCAGTGCGTGCGCCAGCCCAAGCGACGCGTTTGGGCAGAGCCCTAG 8339

Qy   8380 CGAGCTACGGGTACGCCATCGCAGCCTTCGTCACTCACTGACACGGCCCCCCCTTCT 8439
          ||||| |||||||| ||||| |||||| |||||||| |||||| ||||||||||||
Db   8340 CGAGCTATGGGGTACGCGTCGCGAGCCCTCATATCATCCTTGGCACGGCGCCCCCCTTCT 8399

Qy   8440 GCTCCACTTGGCTACGTGACTGAGTCGATGCAATGCGGAAACCCCATTTCTTCCTGACCACGG 8499
          ||||||||||||||||  | |||  |||||||||||||  |||||||||||||||||||||
Db   8400 GCTCCACTTGGCTTGCTGCCATGCGAGTCGATGCAATGGAAGCCCATTTCTTCCTGACCACGG 8459

Qy   8500 ACTTTCGGAGGCCCCCTCGCCTATACCCGGGCCAATGGCTTCGGCCA 8559
          ||||| |||||||||||||| |||| ||||||||||| ||||| |||
Db   8460 ACTTCCCGGAGGCCGCGGCCCTGCCTCGTGAGTGGGATTGGGCTCGGCGA 8519

Qy   8560 TCGGTTACATCCTCCTATACCCTTATCCTTTGGCACCCCATCACCCTTCACG 8619
          ||||||  ||||||| || |||| |||  ||||||||||||||||| || ||
Db   8520 TCGGTTTACATCCTCTCTTTATTCCTGGCACCCATGCACGGTCATCATCCTCATG 8579

Qy   8620 TGCTCACCTTGCGCGGTTAGGGTGTGGCCACACCGCTGATCCGTGTGTGGCCACACGG 8679
          ||| |  ||||||||||||||||||||||| || ||||||||||||||||||||||||
Db   8580 TGCTAAGTGCGCGTTCAGGGTTACCGGCACCACCGTTGATCCGTCTGGTTGTGGCCAGGTAC 8639

Qy   8680 ATGTAATTACTACAAGTTCCACTGACAAACTGCCTAACATCGCCGACAACGAGGCGGCAATAA 8739
          ||||| ||||||||||| ||||||| ||||  |||| ||||||||||||||||||||||||||
Db   8640 ATGTAACTACTACAAGTTCCACTGACAAACTCCTAACATCGCCGACAACATCGAGGCCCACCG 8699

Qy   8740 GACCAGCAGCGTTGAGGGTTACCCGCAGACACAACTAAGACAAAAATGGAGGCCTGGCAAGG 8799
          |||||||||||| ||||||||||||||| ||  ||||||| ||||| |||||||||||
Db   8700 GACCAGCAGCGTTGAGGGTTACCCGGCGACTCCAGACCAACAACTAAAAACAAAAGGAGGCCTGTAAGG 8759

Qy   8800 TGCTGAGCGACCTCAAGCTCCCTGCCTCCCGCAGTTCCACCGGGGCGGGCATTGC 8859
          |||||||||||||||||||||||||||  |||||||||||||||  |||||| |||
Db   8760 TTCTGAGCGACCTTCAAGCTCCGTGCTTAGCAGTCCAGTACAGGGCGGCCGTTGC 8819
```

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Qy  8860 GAACGCGTATGCTCCGGTCGCGCCGGTCGGGCTCGAGTTGGCTAGGGGCGCTGTTGTGGCGTC 8919
         ||||| || ||||||| |||||||||||||||||||||||||||||||||| |||||||| ||
Db  8820 GAACACGCATGCTCCGCGCGGTTGGCTGGCGCGGTTGGCTAGGGGCTTGGCTAGGGCCATC 8879

Qy  8920 CAGGCCTGCGGCTTCCCCCTCCGAGATTGCTGGTATCCCGGGGGTTTCCCCCTTTCCC 8979
         ||||||| ||||||||||||||| |||||||| |||||||| | ||||
Db  8880 CAGGCCTAGGCGGCTTCCCCCCTCCGAGATTGCTGGTATCCCGGGGGGTTTCCCCTCTCCC 8939

Qy  8980 CCCCTATATGGGGTGGTTCATCAATTGGATTTCACAGAGCCAGAGAGTCGCTGGCCGT 9039
         |||||||| ||||||| || |||||||| |||||||||||||||||| ||||||||||
Db  8940 CCCCTATATGGGGTGGTACACCAATTGGATTTTACAGCCAGAGAGTCGCTGGCCGT 8999

Qy  9040 GGTTGGGGTTCTTAGCCCTGCTCATCGTAGCCCTTCGGTGAACTAAATTCATCTGTT 9099
         ||||||| ||||||||||||| |||||||||||||||||||||||||||||||||||
Db  9000 GGTTGGGGTTCTTAGCCCTGCCTCATCGTAGCCCCTTCGGGTGAACTAAATTCATCTGTT 9059

Qy  9100 GCGCAAGTCCGGTGACTGATCATCACTGGAGGAGGTTCCCGCCCTCCCCGCCCCAGGG 9159
         | |||||||||||||||| |||| ||||||||| ||||||||||||||||||||||||
Db  9060 GCGGCGAGGTCGGTGACTGATCGTCACCGGAGGAGGTTCCCGCCCTCCCCGCCCCAGGG 9119

Qy  9160 GTCTCCCCCGCTGGGTAAAAAGGGCCCGGCCTTGGAGGCATGGTGGTTACTAACCCCCTG 9219
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9120 GTCTCCCCCGCTGGGTAAAAAGGGCCCGGCCTTGGAGGCATGGTGGTTACTAACCCCCTG 9179

Qy  9220 GCAGGGTCAAAGCCTGATGGTGCTAATGCACTGCCACTTCGGTGGTGGGTCGCTACCTTA 9279
         ||||||| ||||||||||||||||||| ||||| |||||||||||||| ||||||||||||
Db  9180 GCAGGGTTAAAGCCTGATGGTGCTAATGCACTGCCACTTCGGTGGTGGGTCGCTACCTTA 9239

Qy  9280 TAGCGTAATCCGTGACTACGGGCTGCTCGCAGAGCCCTCGCAGAGCCCCGATGGGGCACAGTGCAC 9339
         |||||||||||||||||||||||||||| ||||||||||||||||||| ||||||||||||||||
Db  9240 TAGCGTAATCCGTGACTACGGGCTGCTCGCAGAGCCCTCGCAGAGCCCCGATGGGGCACAGTGCAC 9299

Qy  9340 TGTGATCTGAAGGGGTGCACCCCGTAA 9367
         || ||||||||||||||||||||||
Db  9300 TGAGATCTGAAGGGGTGCACCCCGGGAA 9327
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RESULT 11
AAV56242
ID AAV56242 standard; cDNA; 9327 BP.
XX
AC AAV56242;
XX
DT 06-NOV-1998 (first entry)
XX
DE HGV isolate 3ZHGV-6 cDNA from PNF2161.
XX
KW Immunoreactive; detection; antibody; alanine aminotransferase;
KW Non-A, Non-B, Non-C, Non-D, Non-E hepatitis virus; ds.
XX
OS Hepatitis G virus.
XX
PN US5766840-A.
XX
PD 16-JUN-1998.
XX
PF 05-JUN-1995; 95US-0466033.
XX
PR 19-MAY-1995; 95US-0444733.
PR 20-MAY-1994; 94US-0246985.
PR 03-AUG-1994; 94US-0285543.
PR 03-AUG-1994; 94US-0285558.
PR 03-AUG-1994; 94US-0285561.
PR 26-OCT-1994; 94US-0329729.
PR 23-NOV-1994; 94US-0344271.
PR 16-DEC-1994; 94US-0357509.
PR 15-FEB-1995; 95US-0389886.
PR 05-JUN-1995; 95US-0466033.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fry KE, Kim JP, Linnen JM, Wages J, Young LM;
XX

DR WPI; 1998-361677/31.
XX
PT Antibody to hepatitis G virus protein - useful for diagnosis of
PT hepatitis G virus infection
XX
PS Example 18; Column 337-346; 204pp; English.
XX
CC This sequence is a used in a method which detects Non-A, Non-B, Non-C,
CC Non-D, Non-E hepatitis G virus (HGV) in a biological fluid sample, e.g.
CC from a test subject, especially using a kit comprising an anti-HGV
CC antibody preparation and a reporter for detecting binding of an HGV
CC polypeptide antigen to the antibody, preferably where the antibody is
CC monoclonal and/or is attached to a solid support and where the reporter
CC is a labelled monoclonal antibody or a labelled competing antigen. The
CC HGV is characterised by producing elevated serum alanine aminotransferase
CC levels in an infected primate, being serologically distinct from
CC hepatitis A, B, C, D and E viruses and having a viral genome containing a
CC nucleic acid region that is selectively hybridisable with a polypeptide
CC having 203 base pairs as given in the specification.
XX
SQ Sequence 9327 BP; 1682 A; 2532 C; 2984 G; 2129 T; 0 other;

Query Match   83.9%; Score 7885.6; DB 19; Length 9327;
Best Local Similarity   90.4%; Pred. NO. 0;
Matches 8433;   Conservative   0; Mismatches 894; Indels 1; Gaps 1;

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Qy    40 GCAAGCCCCATAAACCGACGCCTATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCG  99
         ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GCAAGCCCCAGAAACCGACGCCTATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCG  60

Qy   100 ACCGGCCAAAAGGTGGTGAATGGTGGTTGGTGACAGGTTGGTAGGTCGTAAATCCCGTCAT 159
         |||||||||| |||||||||||||||||||||||||||||||||||||||||||||| |||
Db    61 ACCGGCCAAAAGGTGGTGAATGGTGGTTGGTGACAGGTTGGTAGGTCGTAAATCCCGTCAC 120

Qy   160 CCTGGTAGCCACTATAGTGGTCTTAAGAAGTGCAAGACTCCTCTTGTGCCTGCGGCC 219
         | |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   121 CTTGGTAGCCACTATAGTGGTCTTAAGAAGTTAAGATTCCTCTTGTGCCTGCGGC 180

Qy   220 GAGACCGGCACGGTCCACAGTGCTGGCCCTACGGTGTGAATAAGGGCCCGACGTCAG 279
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   181 GAGACCGGCACGGTCCACAGTGTTGGCCCTACGGTGGGAATAAGGGCCCGACGTCAG 240

Qy   280 GCTCGTCGTTAAACCGAGCCCTATCACCCACCTGGGCAAACGACGCCCACGTACGGTCCAC 339
         ||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   241 GCTCGTCGTTAAACCGAGCCCGTTACCCACCTGGGCAAACGACGACGCCCACGTACGGTCCAC 300

Qy   340 GTCGCCCTTCAATGTCTCTCTGACCAATAGGTTTATCCGCGAGTTGACAAGGACCAGT 399
         ||||||||||||||||| |||||||||| | ||||||||||||||| |||||||||||
Db   301 GTCGCCCTTCAATGTCTCTCTGACCAATAGGCGTAGCCGCGAGTTGACAAGGACCAGT 360

Qy   400 GGGGGCGGGGTTATGGGAAGGACCCCAAACCTGCCCTTCCCGCCGCGGGTAGCCCAAGAATCCTTCGGG 459
         |||||||||||| ||| || |||  || |||||||||||||| ||||||||||||||||||||||||||
Db   361 GGGGGCGGGGGCT TGGAGAGGGAGCT CCAAGTCCAAGTCCGGCCGCGGGTAGCCCAAGAATCCTTCGGG 419

Qy   460 GCATGGGGCCACCCAGCTCCGCGGCGCCCGGCCGCGGCCTGCAGCCGGCGCTGCAGCCGAATCCTTCGGG 519
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 GCATGGGGCCACCCAGCTCCGCGGCGCCCGGCCGCGGCCTGCAGCCGGCGCTGCAGCCGAATCCTTCGGG 479

Qy   520 TGAGGGCGGGTGGCATTTCTCTTTCTCTTCTATACCATCATGGCAGTCGCAGTCCTTCTCG 579
         |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   480 TGAGGGCGGGTGGCATTTCCTTTTCTATACCATCATGGCAGTCGCAGTCCTTCTCG 539

Qy   580 TGGTTGAGGCCGGGGCCATTCTGCCCCGGCCACCCCAGCCGCCAATGGGCAAT 639
         ||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   540 TGGTTGAGGCCGGGGCCATTCTGCCCCGGCCACCCCAGCGTCTGCGCCGAATGGGCAAT 599

Qy   640 ATTTCCTCACAAATTGCTGTGCCCGGAAGGACACATCGGGTTCTGCCTGGAAGGCGGATGCC 699
         ||||||||||||||||||||| ||||| ||| ||||||||||||||||||||||||||||||
Db   600 ATTTCCTCACAAATTGTGTGCCCCGGAGGACAATCGGGTTCTGCCTGGAGGGGTGGATGCC 659

Qy   700 TGGTGGCCCTGGGTGCACGGTTTGCACCGACCGGTTGCTGCCCACTTGGCCCACTGTATCAGGCGGGTT 759
         ||||||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   660 TGGTGGCCCTGGGTGCACGATTTGCACTGACCAATGCTGGCCACTTGGCCCACTGTATCAGGCGGGTT 719
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Db  2880  |||||||||||||||||||||||||| ||| ||||||||||||||
          TTGAGTTGCTGTGTGATGGCGGCTACCTGTTGACCAGAGGGGCCACAACCGTCCGGCTGGTCTCCAAGATGT  2939

Qy  2980  GCCCAAGAGGGGCCTACCTGTTGACCAGAGC
          || | ||||| ||| || |||| ||||||||||||||||||||
Db  2940  GTGCGGAGGAGCTTATTGTTCGATCATATGGGCTTCATTTTCGCGTGCTGTGCCAGAGC  2999

Qy  3040  GCTTGTTGGAATGGGACGCGCTTGGAGCCCGCTCACTAGGACGGACTGTCGCA
          |||||||| ||||||| |||| |||||||||||||||||||||
Db  3000  GCCTGTTGGAATGGGACGCGCTTGAACCTCGTCATTCACTAGGACGGACTGTCGCA  3059

Qy  3100  TCATCAGAGATGCCGCGAGGACCCTGTCTGCGGACAGTCGCTCATGGGTTTACCCGTGG
          |||| |||||||| ||| ||||||||||||||||||||
Db  3060  TCATACGGGATGCCGCGGCCTGAGGACTTGTCTCTGCGGCAATGCGTCATGGGTTTACCCGTGG  3119

Qy  3160  TAGCACGGCGGTGATGAGGTTCTCATCGGCGTCTTTCAGGATGTGAATCATTTGCCTC
          | || ||||| ||||||||| |||||| |||||||||||||||
Db  3120  TTGCGCGCGGTGATGAGGTTCTCATCGGCGTCTTCCAGGATGTGAATCATTTGCCCTC  3179

Qy  3220  CCGGGTTTGTTCCGACTGCCACCAGTTGTCATCCGTCGGTGCGGAAAGGGCTTCCTGGGGG
          | |||||| ||||||| |||||||||||||||| ||||||||||||||
Db  3180  CCGGGTTTGTTCCGACCGCGTGTTGTCATCCGTCGGTGCGGAAAGGGCTGCCTGGGGG  3239

Qy  3280  TCACGAAGGCAGCCTTGACAGTAGGAGGATCTGACTTACATTCCAGGGAACGTCATGGTGT
          |||| ||||||||||||||||||| |||||| ||||||||||||||
Db  3240  TCACAAGGCTGCCTTGACAGGTCCGGATCGTCCTGACTTACATTCCAGGGAACGTCATGGTGT  3299

Qy  3340  TGGGGACGGCTACGTCACGGAAGCATGGGCACATGTCTGAATGGCCACTTCACAACTT
          || |||||||| |||||| |||||||||||| | ||||||||
Db  3300  TGGGGACGGCTACGTCCGAGAACATGGGAACATGTTGAACGGCCGTCTGTTCACGACCT  3359

Qy  3400  TCCATGGGCTTCATCCCGAACCATCGCCACGCCCGTGGGGCCCTTAATCCCAGTTGGT
          ||||||||||||||||||| ||||||||||||||||
Db  3360  TCCATGGGCTTCATCCCGAACCATCGCCACACCCGTGGGGCCCTTAATCCCAGATGGT  3419

Qy  3460  GGTCAGCCAGTGATGACGTCACGGTCTACCCGGCTTCCAGATGGGCCAACTTCGTTGACGC
          |||||||| |||||| ||||||| ||| |||| ||||||||||||||
Db  3420  GGTCGTGCTCGGCTGATGTGCACGGTCTATCCACTCCCGGATGGGCTACTTCGTTAACGC  3479

Qy  3520  CCTGCACTTGCCAGGCGGAGTCCTTGTTATTAGATCCGACGGGCTTTGTGCCCATG
          | |||||||| |||||||||||| | |||||||||||||||
Db  3480  CTTGTACTTCCGGTGTGCCAGGCTGAGTCCTTGTCATCAGATCCGACGGGCCCCTATGCCCATG  3539

Qy  3580  GCTTGAGCAAGGGGACAAGGTTGAGCTGGAGGTTCTCTGAGTTCCCGTG
          ||||||||||||||||||||||||||||||
Db  3540  GCTTGAGCAAGGGGACAAGGTGGAGCTGGAGGTCCCTGAGTTCCCGTG  3599

Qy  3640  GTTCGTCTGGTTCACCGGTCCTTCTTGCGCACAACGTCACGCACCAGTCAAGGTAAGCGTCGTGCAG
          |||||||| ||||| |||||||| ||||||| ||||||
Db  3600  GCTCGTCTGGTTCACCGGTCCTTATGTGACGAGGGGCACGCAGTCAAGGTAAGCGTCGTGTCTG  3659

Qy  3700  TGCTTCCACTCTGGCGGCCAAGGTCTTGATCTTGAAATCCTGCGGCGGCAGTTCACTAGGCCGTCAAGTAC
          |||||||| |||| || | | ||||||||||||| |||||
Db  3660  TGCTTCCACTCCGGTGTTACTTGGCACAAGGTCTTAGTCTTGAACCGTTCATGTGCCACTGTCGCGGGCCAAGTGC  3719

Qy  3760  CAACAGATGCCAAGACTACCACAGAACCCCTCGGGCGGGAAAAAGGAGTTTTCAAGG
          ||||||||||||||||||||||||||||
Db  3720  CAACAGATGCCAAAACCACCACCACCGAACCCCTCGAACCCTCCGGGCGGGAAAGGAGTTTTCAAAG  3779

Qy  3820  AGGCCCCGTGTTTATGCCTACGGGGCCTGGGAAAGAGCACCCGCGTACCCGCGTCGCGTCCGTGTCAG
          ||||||||||||| ||| ||||||||||||||||||||||
Db  3780  AGGCCCCGTGTTTATGCCTCACGGGGCGGGAAAGAGCACTCGCGTCCCGTTGGAGTACG  3839

Qy  3880  GCAACATGGGCGCCACAAGGTCTTGATCTTGAACCGTGTAGCTTACGGCCCTCGAGGGCCATGG
          |||||||||||||| |||||||| |||||| |||| |||||||||
Db  3840  GCAACATGGGCGGCACAAGGTCTTAGTCTTGAACCGTCCAGTTCACTGTCGCGGGGCCATGG  3899

Qy  3940  GCCCATACACGAGCGGCTGCGCCCCAGTATTTACTTGTGGCCATGACACCA
          ||||| ||||||||||||||| |||||||||||||||||||||||
Db  3900  CCCCGTACACGAGCGGCTGCGCCCCGGGTAAACATCCAAGTATATATACTGTGGGCATGATACAA  3959

Qy  4000  CTGCTTTCACAAGGATCACTGACTCCCCCCTGACGTATTCCACTTACGGAAGGTTTTTGG
          ||||||||||||||||||||| || ||||||||
Db  3960  CTGCTTTCACAAGGATCACTGACTCCCCCCTGACGTATTCAACCTATGGGAGGTTTTTGG  4019
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Qy  4060  CCAACCCTAGGCAGCAGATGCTGAGGGGTGTGTCGGTGTCATTTGTGCAGAGTGCCACAGTC
          |||||||||||||||||||||||| ||||||| |||||||||||||||||
Db  4020  CCAACCCTAGGCAGCAGATGCTACGGGGCGTTTCGGTGGTCATTTGTGATGAGTGCCACAGTT  4079

Qy  4120  ATGACTCAACTGTGTTGTGGGCATTGGGCGTGTCAGGGAGCTGGCGCGGAGGATGTGGAG
          ||||||||||||||||||||||| ||||||||||||||| ||||||||||||
Db  4080  ATGACTCAACCGTGCTGTGTTAGGCATTGGGAGTGTCAGGGAGCTGGCAGCTGGCGCGGAG  4139

Qy  4180  TGCAATTGGTGCTCTACGCCACTGCCACCCTCCCGGATCCCCGATGACCCAGCACCCAT
          ||||||| |||||||| ||||||||||||| |||||||||||||||||
Db  4140  TGCAACTAGTGCTCTACGCCACCGCCACCGTCCGGATCCCCGATCCCCGGTCCCCTATGACGCAGCACCCTT  4199

Qy  4240  CAATCATTGAGACAAAACTGGACGTGGGAGAGATCCCCTTCATGGGCATGCGCATACCTC
          | ||||||| |||||||||||| || |||||||||
Db  4200  CCATAATTGAGACAAAATTGGACGTGGGCGAGATTCCCTTTTATGGGCACGGAATACCCC  4259

Qy  4300  TTGAGCGGATGGGACCGGAAGGCATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGC
          | ||||||||||| |||||||||||| |||||||| ||||||| ||||| ||||||
Db  4260  TCGAGCGGATGCGAACCGGAAGGCACCTCGTGTGTCCATTCTCTAAGGCTCTAAGGTGCGAGC  4319

Qy  4360  GCCTGGCGGCCAGTTTTCGGCTAGGGGGTAAATGCCATTCGCCTATTACAGGGGAAAG
          ||||||||||||||||| |||||||||||||||| |||| ||||||||
Db  4320  GCCTTGCTGGCCAGTTCTCCGGCTAGGGGGTCAATGCCATTGCCTATTATAGGGGTAAAG  4379

Qy  4420  ACAGTTCTATCATCAAAGATGAGACGTGGTGGTGTGCTACAGACGCCACTATCCACTG
          | ||||||||||| |||||| |||||||| ||||| ||| |||||
Db  4380  ACAGTTCTATCATCAAGGATGGCTGGTCGGTGTCTGTGCCACAGACGCGCTTCCACTG  4439

Qy  4480  GGTACACTGGGAACTTCGTCTCACCGATTCGTGGGTTAGTGGTGGAGGTCGTCG
          |||||||||| ||||||||| |||||||||||||||||||||||
Db  4440  GGTACACTGGGGTGAAATTTCGACTGTGGTGGAATTAGTGGTGGGTGGAGGTCGTTG  4499

Qy  4540  AGGTGACCCTTGATCCCACCATTACCATTCCTCCCTGCGCACGTGCCCCGCGTGCGGTGGCTGAAC
          ||||||||||||||||||||||| |||||||| |||||||||||||||||||
Db  4500  AGGTGACCCTTGATCCCATCCTACCATTACCATCTCCCTGCGACAGTGCCCTGCGCCTGCGGTGGCTGAAC  4559

Qy  4600  TGTCGATGCAGGCGGAGTCCGTTGTTGTGGAGTCTTGCGGCGCTACTACCGCGG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4560  TGTCGATGCAGACGAGGACGAGGACGCACGGGGTAGGGGCAGGGTCTCGACGCTACTACCGCGG  4619

Qy  4660  GGGTCGGCAAGGCCCTGCGCGTGTGGTGCGGCTCAGGTCTCGACTTCCGTG
          | |||||||||||||| |||||||||||||||||||||||||||||||||||
Db  4620  GGGTGGGCAAGGCCCCTCGCGGTGTGGTGCGCCTCAGGTCCTGTCAGGTGCGGTGGAAG  4679

Qy  4720  CCGGTGTGACCTGGTACGGAAGTCGCTGACCAGCAGCAAAACCTACTGAGACTTTACG
          ||| ||||||||||||| ||||||||||||| ||||||||||
Db  4680  CTGGGAGTGACCTGGTACGGGAGGTCGCTGACCTGCAGCTAACCTACTGAGACTTTACG  4739

Qy  4780  ACAACTGCCCTTACACCGCGTTGCAGCTGTCGCACATTGGGGAGCCCGGCGTGGTTGTTTT
          ||||||||||||||| ||||||||||||||||||||||||||||||||
Db  4740  ACGACTGTCCTTACACCGCGTTGCGGCTGTGATATCGGAGAAGCCCGGCGGTGGTTGTTCTCT  4799

Qy  4840  CGGGGCTTGCCCCGTTGAGGATGCATCCCGATGTTAGCTGGCAAAAGTTCGCGGCGTGGAAG
          | ||||||||||||| ||| ||||||| ||||||| ||||||||||||||||
Db  4800  CTGGGCTCGCCCCGTTGAGGATGCATCCCGATGTCAGCTGGCAAAAGTTCGGCGGCGTCA  4859

Qy  4900  ACTTGCCCTTCCTGGGTGGTTGTTCAGCGGACCCATGTGCCGGGGGAAAACACTGTCTCCCGGCC
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  4860  ACTGGCCCCCTTCCTGGGTGGTTGTTCAGCGGACCCATGTGCCGGGGGAAAACACTGTCTCCCGGCC  4919

Qy  4960  CATCGGATGACCCCCAGTGGCCCCGAATCCTGTCCCACTCCTGCTGA
          |||||||||||||||||||||||||||||||||||||||||
Db  4920  CATCGGATGACCCCCATGGGCCCCCAAATCCTGTCCCACTCCTGCTGA  4979

Qy  5020  GGTGGGGCAATGATTTACCATCTAAAGTGGCCGGCCATCACATCGTGGACGACCTGGTCC
          |||||||||||| |||||||||||||||||||| ||||| ||||||||||||
Db  4980  GGTGGGGCAATGATTACCATCTAAAGTGGCCGGCCACCACATAGTGACGACCTGGTCA  5039

Qy  5080  GTAGGCTCGGGTCGGTGGCGGAGGTTACGGTCACCGGCGGCGGCTGCGGATGCGGTGG
          | ||||||| |||||| |||||||||| |||||||||||||||||||| |||||
Db  5040  GGAGACTCGGGTCGGTGGCGGAGGGTTACGCCGGCGGGCTGCGGATCTTGATGATCG  5099
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This page contains a two-column nucleotide sequence alignment between a query sequence (Qy) and database sequence (Db), with position coordinates labeled at the left and right of each alignment block.

Left column position coordinates (Qy / Db):
5140 / 5100, 5200 / 5160, 5260 / 5220, 5320 / 5280, 5380 / 5340, 5440 / 5400, 5500 / 5460, 5560 / 5520, 5620 / 5580, 5680 / 5640, 5740 / 5700, 5800 / 5760, 5860 / 5820, 5920 / 5880, 5980 / 5940, 6040 / 6000, 6100 / 6060, 6160 / 6120

Right column position coordinates (Qy / Db):
6220 / 6180, 6280 / 6240, 6340 / 6300, 6400 / 6360, 6460 / 6420, 6520 / 6480, 6580 / 6540, 6640 / 6600, 6700 / 6660, 6760 / 6720, 6820 / 6780, 6880 / 6840, 6940 / 6900, 7000 / 6960, 7060 / 7020, 7120 / 7080, 7180 / 7140, 7240 / 7200, 7300 / 7260, 7359

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Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     7260 GCACCCGCTTGAATTGCAGGTTGGGTGCTTGGTGGCAATGAACTTACCTTTGAATGTG        7319

Qy   7360 ACAAGTGTGAGGCTAGGCAAGAGACCTTGGCTTCCTTCTCTTACATTTGGTCTGGGGTGC        7419
          ||||||||||||| ||||||| | ||||||||| |||||| ||||||||| || ||||
Db   7320 ACAAGTGTGAGGCTAGGCAAGAAACCTGGGCTCCTTCTCCTTACAATTGGTCTGGGAGTGC        7379

Qy   7420 CACTGACGAGGGCCACTCCAGGCCAAGCCCCTGTGGTGAGGCGGTTGGCTTCCTTGCTGG        7479
          |||||||| | |||||||| |||||||||||| | |||||||||||||||||||||||||
Db   7380 CGCTGACTAGGGCCACCGCCGCCAAGCCTCCCGTGTGAGGCGGTTGGCTCTTTATTAG        7439

Qy   7480 TGGCCGACACCAAGGTGTATGTCACCAACCGGACAAGTGTGGGAGAGAGTTGACA        7539
          ||||| ||||||||| ||||| ||||| || |||| || ||
Db   7440 TGGCCGACACTACTAAGGTGTATGTTACCAATGCAGACAATGTGGGACGGAGGGTGGACA        7499

Qy   7540 AGGTTACCTTCTGGCGTGCCCCTAGGGTTCATGACAAATTCCTCGTGGACTCCATAGAGC        7599
          |||||||||| || || ||||| |||||||||| ||||| |||| ||||| ||||||||
Db   7500 AGGTGACCTTCTGGCGTGCTCCTAGGGTTCATGATAAGTACCTCCGTGGACTCCTATTGAGC        7559

Qy   7600 GGCTAAGAGAGGCAGTCAAGCCTGCCTAAGCCTGCCATGGCTTACACTTATGAGGAGCAATAA        7659
          |||||||||||||||||||||||||||| || ||||| |||||| |||||||||||||||
Db   7560 GGCGTAAGAGAGGCCGCTCAAGCCTGCCTAAGCCTGCCATGGGTTACACTTATGAGGAGCAATAA        7619

Qy   7660 GGACTGTAAGGCCACATGCTGCCATGGGCTGGGGATCTAAGGTGTCGGTCAAGGACCTCG        7719
          |||||||||||||||||| |||||| ||||||||||||||||||||| ||||||||||
Db   7620 GGACTGTAAGGCCACATGCTGCCATGGGCTGGGGATCTAAGGTGTCGGTTAAGGACTTAG        7679

Qy   7720 CCACCCCTGCGGGGAAGAGATGGCGTGTCCATGACCGGCTCCAGGAGATACTTGAAGGGACGC        7779
          || |||||||||||||| |||||||| |||||||||||||||||||||||||||||||||
Db   7680 CCACCCCCGCGGGGAAGAGATGGCGTGTCCATGACCGGCTCCAGGAGATACTTGAAGGGACTC        7739

Qy   7780 CAGTCCCCTTTACTCTTACTGTGAAAAAGGAAGTGTTCTTCAAAGACCGAAAGGAAGAGA        7839
          | ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   7740 CGGTCCCCTTTACTCTGTGTGTGTAAAAAGGAGTGTTCTTCAAAGACCGGAAGGAGGAGG        7799

Qy   7840 AGGCCCCCCGCTCATTGTTCCCCCCTGGACTTCCGGATAGCTGAAAAGCTTATTC        7899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7800 AGGCCCCCCGCTCATTGTTCCCCCCTGGACTTCCGGATAGCTGAAAAGCTCATCT        7859

Qy   7900 TGGGAGACCCTGGACGGGTAGCCAAGGCGGTGTTGGGGGCCTACGCCTTCCAGTACA        7959
          ||||||||||| | |||||||||||||| ||||| ||||||||||||||||||||||
Db   7860 TGGGAGACCCCGCAGCCAAGGCGGTGTTGGGGGCCTACGCCTTCCAGTACA        7919

Qy   7960 CCCAAATCAGCGAATTAGGGAGATGCTCAAACTGTGGAATCAAAGAAGACACCATAGCG        8019
          |||||||||||||||| || || |||| |||||||||||| |||||||||||| ||||||
Db   7920 CCCAAATCAGCGAGTTAAGGAGATGCTCAAGCTCTAAGAGAGAACCCCCTTGCG        7979

Qy   8020 CCATCTGTGTGACGCGCCACATGCTTCGACAGTAGCATAACTGAAGAGGACGTGGCGCTGG        8079
          ||||||||||||||||||||||| | ||| ||||||||||||||||||||| ||
Db   7980 CCATCTGTGTGACGCGCCACCTGCTTGGACAGTAGCATAACTGAAGAGGACGTGGCTTTGG        8039

Qy   8080 AGACAGAGCTTTATGCCCTGGCTTCAGACAATCCAGAATGGTGCGCCTGCCCTGGGAAAT        8139
          |||||||||||| || ||||||||||| || |||||||||||||||||||||||||||
Db   8040 AGACAGCGTGTACGCGTCTGGCCTCTGGCCCTCTGACCATCCAGAATGGTGCGCCCACTTGGGAAAT        8099

Qy   8140 ACTATGCCTCTGCAACAATGTCGTAACCCCCGAGGGGTGCCAGTGGGTGGAGGTATTGTA        8199
          |||||||||||| || || |||| || || |||||||||||| ||||| ||||||||
Db   8100 ACTATGCCTCAGGCAGCACCATGTCAAGCACCCGAGGGGTGCCAGTGGGTGGAGGTATTGCA        8159

Qy   8200 GATCCTCAGGGGTGTGACGCGCCAGTGCACACCAAACCTTGCTTGACTTGCTATATCAAGGTGA        8259
          ||||||||||||| ||| |||| |||||||||||| || ||||||||||||||||||||
Db   8160 GATCCTCGGGGTGTCCTTAACACTAGCCGCGAGCCAAACTGCTTTGACCTGCTTCTACACTGTAAGGTGA        8219

Qy   8260 AAGCCGCCTGTGAGAGGTGGGGCTGAAAAATGTCTCGCCTCCATCGCTGCGATGACT        8319
          |||||||||||||||||||||| || |||| ||||||||||| ||||||||||||||
Db   8220 AAGCCGCCGTGTGAGAGGTGGGGCTGAAGATGTCTTCTCAGTCTCCATAGCCGGCGATGACT        8279

Qy   8320 GTTTGATCATATGCGAACGACGTGGGCGATCCTAGCCGACGCTTTGGGCAGAGAGCCCTGG        8379
          | |||||||||| ||||||||||| | |||||||||||||| ||||||||| ||||||||
Db   8280 GCTTTGATCATATGAGCTGAGCGGACGACCCTAGCCGACGCTTTGGGCAGAGAGCCCTAG        8339

Qy   8380 CGAGCTACGGGTACGCATGCGAGCCTTCGTATCATCACTGACACCGCCCCCTTCT        8439
          |||||||| |||||||| ||||||| ||||||||||||||||
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Db   8340 CGAGCTATGGGTACGCTGCGGAGCCCTCATATCATGCATCCTTGGACACGGCCCCCTTCT        8399

Qy   8440 GCTCCACTTGGCTAGCTGAGTGCAATGCAGATGGAAACGCCATTTCTTCCTGACCACGG        8499
          |||||||||||| ||||| ||||||||||| |||| ||||| |||||||||||||||||
Db   8400 GGTCCACTTGGCTTGCTGAGTGCAATGCAGATGGAGCGGCCATTTCTTCCTGACCACGG        8459

Qy   8500 ACTTTCGGAGCCCCTCGCTCGCCATGTCGAGCGAGTACAGTGCAGTACAGTAGTGCTTCGCGCCA        8559
          ||| |||||||||||| |||||| |||||| ||||| || ||||| |||||||||| ||||| |
Db   8460 ACTTCCGGAGGCCGTCGCTCGCCATGTCGAGCGAGTACAGTAGTAGTGACCCGATGGCTTCGGCGA        8519

Qy   8560 TCGGTTACATCCTCTCTATACCCTTGGCATCCTATCACACGGTGGGTCATCATCCCTCACG        8619
          |||||||| ||| |||||| | ||||| ||||||||||||||||||||||||||||
Db   8520 TCGGTTACATCCTCCTTTATCCTTGGCACCCCATCACACGGTGGGTCATCATCCCTCATG        8579

Qy   8620 TGCTCACCTGCGCGTTAGGGGTGGTGGCACACCGTCTGTGTGGTGCCAGTGAC        8679
          || |||||||||||| |||| |||| ||||||||||| | ||||| |||||||||
Db   8580 TGCTAACGTGCGCATTCAGGGGTGAGGCACACCGTTGGTCCAGGTTGGTACCAGTGTAC        8639

Qy   8680 ATGGTAATTACTACAAGTTCCACTGGACAAACTGCCTCAACATCATCGTGGCCCTCCACG        8739
          ||||| ||||||| || ||||| |||||| |||||| ||||||| || |||||||||||
Db   8640 ATGGTAACTACTACAAGTTCCACTGGACAAACTGCCTCAACATCATCGTGGCCCTCCACG        8699

Qy   8740 GACCAGCAGCGTTGAGGGTTACCGCAGACACAACTAAGCACAAAAATGGAGGCGTGGCAAGG        8799
          |||||||||| ||||| ||||| ||||||||||| || |||| |||||||||||||
Db   8700 GACCAGCAGCGTTGAGGGTTACCGCAGACACAACTAAAACAAGATGGAGGCGTGGTAAGG        8759

Qy   8800 TGCTGAGCGACCTCAAGCTCCCTGGCCTTGCGGCCGCGTGTTGCGTGTTGTGGCCTC        8859
          || ||||||||| |||||||||| || |||||||||||| || ||||||||||||
Db   8760 TTCTGACCGACTTCAAGCTCCCTGGCTTTAGCAGTCACCCCTTAGCAGTCCGCCGTTGC        8819

Qy   8860 GAACGCGTATGCTCCGGTCGGTTGGCTAGGTTGGCTGTTGCGTGTTGTGGCCTC        8919
          ||||||||| | |||||| ||||||||||||||| ||||||||||||| |||||
Db   8820 GAACACCGTGTCTCCGGTCCGCGTGGGTTGGCTGTTGCGTGTTGTGGCATC        8879

Qy   8920 CAGGCCTTGCGGCTTCCCCCTCCGGAGATTGCTTGGTATCCCCGGGGGGTTTCCCCCTTTCCC        8979
          |||||||||| |||| ||||||||||||||| |||| | ||||| ||||||||||||||||
Db   8880 CAGGCCTACGGCGTTCCTCTCCCGGAGATTGCTGCGTATCCCGGGGGGGTTTCCCTCTCTCCC        8939

Qy   8980 CCCCTATATGGGGTTCATCAATTGGATTTACAACCAATTGAATTTACATCATCTGTT        9039
          |||| ||||||||||||||| |||||||| |||| ||||||||||||||||||||||
Db   8940 CCCCTATATGGGGTTCTTGGTATACAACCAATTGGATTTTACATCATCTGTT        8999

Qy   9040 GGTTGGGGTTCTTTAGCCGTGCCCTTCGTCATCGTGAACTAAATTCATCTGTT        9099
          |||||||||||||||||| ||||| ||||||||||| ||||||||||||||||
Db   9000 GGTTGGGGTTCTTTAAAGCCGTGCCCTTCGTCATCGTGAACTAAATTCATCTTTA        9059

Qy   9100 GCGGCAAGGTCCGGTGACTGATCATCACTGCCCCCCAGGG        9159
          |||||||||||| |||||||||||| || ||||||||||||
Db   9060 GCGGCGGAGGTCGGTGACTCGTGACTGATCGTCACCGGAGGAGTTCCCGCCTCCGCCCCAGGG        9119

Qy   9160 GTCTCCCCGGCTGGGTAAAAAGGCCGCCTGCCCTGGGCACTTCGGAACTGGTTACTAACCCCCTG        9219
          ||| ||||||||||||| |||||||||||||||||||||||| || |||||||| ||||||||
Db   9120 GTCTCCCCGCTGGGTAAAAAGGGCCATGCCCTGGGCACTTGGTTACTAACCCCCTG        9179

Qy   9220 GCAGGGTCAAAGCCTGATGGTGCTAATGCACTTCGGTGTGCGCCACTTACCTTA        9279
          || |||||| |||||||||||| || |||||||||||| || ||||||||||||
Db   9180 GCAGGGTTAAAGCCTGATGGTGCTAATGCACTTCGGTGTGCGCCTTCGGCTCGCTACCTTA        9239

Qy   9280 TAGCGTAATCCGTGACTACGGCGCTCGCGAGAGCCCTTCGCGAGGCACCAGTGCAC        9339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9240 TAGCGTAATCCGTGACTACGGCGCTCGCGAGAGCCCTTCGCGAGGCACAGTGCAC        9299

Qy   9340 TGTGATCTTGAAGGGTGCACCCGGTAA        9367
          || |||||||||||||||||| | ||
Db   9300 TGAGATCTATATGAAGGGTGCACCCCGGAA        9327
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RESULT 12
AAX16505
ID   AAX16505 standard; cDNA; 9327 BP.
XX
AC   AAX16505;
XX

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DT   22-JUL-1999  (first entry)
XX
DE   Polynucleotide sequence of HGV clone 3Z-HGV94-6.
XX
KW   Hepatitis G virus; HGV; HGV-E2 antigen; vaccine; viral replication;
KW   treatment; HGV infection; antisense; ds.
XX
OS   Hepatitis G virus.
XX
PN   US5874563-A.
XX
PD   23-FEB-1999.
XX
PF   05-JUN-1995;   95US-0485910.
XX
PR   19-MAY-1995;   95US-0444733.
PR   20-MAY-1994;   94US-0246985.
PR   03-AUG-1994;   94US-0285543.
PR   03-AUG-1994;   94US-0285558.
PR   26-OCT-1994;   94US-0329729.
PR   23-NOV-1994;   94US-0344271.
PR   16-DEC-1994;   94US-0357509.
PR   15-FEB-1995;   95US-0389886.
PR   05-JUN-1995;   95US-0485910.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fry KE,  Kim JP,  Linnen JM,  Wages J,  Young LM;
XX
DR   WPI; 1999-180067/15.
XX
PT   Isolated polynucleotide sequences derived from the Hepatitis G Virus
PT   that encode the E2 antigen - useful for producing vaccines and
PT   inhibitors against Hepatitis G, and for assays to detect the virus
PT   in a sample
XX
PS   Example 18; Column 337-344; 206pp; English.
XX
CC   The specification describes isolated polynucleotide sequences, derived
CC   from a Non-A, Non-B, Non-C, Non-D, Non-E (N-(ABCDE) Hepatitis virus
CC   (designated Hepatitis G or HGV). HGV is characterised by stimulating
CC   production of serum alanine aminotransferase in primates infected with
CC   the virus, being serologically distinct from the Hepatitis A, B, C, D
CC   and E viruses, and being a member of the Flaviviridae virus family.
CC   The HGV-E2 antigens, encoded by the polynucleotide sequences of the
CC   invention, may be produced by standard recombinant DNA techniques,
CC   and used in the preparation of vaccines. Anti-sense oligonucleotides
CC   (and oligonucleotide analogues which encode portions of the sequences
CC   disclosed in the specification) may be used to prevent expression of
CC   the HGV-E2 genes by blocking transcription and preventing them
CC   functioning normally in viral replication. Antisense sequences may be
CC   used in this way as part of a treatment strategy against HGV infection.
CC   The single stranded nature of the viral genome makes HGV highly
CC   susceptible to inhibition in this way. The present sequence represents
CC   the polynucleotide sequence of HGV clone 3Z-HGV94-6.
XX
SQ   Sequence 9327 BP; 1682 A; 2532 C; 2984 G; 2129 T; 0 other;

Query Match        83.9%;   Score 7885.6;   DB 20;   Length 9327;
Best Local Similarity   90.4%;   Pred. No. 0;
Matches 8433;  Conservative   0;  Mismatches  894;  Indels   1;  Gaps   1;
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Qy    40 GCAAGCCCCATAAACCGACGCCTATCTAAGTAGACGCAATGACTCGGCCGACTCGGCCG    99
         ||||||||||| ||||||||||||||||||||||||| ||||||||||||||||||||||
Db     1 GCAAGCCCCAGAAACCGACGCCTATCTAAGTAGACGCCAATGACTCGGCCGACTCGGCCG    60

Qy   100 ACCGGCCAAAAGTGGTGGATGGTGACAGGGTTGGTAGGTCGTAAATCCCGGTCAT   159
         |||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db    61 ACCGGCCAAAAGTGGTGGATGGTGATGACACAGGGTCGGTAGGTCGTAAATCCCGGTCAC   120

Qy   160 CCTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTCAAGACTCCTCTTGTGCCGGCG   219
         | |||||||||||||||||||||||||||||||||| |||| ||||||||||||||||
Db   121 CTTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTTAAGATTCCTCTTGTGCCTGCCGGC   180
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Qy   220 GAGACCGCCACGTGCCACAGTGCTGGCCTACCGTGTGAATAAGGGCCCGACGTCAG   279
         |||||||||||||||||||||| ||||||||||||||  ||||||||||||||||
Db   181 GAGACCGCCACGTGCCACAGTGTTGGCCTACCGTGTGGGAATAAGGGCCCGACGTCAG   240

Qy   280 GCTCGTCGTTAAACCGAGCCGTCACCCACCTGGGCAAACGACGCCCACGTACGGTCCAC   339
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCTCGTCGTTAAACCGAGCCGTCACCCACCTGGGCAAACGACGCCCACGTACGGTCCAC   300

Qy   340 GTCGGCCCTCAATGTCTCTCTTGACCAATAGTTTATCCGGCGAGTTGACAAGGACCAGT   399
         ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||
Db   301 GTCGGCCCTCAATGTCTCTCTTGACCAATAGGCGTAGCCGGCGAGTTGACAAGGACCAGT   360

Qy   400 GGGGGCCGGGGGTTATGGGAAGGAGACCCAAACCTGCCCTTCCCGTGGCCGGGAAAT   459
         ||||||||||||| |||  | |||||||| ||||| |||||||||||||||||||||
Db   361 GGGGGCCGGGGGGCT-TGGAGAGGGACTCCCAAGTCCCGCCCTTCCCGTGGCCGGGAAAT   419

Qy   460 GCATGGGGCCACCAGCTCCGCGGCGGCCTGCAGCCGGGTAGCCCAAGAATCCTTCGGG   519
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 GCATGGGGCCACCAGCTCCGCGGCGGCCTGCAGCCGGGTAGCCCAAGAATCCTTCGGG   479

Qy   520 TGAGGGCGGGTGGCATTCTCTTTCTATACCATCATGGGAGTCCTTCTGCTCCTCTCG   579
         |||||||||||||||||| |||||||||||||||||||  ||||||||||||||||
Db   480 TGAGGGCGGGTGGCATTTCCTTTTCTATACCATCATGGCCAGTCCTTCTGCTCCTCTCG   539

Qy   580 TGGTTGAGGCCGGGGCCATTCTGGCCCCCGGCCACCCACGCTTGTCGAGGCGAATGGGCAAT   639
         ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540 TGGTTGAGGCCGGGGCCATTCTGGCCCCCGGCCACCCACGCTTGTCGAGGCGAATGGGCAAT   599

Qy   640 ATTTCCTCACAAATTGCTGTGCCCGGAGACATCGGTTCTGCCTGGAAGGCCGGATGCC   699
         ||||||||||||||| |||||||| |||||||||||||||||||||   ||| ||||
Db   600 ATTTCCTCACAAATTGTTGTGCCCCGGAGACATCGGTTCTGCCTGGAGGGTGGATGCC   659

Qy   700 TGGTGGCCCTGGGGTGCACGGTTGCACCGACGGTTGCTGCCACTGTATCAGGCGGGTT   759
         ||||||||||||||||||||  ||| ||  |||||||||||||||||||||||||||
Db   660 TGGTGGCCCTGGGGTGCACGATTGCACTGACCAATGCTGCCACTGTATCAGGCGGGTT   719

Qy   760 TGGCTGTGCGGCCTGGCAAGTCCCGCGCCCAGCTCGTTGGGGAACTGGGAGGCCTGTACG   819
         ||||||||||||||||||||||||||||||  ||  |||||| |||||| ||||| |||
Db   720 TGGCTGTGCGGCCTGGCAAGTCCCGCGCCCCAACTGTGGGGAGCTGGGTAGCCTATACG   779

Qy   820 GGCCCTGTCGCTCGGCTTACGTAGCCCGGGATCCGGATCCTGGGCGTCGGCGAGGTTACTCCG   879
         |||| ||||| |||| |||| |  ||| |||||| ||| ||| |||| |||| ||| ||||| |
Db   780 GGCCCCGTCGTCGGCCTATGTGGATCCTGGGATCCTGGGTGGTGAGGTGTACTCGG   839

Qy   880 GGGTCCTGACAGTTGGTGTGTCGTTGAGGCGCCGGGTCTACCTGATGCCCAACCTGAAGT   939
         | |||||| || |||| ||| |||||| ||| | |||  ||| ||||| ||||||| |||
Db   840 GTGTCCTACGTGGGAGTCGCCGTTGACGCGCGTCACCCGGTGCCTAACCTGACGT   899

Qy   940 GTGCAGTAGAAATGGACGTTAAGTGGGAGAGTGAGTTTTGGAGATGGACTGAGCAGTTGG   999
         ||||||| |  |||||  | ||||||| ||||||||||| |||||||||||| |||||||
Db   900 GTGCAGTGCGTGTGAGTTAAAGTGGAAAGTGAGTTTTGAGATGGACTGAACAGCTGG   959

Qy  1000 CCTCCAATTACTACTGGATTTGAATACCTTTGGAAATACCTCTGGAAGTCCCATTGCTTT   1059
         |||||| |||| |||||||  ||| |||| |||||||||||||||||||||| ||||||
Db   960 CCTCCAACTACTGGATTCTGGAAATACCTCTGGAAGTCCCCATTGCTTT   1019

Qy  1060 TGATGAGCCTGACCCCCTCTGTTGGTTGGTCGCCCCCATTGCTTGCTTTGCTCTGGAGCAACGGA   1119
         |||| |||||||| | ||||||||||||| |||||||||||||||||| ||||||||||||||
Db  1020 TGATAAGCCTGACCCCCTTGTTGGTTGGTCGCCCCCATTGCTTGCTTGCTCTGGAGCAACGGGG   1079

Qy  1120 TTGTCATGGTTTTCCTGCTGGTGACGATGGCGGGGATGTTGCAAGGCGCCCCGCCTCCG   1179
         ||||||||| ||||||  |||||||||||||| |||||| |||||||||||||||||||
Db  1080 TTGTCATGGTCTTCCTGTTGGTGACGATGGCGCCGGGATGTCGCAAGGCGCCCCGCCTCCG   1139

Qy  1180 TTTTGGGGTCCGGCCCCTTTGACTACGGTTGAAGTGGCAGTCATGCCTCCCAGGCTA   1239
         |||||||||| | ||||||||||  |  |||||| |||||| || |||||||||| |
Db  1140 TTTTGGGGTCACGCCCCCTTTGACTTGGCCGGTTGACTTGGCAGACCTGCTCTTGCAGGGCCA   1199

Qy  1240 ACGGTCGCGTATTCCCACTGGGGAGAGAGGGTGTGGGATCGAGGGAATGTCACGCTCTTGT   1299
         |||| ||||| |||   ||||||||| |||||||||| ||| ||||| ||  ||| |||| |
Db  1200 ACGGTTCGCGTTTTCGACTGGGGAGAAGGTGTGGGACCGTGGGAACGTTACGCGTTACGTCAGT   1259
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Qy    1300  GTGACTGCCCAACGGCCCCTGGGTTGGGTCCCGCCTTTGCCAGGCCGGTTGGGTGGG  1359
            ||||||||||| ||||||||||  ||| ||| ||||||||||||| || ||| |||
Db    1260  GTGACTGCCCTAACCCCTGGGTGTGGTGTCGGGTGCCAGCCGTTTGCCAAGCAATCGGCTGGG  1319

Qy    1360  GCGACCCCATCACCCATTGAGACCACGACAAAACCAGTGCCCCTATCATGCCCCCAAT  1419
            ||||||||||||||| |||||||||||||| ||||||||| |||||||||||||||||
Db    1320  GTGACCCCATCACTTATTGGAGACCACGGCACGGGCAAAATCAGTGCCCTTCATGCCCCCAGT  1379

Qy    1420  ATGCTATGGGTCGTGTCCGTAACGTGCCTGTCGTGTGGTTCCGGTTCCGTGTTGCCTCGA  1479
            ||||||||||||||||| ||| || |||||||| ||||| |||| ||| |||||||||||
Db    1380  ATGTCTATGGGTCTGCTACAGTCACTTGCCGTGTGGGTTCTTCTTGTATGCCTCCA  1439

Qy    1480  CCGGCGGTCGTGATTCGAAGATCGATGTGTGGAGTTGGTGCCGGTTGGATCTGCCAGCT  1539
            || |  |||||| || ||||||||| |||| |||||| ||||| ||| ||| |||||||
Db    1440  CCAGTTGGTCGCGCGACTCGGACAGTGTGGCGAGTTGGCCAGTTGCCTCTGCCCACCT  1499

Qy    1540  GCACCATAGCCGCTCTAGGGTCATCGGATGCGACACGGTGGTTGAGCTCTCCGAGTGGG  1599
            ||||||||||||||||||||||||||| ||||  || |||||||||||||||||||||||
Db    1500  GCACCATAGCCGCCACTTGGATCATCGGATCGCGACACGGTGCCTGGGCTCTCCGAGTGGG  1559

Qy    1600  GAGTCCCGTAACGTGTATTCTGAAGCTGTCCGCCTCGGCCTCATGTGCGACCTTGTGTGC  1659
            |||||||| |||||||||   |||||||||||||||||||| |||||||||||||||||||
Db    1560  GAATCCCGTGACGTGTGTTCTTGGAGCTGTCCGCCTTCATGCGGCCACCTTGTGTGA  1619

Qy    1660  GGGACTGCTGGCCCGAAACCGGTCGGTTAGATTCCCTTTCATCGGTGCGCACGGGGC  1719
            ||||||||||||||||||  |||||||||||||||| ||| ||||||||||||||||
Db    1620  GGGACTGCTGGCCCCGAGACCGGTCGGTTAGGTTCCATTCCATCGGTGCGCGGGGGC  1679

Qy    1720  CTCGGCTGACAAAAGGACTTGGAAGCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCA  1779
            |||||||||||||| |||||| ||  | | |||||||||||||| |||||||||||||||||
Db    1680  CTCGGCTGACAAAGGGCTTGGAAGCTGTGCCCTTCGTCAATAGGACAACTCCCTTCACCA  1739

Qy    1780  TAAGGGCCCCCTGGGCAACCAGGGAGAGGCAACCCGGTGCGGTGCGCCCCCTGGGTTTTG  1839
            | |||||||||| ||||||||||| |||| |||||||||||| ||||  ||||||||| ||
Db    1740  TTAGGGGAGGTGGCAACCAGGGCCGAGGCAACCCGGTGCGGTGCGCCTGGGGCCTTGGGTTTTG  1799

Qy    1840  GGTCCTACACCATGACCAAGAGATCCGGGATTCCCTGCATTTGGTGAAATGTCCCACACAG  1899
            |||||||||||||||||| |||||||||||||  ||| ||||||||||||| |||||||||
Db    1800  GGTCCTACGCCATGGCCAACAGATAGCCCGAGATCTGGTGAGTGTCCCACACAG  1859

Qy    1900  CCATAGAGCCTCCGACTGGAACGTTCGGTTCTTCCCCGAGTCCGCCATTAACAACT  1959
            ||||| ||||||||||  | ||||||||| || ||||||| ||||||||| ||||||
Db    1860  CCATGAGCCTCCGACTGGAACGTTTGGGTTCTTCCCCGGGACGCGCCGCCTCTCAACAACT  1919

Qy    1960  GCATCGCGCTAGGCACGGAAGTGTCTGAGGCATTGGCCGGAGCTGGCTTACGGGGGGT  2019
            |||| || ||||| ||| |  |||||||||||  ||||| |||||||||||||||||
Db    1920  GCATCGCGTTGGGCACGGAAGTGTCTGAGGCATCGGTCGGAGCTGGCTTACGGGGGGT  1979

Qy    2020  TCTACGGAGCCTCTGGTTCCCAGGTGTTCGGAGCTGATGGAGACGCGGGAAATCCGGTTTGCC  2079
            ||||||||||||||||||| ||  |||||||||| ||||||||||||||||| ||||||||||
Db    1980  TCTATGAACCCCTGTTCCGGTTCGGAGCTGATGGAGACTCGGTTTTGTC  2039

Qy    2080  CGGGTACGGCATGGCGTCCTCGTGGTAGACCTGACGGTTCATCACGCGTCAGGGGCACC  2139
            ||| || |||||| |||||| ||||||||| |||||||| ||||| ||||||||||||||
Db    2040  CGGGTTTGCATGGCGTCCTCTCTTCGGGCGACGAGCTGGTTTATACATGTCCAGGGTCACT  2099

Qy    2140  TGCAGGAGGTGATCGGGGACAACTTCATCCCCTCCGGTTGCTCTTGGATTTTG  2199
            ||||||||||| |||| |||||||||||||||||||||||||||||| |||||
Db    2100  TGCAGGAGGTGATCGGGGACAACTTCATCCCCTCCGGTTGCTCTTGGACTTTG  2159

Qy    2200  TATTTGTCCTGCTCATCTGTATCTGATGAAGCTGATGAAGCTGTCCCGTTCCTGC  2259
            |||| ||||  ||||||||||| ||||||||||||  |||||||||| ||||||||
Db    2160  TATTTGTCCTTTATACCTGTTATCTGATGAAGCTGGTGGGTGTCCCGTGATCTTGC  2219

Qy    2260  TTCTGCTGTGGTGGTGAACCAGTTGGCCCGTTCTAGGACTGGTCGACGCTG  2319
            | ||||||||||||| ||||||||||||||||||||||||| |||||||||
Db    2220  TGCTGCTATGTGGTGGTGAACCAGCTGGCCCTCTAGGGCTGCCGGCTGTGGAAGCCG  2279

Qy    2320  CCGTGCGCGGTGAAGTTTTGCGGCCTTCATGTGTTTGGGCCTTCCCACTG  2379
            ||||||| |||| |||| |||||||||||| |||||||||||||||| |||
Db    2280  CCGTGCGCAGGTGAGGTCTTCGGGGACTCCCGGTCG  2339

Qy    2380  TCAGTATGATACTAGGTCTAGCAAACCTGTGTTGTACTTTCGGTGGATGGGCCCTCAGC  2440
            |||||||||||| ||||||||| |||||||||| ||| ||| || | |||||||||||||
                                                                         (continued)
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Db    2340  TCAGTATGATATTGGGTTGTGTTTGCAACCTGGTTGCTGCTTTTAGATGGTTGGGACCCCAAC  2399

Qy    2440  GCCTCATGTTCCTCGTGTGTTGGGAAGCTCGGCGGGGACGCCCTCTGCTTCTGTGCTTCGATG  2499
            |||| |||||||| ||||||||||||||||||| ||||||| ||||| |||| |||||||||||
Db    2400  GCCTGATGTTCCTCGTGTGTTGGGAAGCTTGCTCGGGGAGCTTGCCCTGGCCCTGA  2459

Qy    2500  TGGGGATTTCGGCGACCCGGCGGGCGACCTGTGCTCGGCGGGCGGCCGAGTTCTGTCTTCGATG  2559
            |||||||||||||||||||||| |||||| ||||||||||||||| |||||| ||| |||||||
Db    2460  TGGGGATTTCGGCGACCCGGCGGGCGACCTCAGTGCTCGGCGGGCCGAGTTCTGCTTCGATG  2519

Qy    2560  TCACATTCGAGGTGGACACTTCGGTTGCCGGTTGGTGCGGTGGTCGGCCAGCCTGGTGGCTTGGG  2619
            |||||||||||||||||||||||||||||| ||||||||||||| ||| |||||| |||||||||
Db    2520  CTACATTCGAGGTGGACACTTCGGTTGGGTGGTTGGTGGCCAATGTGGTAGCTTGGG  2579

Qy    2620  CCATAGCGCTCTGAGCTCAATGAGCCAGGGGGTGGAAGCACAAGGCCGTGATCTATA  2679
            |||| |||||||| ||||||||||||||||||||| ||| ||||| ||||||||||||
Db    2580  CCATTGCGCTCTGATGAGCTGAGCCAGGGGTGGAGGCACAAAGCCGTGATCTATA  2639

Qy    2680  GGACGTTGGTTAAAGGTACCAGGCTGTGCGCCAGAGGGTGGTGCGGCCACTGG  2739
            ||||| |||| ||||| |||||| || ||| ||||| |||| ||||| ||||||
Db    2640  GGACGTTGGTGAAGGGTACCAGGCAATCGTCAAAGGTGTGAGGAGCCCCTCGGGGG  2699

Qy    2740  AGGGGCGTCTACCAAGCTTCTGACGTTCGCCTGGTGCTTGCCGCTTCATACATCTGCCCGG  2799
            ||||||||||||||||||| |||||||||||| ||||| |||||||||||| |||||||||
Db    2700  AGGGGCGGCCTGCCCAAACCCCTGACCTTTGCCCCTGGTGCTTGCCGCTTCATACATCTGCCCAG  2759

Qy    2800  ATGCTGTGATGATGGCGCCCTTGGTCTCCTGGTCTCCCGGCCCTCGTTCCTGGTCGACGCCACTGG  2859
            ||||||||||||||||||||||||| |||||||||| |||||||||||| ||| ||||||| |||
Db    2760  ATGCTGTGATGATGGCGTCCTGGTGTTCGATCATATGGGTCCTTGGCCGTGTGTTTCAAGGAGC  2819

Qy    2860  ACTGGGCCCTGGAGGAGCTCTCCGGGTCTCCCGGCCCTCGTACGGCCACGGGTGG  2919
            || ||||| |||||| |||| ||||||||||||||||||||||| ||| |||||||
Db    2820  ATTGGGCCTTTGGAAGGGAGATCTTTGGTGTCCCGGCCCTCTGAAACCTCTGTCATTCACTGGTGG  2879

Qy    2920  TTGAGTCGTGTGGATGGCGGGGGCGAGAAGGCCACCACCAGCTGGTCTCCAAGATGT  2979
            ||||| |||||||||| ||||||||||||| |||| ||| ||||||||||| ||||||
Db    2880  TTGAGTCGTGTGGATGCGGGGGGTGAGAAGGCCACCACCAGTTTGCCTGGTCTCCAAGGATGT  2939

Qy    2980  GCGCAAGAGGGGGCCTACCTGTTTGACCACATGGGCTCTTCTCGCGCGCTGTCAAGGAGC  3039
            ||| |||||| | ||   |||||||||| ||||||||| |||||||||||| ||||||||
Db    2940  GCGCGGAGAGGAGCGTATTTGTTGGATCATATAGGGTGGCTGGTGTGCTGTCAAGGAGC  2999

Qy    3040  GCTTGTTGGAATGGACGCGGCTTTGGACGCCCTTTGCATTCACTACTAGGACGACGTCGCCA  3099
            ||||| |||||||||| ||||||||||||||| | |||||||||||||||| ||| |||||
Db    3000  GCCTGTTGGAATGGGACGCGGCTCTGTCATCTCGTGTCATTCACTAGGACGACGTCGCA  3059

Qy    3100  TCATCAGAGATCGCCGAGGACCCTGCTCCTGCGACAGTGCGTCATGGGTTTACCCCTGG  3159
            |||| |||||||||||||||||| | ||||| |||| |||||||| |||| |||||||||
Db    3060  TCATCAGGGATGCCCGAGGACACTTGTCCTGCGGATGCCCAATGCCATGGGTTTACCCCTGG  3119

Qy    3160  TAGCACGGCGTCGACTGAATGAGTTCTCATCACGGATGTGAATGCATTTGCCTC  3219
            ||| ||||| | |||| |||| ||||||||| ||||| ||||||||| ||||||||
Db    3120  TTGCGCACGGCTACGTCGTGATGAGTTCTCATCGCGGATGTGAATCATTTGCCTC  3179

Qy    3220  CCGGGTTTGTTCCCGACTGTCATCCCTCCGGTTGCGTTCCTGTGGGGG  3279
            |||||||||||||||| |||| ||||||||||||| ||||||||||||
Db    3180  CCGGGTTTGTTCCCGACTGTCATCCCTCCGGTTGCGTTCCTTTGGGGG  3239

Qy    3280  TCACGAAGGCAGCCTTGACAGGTGGATCCCTTGACTTACATCCGAAGCGTCATGTGT'  3339
            |||| ||||||||||||||||| |||||  |||||||||||| ||||||||||| ||||
Db    3240  TCACAAAGGCTGCCTTGACAGGTCGGATCCTTGACTTACATCCGGAAGCCATCATGTGT  3299

Qy    3340  TGGGGACGGCTACGTGCTAGGACTCGGTGGTGCGCTGGAATGTGCTTGGTCACAACTT  3399
            ||||||||||||||| |||||||| ||||||| ||||| |||||||||||||||||||||
Db    3300  TGGGGACGGCTACGTGCTAGGACTTCTGGAACATGGAACATGCTTGTGTTGCTCGTGTCGTCGTTCACGACCT  3359

Qy    3400  TCCATGGGCCTTCATCATCCCGACCACCCGGGCCCTTAATCCCAGTGGT  3459
            |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    3360  TCCATGGGCTTCATCATCCCGACCACCGGGCCCTTAATCCCAGATGGT  3419

Qy    3460  GGTCAGCCAGTGATGACGTCACGGTGTACCCGTTCCAGATGGGGCAACTTCGTTGCGC  3519
            ||||||| |||||||||||||||||| ||||| |||||||| ||| |||||||||| |||
                                                                       (continued)
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Qy  5680 CTCTCCTACTAGGGCCGCGCTCTGGGCACGCGCTGTCTGTGGGGTTAACCATGG 5739
         |||||||| | |||||| ||||   ||||||  ||||||||||||| || |||||
Db  5640 CCCTCCTATTGGGGCCGCTGCTGGAACGCGCTGGGCGCTGTCCGTGGGCTTGACCATGG 5699

Qy  5740 CGGGCGCGGTTCATGGGAAGTGCTAGCGTCTCCCCCTCCTTGGTCACCATTTACTTGGGG 5799
         ||||| ||| || || | |||| ||||||  || |  |||||||| |||||||| |||||
Db  5700 CAGTGCGTTCGTCATGGGGGCGCCACAGTGTCTCCCCCTCCTTGGTCACCATTTATTGGGG 5759

Qy  5800 CCGTGGGGGCGTGGGAGGGGCGGTGAATGCGGCTAGCCTTGTCTTGACTTTATGGGGG 5859
         ||| ||||||||||||||| ||  | |||||||||||||||||||  |||||||||||
Db  5760 CCGTTGCGGAGGGTGGGAGGGGTGTTGCAACGCGGCAGTCTTTGACTTCATGGGCGG 5819

Qy  5860 GGAAACTATCATCAGAAGATCTGTGGTATGCCATCCCAGTGCTAACCAGTCGGGGGCAG 5919
         ||||||  ||| || |||||||||||||| |||||||||||||| ||  || |||||||
Db  5820 GGAAACTTTCATCAGAAGATCTGTGGTATGCCAACTGCCTGACCAGCCCGGGGGCGG 5879

Qy  5920 GACTTGCGGGGATCGCCCTGGGTTGGTGTACTGGCACTAACAACTCGGCACTACCA 5979
         ||||| ||| ||| || ||||||||||| |||||||||||||||||||| |||||||
Db  5880 GCCTTGCGGGGATCCTCCGGGGTTGGTTTGTATTCAGCTAACAACTCGGCACTACCA 5939

Qy  5980 CTTGTGTTGAACCGTCTGCTGACTACATTGCCAAGGTCCTCATGCATCCCTGACAGTTACT 6039
         |||||| || |||||||||||||||||||  ||||||||| ||||| | ||||||| ||||
Db  5940 CTTGGTTGAACCGTCTGCTGACTACATTGCCAAGGTCTTCATGTATCCCGGACAGTTACT 5999

Qy  6040 TTCAGCAGGCCGATTACTGGCTGAACAAGGTCTCAGCTGCTCCGCAGCGCTTGAGCCTCACTC 6099
         |||||| || || |  || |||| | |||| || |||||||||| |||||| |||||||||||
Db  6000 TTCAGCAAGTTGACTATTGCCACAGGTCTTCGGGGTTCCGGCGCGCCTGAGCCTCACCC 6059

Qy  6100 GCACCTGGTTGCCCTGGTCAACAGGGAGCCTAAGGTGATGAGGTTCAGGTGGGTACG 6159
         |||| || |||||  |||||||||| || ||||||||||||||||||||||||||| |
Db  6060 GCACAGTGGTTGCCCTGGTCAACAGGGAGCCTAAGGTGATGAGGTACAGGTGGGTATG 6119

Qy  6160 TCTGGGACTTGTGGAGTGATCATCGTCAAGTGCGCATCGTGATGGCCGACTTCGGG 6219
         |  ||||| ||||||| || | ||| |||||||||||||  ||||||||||||| |
Db  6120 TCTGGGACCTGTGGAGTGATCATCGTCAAGTGCGCATCGTGATGGCCGACTTCAGG 6179

Qy  6220 CCCTCTGCCCCGTGGTGTGTCATTACCCCTTATGGCACTGCGCGGGGGAGGGGTGTCCGGGAGAAT 6279
         |||||| |||| || ||| ||||||||| ||||| |||||||||||| || |||||||||||||||
Db  6180 CCCTCTGCCCCGTGGTGTGTCATTACCCCTTGGCACTGCGCGGGGGAGGGGTGTCCGGGGAAT 6239

Qy  6280 GGTTGTTGGACGATGTGGAGCATGTCGTTCGTTGTGTTGCGTGATCACCGTGATG 6339
         ||| | |||||||||||||| || | |||||||||||||| |||||||||||||
Db  6240 GGTTGCTTGACGGTCATGTGAGCATGTCGTTCGTTGTGTTGCGTGATCACTGGTGACG 6299

Qy  6340 TTTTGAATGGGCAACTCAAAGATCCAGTTTACTTCTACCAAGCTGTGCAGGCATTATTGGA 6399
         || ||||||||||||||||| | |||| ||||| |||||||||||||| || |||||||||
Db  6300 TTCTGAATGGGCAACTCAAAGAACCAGTTTACTTCTACCAAGCTGTGAAACTGTCCCACTATTGGA 6359

Qy  6400 TGGGGACAGTCCCTGTGAACATGTCTATGGCGTATACTGCGAGACGTTGCTCGCCTCAG 6459
         |||||| |||| ||||||||||||| |||| | ||||||| || |||||||||||||||
Db  6360 TGGGGACGTCCCTGTGAACATGTCGTGGGCTGTGAAACGTGAAGCTCGGCTGCTCTCCTGCCCTCCG 6419

Qy  6460 ACACCCGGAAGGTTGTGCCTCGCCTACAAACTGCCGCGCGAGCAAATCCTGTCGCG 6519
         ||||||||||||  |||| || | |||||  ||| || |||||||||  ||| |||
Db  6420 ACACCCCGAAGGTTGTGCCTCGCCTACAAGCTGCTGCGCGAGCAAATCTGGTCGTCG 6479

Qy  6520 CCCACGTTGTGATCAGGCGAACATCCGCCTACAAACTGCGCGCGGCAAATCTGTCGG 6579
         ||||| ||||   ||| || |||||||||| |||| |||||||||||||  || |||
Db  6480 CCCACGTGTAATCAGGAGAACCTCCGCCTATAGCTGCTGCGCGGCAAATCCTATCGG 6539

Qy  6580 CTGCTGTTGCTGAGCCCGAGTCGACGGCCATTACGTCCGACGCACCGGTCCATGGGGGACCGGGCC 6639
         ||||| | |||||||||||||||| | ||||||  ||||||||||||||||||||||||||||||
Db  6540 CTGCTGTAGCTGAGCCCGAGTCGACGCGCTCAACATGGGGACGCACCGGTCCATGGGGGACGCGTC 6599

Qy  6640 GAGCCGCTGCAGCCCATGGTCTATGGCCCTGGGCAAAGTGTCACCATTGGCAGGGAAAACGGCTACA 6699
         |||||||||||||||| || ||||||  || ||| | |||| ||||| |||||||| || || |||
Db  6600 GTGCGCCCCGCATGTGCTATGGCCCTGGGCAAAGTGTTACCATTGACGGGGAGCGCTACA 6659

Qy  6700 CCCTTCCGCATCAACTGCCGCTTAGGAATGTGGCGCCCCTGAGGTGTCATCCGAGGTGT 6759
         |||||  | ||||| |||||  |||||||||||||||| ||||||||||||||||||||
Db  6660 CCCTGCTCATCAACTGCCTCAGGAAGTGTGGCGCCCCCTCTGAGGTTTCATCCGAGGTGT 6719

Qy  6760 CCAATTGACATTGGGACGGAGACTCGAAGACTCAGAACTGACTGAGGCCGCTGCCGCCCG 6819
         |||| |||||||||||||| ||||  ||||||||||||||||||||||||||||||||||
Db  6720 CCATTGACATTGGGACGGAGACTGAGACTCAGAACTGACTGAGGCCGATCTGCCGCCGG 6779

Qy  6820 CGGCTGCAGCCCTTCAGGCTGTCCATCGAGAATTCTGCGAGAATTCTTGAACCTCACATAGATG 6879
         |||| || |||| || |||| ||| || ||| | | |||||| ||||| ||||| ||||| |||
Db  6780 CGGCTGCTGCTGCTCCAAGGCGATCGAGAATCTGAACCGCCACATTGATG 6839

Qy  6880 TCATCATGGAAGATTGCAGTACACACCTCTCTTTGTGGGAGTAGCCGAGAGATGCCTGTGT 6939
         ||||||||||| || |||||||| | |||||||| ||| || | ||||| ||||||||| |
Db  6840 CCAATCATGGAGGACTGCAGTAGCACACCTCTCTTGGTAGTAGCCGAGAGATGCCTGTAT 6899

Qy  6940 GGGGAGAAGACATACCCCACTCATCTCGGTACTCGGTACTCGGTACTGAGAGCAGCC 6999
         ||||||||||||||||| | |||| | ||||| |||||||| |||||||||||||||
Db  6900 GGGGAGAAGACATCCCCGTACTCCTCCGGTACTCCTATCTCGGTACTGAGAGCAGCT 6959

Qy  7000 CAGATGAGAAGAGACCCCGTCGTGTCTTCCTCGCAGGAGTACCCCGTCTTCAACTGGTGGCTCAT 7059
         |||||||||||||| ||||| ||| || ||||||||| ||| |||| ||||||||| || ||||
Db  6960 CAGATGAGAAGAGACCCCGTCGTGTCCTCCTCGCAGGAGTACCCCGTCTTCAACTGGTGGCTCAT 7019

Qy  7060 TCGAGGTCATCCAAGAGTCCGAGACAGCAGCCCAAGGGGGAGAAAGCGTCTTCAACGTGGCTC 7119
         |||||||||||||||||| |||||||| |||||||||| ||||||||| |||||||||||||
Db  7020 TCGAGGTCATCCAAGAGTCCGAGACAGCAGCCCAAGGGGAGAAAGCGTCTTCAACGTGGCTC 7079

Qy  7120 TTTCCTACTAAAAGCCTTGTTCCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGA 7179
         ||||| || ||||||| |||||||||| |||| | |  ||||||||| ||||||| |
Db  7080 TTTCGTATTAGAAGCCTCATTCCACAGAGCGATGCCACAGGAAAGCTTACCGTTCAAGA 7139

Qy  7180 TGTCATGCGTGTTGTGAGAAGAGCGTAACACGCTTCTTTCATTGGGATTGACGGGTCGCTG 7239
         ||||| | |||||||||||||| ||||| |||||||  | ||||||| |||||||||||||
Db  7140 TGTCGTGCTGCTGTTGAAAAGAGCGTCACGCGTTCCATGGGTTGCTGGAGTGC 7199

Qy  7240 ACGTGGCAAGCCTGTGTGAGATGGAAATCCAGAACCATCCAGCTATTGTGACAAGGTGC 7299
         | | | |||||||||| |||||||||||||||||| |||||||||||||||||||||||
Db  7200 ATGTTGCTAGCCCTGTGTGAGATGGAAATCCAGAACCATCACAGCCATTGTGACAAGGTGC 7259

Qy  7300 GCACTCCGCTTGAATTGCAGTTGGGGTGGTGGTCCGGGAGAAT 7359
         ||| || |||||| |||||||||||| |||| ||||||||| |
Db  7260 GCACTCCGCTTGAATTGCAGTTGGGGTCGGTTGGTCCGGGAATGTG 7319

Qy  7360 ACAAGTGTGAGGCTAGGCAAGAGACCTTGGCTTCTCTTCACATTGGTCTGGGGTGC 7419
         |||| |||||||||||||||| ||| |||| |||||||| |||||| |||||||||
Db  7320 ACAAGTGTGAGGCTAGGCAAGAAACCTTGGCCTCCTCTTTACATTGGTCTGGAGTGC 7379

Qy  7420 CACTGACGAGGCCCACTCTGTGGAGCGCGGCCGTTGCCGTTCCTCTGG 7479
         ||  | | | || | |||||||| || ||||||||||||||||||||
Db  7380 CGCTGACTAGGCCACTCTGCCGTGGTGAGGCCGTTGGCGTCTCTTATTAG 7439

Qy  7480 TGGCCACACCACCAAGGTGTATGTCCAACCCGACAAGTGTGGGAGAAGAGTTGACA 7539
         ||||  ||||  ||||||| |||  ||||| |||||||||||| ||||||||||||
Db  7440 TGGCCGACACTACTAAGGTGTATGTTACCAATCCAGAACTAAGTACGTGGGAGCTGTGGACA 7499

Qy  7540 AGGTTACCTTCTGGCGTGCCTAGGGTTCATGACGACCAAATTCCTCCTGGGACTCCATAGAGC 7599
         ||||| || ||||||||| || |||||||| || ||| |||||| |||||||||||||||||
Db  7500 AGGTGACCTTCTGGCGTCCTAGGGTTCATGACGACCTCGGTTGGACTCTATTGAGC 7559

Qy  7600 GCGTAAGAGGGCAGCTCAAGGTGTACACTTATGAGGAGCAATAA 7659
         |||| |||||| ||| ||||||||||  || | |||| || |||
Db  7560 GCGCTAAGAGGGCCGCTCAAGGTGTTCACTTACTATGAGGAAGCAATAA 7619

Qy  7660 GGACTGTAAGGCCACATGCTGCCATGGGGTCGGGATCTCAAGGACCTCG 7719
         ||| |||||||||||||||||||| ||||| |||||||||||| |||||
Db  7620 GGACTGTTAAGGCCACATGCTGCCACATGGGGTCGGGATCGTAAGGACTTTAG 7679

Qy  7720 CCACCCCTGCGGGGGAAGATGGCTGTTCCATGACCGGCTCCAGGAGATACTTGAAGGGGACCGC 7779
         | | | |||||| |||||| | |||||||||||| ||| |||||||| ||||| ||||||||||
Db  7680 CCACCCCCGCGGGGAAGATGGCCGTCCATGACCGTCATCACCGGCTCCAGGAGATTGAAGGGACTC 7739

Qy  7780 CAGTCCCTTTACTTGTGAAAAGGAAGAGTGTTCTTCAAAGACCGAAAGGAAGAGA 7839
         ||||||  ||||| ||||||| |||| ||||||||||||||||||| |||| |||
Db  7740 CGGTCCCTTTACTTCTTACTTGTGAAAAGAGGAGGTGTTCTTCAAAGACCGAAGAGGAGG 7799

Qy  7840 AGGCCCCCGCCTCAGCCTCATTGTGTTCCCCGCCTGACTGAGCTGAAAGCTTATTC 7899
         ||||||||||||| || ||||||||||||||| ||||||||| ||||| |  | ||
Db
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Left column (Qy / Db alignment):

```
Db  7800  AGCCCCCGCCTCATTCGTTCCCCCCCTGGACTTCCGGATAGCTGAAAAGCTCATCT  7859

Qy  7900  TGGGAGACCCTGCGAGGGCTAGCCAAGGCGGTGTTGGGGGGGCCTACGCCTTCCAGTACA  7959
          |||||||| ||   ||||||||||||||||||||||||| | |||||
Db  7860  TGGGAGACCCAGACCGGGCTAGCCAAGGCGGTGTTGGGGGGGCCTACGCCTTCCAGTACA  7919

Qy  7960  CCCCAAATCAGCGAATTAGGGAGGATGCTCAAACTGTGGAATCAAAGAGACACCATGCG  8019
          ||||||||||| ||  |||||||| ||  ||||||||| || | |||||
Db  7920  CCCCAAATCAGCGAGTTAAGGAGGATGCTCAAGCTATGGGAGTCTAAGAGACACCCCTTGCG  7979

Qy  8020  CCATCTGTGTGACGCCACATGCTTCGACAGTAGCATAACTGAAGAGGACGTTGGCGCTGG  8079
          |||||||||||||| ||||||||| ||||| |||| |||||||||||
Db  7980  CCATCTGTGTGACGCCACCTGCTTCGACAGTAGCATAACTGAAGAGGACGTTGGCTTTGG  8039

Qy  8080  AGACAGAGCTTTATGCCCTGGCTTCAGCACATCCAGAATGGTGCGTGCCCTGGGGAAAT  8139
          ||||||||||| || ||||| | |||  |||||||||| | ||||||
Db  8040  AGACAGAGCTGTACGCTCTGGCCTCTGACCATCCAGAATGGGTGCGGGCACTTGGGAAAT  8099

Qy  8140  ACTATGCCCTCTGCACAATGCTAACCCCGAGGGGGTGCCAGTGGGTGAGAGTATTGTA  8199
          |||||||| |||| |||||| |||| |||||||| | |||||
Db  8100  ACTATGCCTCAGGCACCATGCCACCCCGGAAGGGTCAACCCGGTCGGGTGAGAGGTATTGCA  8159

Qy  8200  GATCCTCAGGGGTCTTGACCACCAGTGCGAGCAACTGCTTGACTTGCTATATCAAGGTGA  8259
          |||||||| ||||| || |||||| ||||||| |||||| || |||||||
Db  8160  GATCCTCGGGTGCCTAACAACTAGCCGCAGCAACTGCTTGACCTGCTACATCAAGGTGA  8219

Qy  8260  AAGCCCGCTGTGAGAGGTGGGGCTGAAAAATGTCTCGCCTCCTCATCGCTGCGATGACT  8319
          |||||||||||||||||||| || ||||||| | || || |||||
Db  8220  AAGCCCGCTGTGAGAGGTGGGGCTGAAGAATGTCTCTCTCATAGCCGGCGATGACT  8279

Qy  8320  GTTTGATCATATGCGAACGGCCTGTGTGCGATCCTAGCGACGCGTTTGGCGCAGAGCCCTGG  8379
          | |||||  ||||| |||||||||||||||||||
Db  8280  GCTTGATCATATGTGAGCGGCCAGTGTGCGACGCGACGCGTTTGGCCAGAGCCCTAG  8339

Qy  8380  CGAGCTACGGGTACGCATGCGAGCCCTTCGTATCATCATGCATACTGGACACGGCGCCCCTTCT  8439
          |||||||| ||||| |||||||| ||||| ||| ||||||||||
Db  8340  CGAGCTATGGGTACGCGCGAGCCCTCATATCTGGACACGGCGCCCCTTCT  8399

Qy  8440  GCTCCACTTGGCTAGCTGAGTGCAATGCAGATGCAGATGCAGAAACGCCATTTCTTCTTCCTGACCACGG  8499
          ||||||||| ||||||||||| |||||||||||||||
Db  8400  GCTCCACTTGGCTTGCTGTGAGTGCAATGCAGATGCAGATGCAGAAGCGCCATTTCTTCTTCCTGACCACGG  8459

Qy  8500  ACTTTCCGAGGCCCCTCGCATGTGCAGTGCAGTGACCCCAATGGCTTCGGCCA  8559
          ||| |||||||||||||||| |||||| |||||| |||||||
Db  8460  ACTTCCGGAGGCCCGCTCGCATGTCGAGTGCAGTGACCCCGATGGCTTCGGCGA  8519

Qy  8560  TCGGTTACATCCTCCTATACCCTTGGCATCCTATCACACGGTGGGTCATCATCCCTCACG  8619
          |||||||||||||  | |||||||||||||||||||||
Db  8520  TCGGTTACATCCTCCTTTATCCTTGGCACCCCATCACACGGTGGGTCATCATCCCTCATG  8579

Qy  8620  TGCTCACCTGGCCGGCGTTTAGGGGTTGGTGGTGCACACCGTCGATCCTGTGTGGTGCCAGGTAC  8679
          ||| | |||||| |||||| ||||||
Db  8580  TGCTAACGTGCGCCATTCAGGGGTTGGAGGCACCACCGTCGATCCTGTGTGGTGCCAGGTAC  8639

Qy  8680  ATGGTAATTACTACAAGTTCCACTGGACAAACTGCCTAACATCATCGTGGCCCTCCACG  8739
          |||||| ||||||||||||||| |||||||||||||||||||
Db  8640  ATGGTAACTACTACAAGTTCCACTGGACAAACTGCCTAACATCATCGTGGCCCTCCACG  8699

Qy  8740  GACCAGCAGCGTTGAGGGTTACCGCACAGACACAAAATGGAGCGGTGGCAAGG  8799
          |||||||||||||||||||||||| ||||||| ||||||
Db  8700  GACCAGCAGCGTTGAGGGTTACCGCACAGACAACACAAACAAAGATGGAGGCGTGGTAAGG  8759

Qy  8800  TGCTGAGCGACCTCAAGCTCCCCGGCTTCACCAGTACCACCGGGAAGAAGGCCGGGGCATTGC  8859
          ||||||||||||||||||| | |||||
Db  8760  TTCTGAGCGACCTCAAGCTCCCTGGCTTAGCAGTCACCACCGGAAAGAAGAGGCCGGGGTTGC  8819

Qy  8860  GAACGGCGTATGCTCCGGTCCCGGCGCGGTCGAGTTGGCTAGGGGGTCTGTTGTGGCCGTC  8919
          |||| || |||||||||||||||||||||||
Db  8820  GAACACGGCATGCTCCGGTCCCGGCGCGGTCGAGTTGGCTAGGGGGCTTGTTGTGCGCATC  8879

Qy  8920  CAGGCCCTGCGGCTTCCTCCCCCCGGAGATTGCTGGTATCCCGGGGGTTTCCCCCTTTCCC  8979
          |||| |||||| |||| ||||||||| ||| ||||
Db  8880  CAGGCCTACGGCTTCCTCTCCCCCGAGAGTTGCTGGTATCCCGGGGGTTTCCCCTCTCCC  8939
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Right column (Qy / Db alignment):

```
Qy  8980  CCCCCTATATGGGGGTGGTTCATCAATTGGATTTCACAAGCCAGAGGAGTCGCTGGCGGT  9039
          |||||||||||||||||||||| ||||||||||| ||||||||||||||||||||
Db  8940  CCCCCTATATGGGGGTGGTTGGTTACACCAATTGGATTTTACAAGCCAGAGGAGTCGCTGGCGGT  8999

Qy  9040  GGTTGGGGTTCTTAGCCCCTCTCGGTGAACTAAATTCATCTGTT  9099
          |||||||||| |||||||||||||||||||| |||||||||||||
Db  9000  GGTTGGGGTTCTTAGCCCCTCTCAGCCCTTCTCGGTGAACTAAATTCATCTGTT  9059

Qy  9100  GCGGCAAGGTCCGGTGACTGATCATCACTGGAGGAGTTCCCGCCCTCCCGCCCCAGGG  9159
          |||| ||||||||||||| |||||  |||||||||||||||||||||||||
Db  9060  GCGGCGAGGTCGGTGACTGATCGTCACCGGAGGAGTTCCCGCCCTCCCGCCCCAGGG  9119

Qy  9160  GTCTCCCCGCTGGGTAAAAAGGGCCCGGCCTTGGGAGGAGGCATGGTGTTACTAACCCCCTG  9219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9120  GTCTCCCCGCTGGGTAAAAAGGGCCGGGCCTTGGGAGGAGGCATGGTGTTACTAACCCCCTG  9179

Qy  9220  GCAGGGTCAAAGCTCGATGCGTGCTAATGCACTGCCACTTCGGTGGTCGCTACCTTA  9279
          |||||  |||||||| ||||||| |||||||||||||||||||||||||
Db  9180  GCAGGGTTAAAGCCTGATGCGTGCTAATGCACTGCCACTTCGGTGGTCGCTACCTTA  9239

Qy  9280  TAGCGTAATCCGTGACTACGGGCTGCTCCGAGAGCCCTCCCCGGATGGGCACAGTGCAC  9339
          |||||||||||||||||||||||||||||||||||||||||
Db  9240  TAGCGTAATCCGTGACTACGGGCTGCTCCGAGAGCCCTCCCCGGATGGGCACAGTGCAC  9299

Qy  9340  TGTGATCTGAAGGGGTGCACCCCGTAA  9367
          || ||||||||||||||||
Db  9300  TGAGATCTGAAGGGGTGCACCCCGGAA  9327
```

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RESULT 13
AAX02517
ID   AAX02517 standard; cDNA; 9327 BP.
XX
AC   AAX02517;
XX
DT   06-MAY-1999   (first entry)
XX
DE   US5856134 Seq ID 234.
XX
KW   Non-A Non-B Non-C Non-D Non-E Hepatitis virus; immunogen; HGV; HAV; HBV;
KW   immunoreactive; serum alanine aminotransferase; hepatitis A virus; HCV;
KW   hepatitis B virus; hepatitis C virus; hepatitis D virus; HDV; HEV;
KW   hepatitis E virus; Flaviviridae; prophylactic; therapeutic; diagnosis;
KW   antibody; vaccine; detection; ds.
XX
OS   Hepatitis G virus.
XX
PN   US5856134-A.
XX
PD   05-JAN-1999.
XX
PF   05-JUN-1995;   95US-0461361.
XX
PR   19-MAY-1995;   95US-0444733.
PR   20-MAY-1994;   94US-0246985.
PR   03-AUG-1994;   94US-0285543.
PR   03-AUG-1994;   94US-0285558.
PR   03-AUG-1994;   94US-0285561.
PR   26-OCT-1994;   94US-0329729.
PR   23-NOV-1994;   94US-0344271.
PR   16-DEC-1994;   94US-0357509.
PR   15-FEB-1995;   95US-0389886.
PR   05-JUN-1995;   95US-0461361.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fry KE,  Kim JP,  Linnen JM,  Wages J,  Young LM;
XX
DR   WPI; 1999-105108/09.
XX
PT   New isolated hepatitis G virus antigens - used to develop products
PT   for the diagnosis, prophylaxis and therapy of hepatitis G virus
```

PT infections
XX
PS Example 18; Column 337-346; 204pp; English.
XX
CC This invention describes a Non-A Non-B Non-C Non-D Non-E Hepatitis Virus
CC (HGV) immunogenic composition which comprises a purified HGV polypeptide
CC antigen at least 10 amino acids in length which is specifically
CC immunoreactive with HGV-positive sera, present in a carrier, where HGV
CC is characterised by (a) production of elevated serum alanine
CC aminotransferase levels in an infected primate (b) its serological
CC distinction from hepatitis A virus (HAV), hepatitis B virus (HBV),
CC hepatitis C virus (HCV), hepatitis D virus (HDV), and hepatitis E virus
CC (HEV) (c) membership in the virus family Flaviviridae. The compositions
CC can be used to develop products useful for prophylactic, therapeutic and
CC diagnosis applications. The immunogenic compositions can be used for the
CC production of antibodies, in vaccines and for detection and diagnosis.
XX
SQ Sequence 9327 BP; 1682 A; 2532 C; 2984 G; 2129 T; 0 other;

Query Match   83.9%; Score 7885.6; DB 20; Length 9327;
Best Local Similarity   90.4%; Pred. No. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;

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Qy      40 GCAAGCCCATAAACCAGCACGCCTATCTAAGTAGACGCAATGACTCGGCGCGACTCGGCG 99
           ||||||||  ||||| ||||||||||||||||||||| ||||||||||||||||||||||
Db       1 GCAAGCCCCAGAAACCGACGCCTATCTAAGTAGACGCAATGACTCGGCGCGACTCGGCG 60

Qy     100 ACCGGCCAAAAGGTGGTGAATGGGTGGTCGTAGGTTGGTAGGTTCGTAAATCCCGGTCAT 159
           |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      61 ACCGGCCAAAAGGTGGTGATGGGTGGTCGTAGGTTGGTAGGTTCGTAAATCCCGGTCAC 120

Qy     160 CCTGGTAGCCACTATAGGTGGTCTTAAGAGAAGGTCAAGACTCCTTGTGCCTGCGGC 219
           | ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     121 CTTGGTAGCCACTATAGGTGGTCTTAAGAGAAGGTTAAGATTCCTTCTTGTGCCTGCGGC 180

Qy     220 GAGACCGCGACGTGCCACAGGTGCTGGCCCTACCGGTGTGAATAAGGGCCCGACGTCAG 279
           ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db     181 GAGACCGCGACGTGCCACAGGTGTGGCCCTACCGGTGGGAATAAGGGCCCGACGTCAG 240

Qy     280 GCTCGTCGTTAAACCGAGCCCGTCACCCACTGGCAAACGAGCGCCACGTACGGTCCAC 339
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GCTCGTCGTTAAACCGAGCCCGTTACCCACTGGCAAACGAGCGCCCACGTACGGTCCAC 300

Qy     340 GTCGCCCTTCAATGTCTCTCTTGACCAATAGTTTATCCGGCGAGTTGACAAGGACCAGT 399
           ||||||||||||||||||||||| ||  || |||||||||||| ||||||||||||||||
Db     301 GTCGCCCTTCAATGTCTCTCTTGACCAATAGGCTAGCCGCGGGTTGACAAGGACCAGT 360

Qy     400 GGGGGCCGGCGGGGTTATGGGGAAGGACCCCAAACCCTGCCCTTCCCGGTGGGCCGGGAAAT 459
           ||||||||||||||| ||| |||  |||||| ||| || |||||||||||||||||||||
Db     361 GGGGGCCGGCGGGGCT-TGGAGAGGGGACTCCAAGTCCCGGCCCTGGGCCGGGAAAT 419

Qy     460 GCATGGGGCCACCCAGCTCCGGCGCCCGGGTAGCCAAGAATCCTTCGGG 519
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 GCATGGGGCCGGGGCCACCCAGCTCCGGCGCCCGGGTAGCCAAGAATCCTTCGGG 479

Qy     520 TGAGGCGGGTGGCATTCTCTTTTCTATACCATCATCATGGCAGTCCTTCTGCCTCCTCTCG 579
           |||||||||||||||||||| ||| |||||||||||||||||||||||||||||||||||
Db     480 TGAGGCGGGTGGCATTCCTTTTTCTATACCATCATCATGGCAGTCCTTCTGCCTCCTCTCG 539

Qy     580 TGGTTGAGGCGGGGCCATTCTGCGCCCCGGGAACATCGGGTTCTGCGCTGGAAGGCGAATGGGCAAT 639
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     540 TGGTTGAGGCGGGGGCCATTCTGCGCCCCGGGAACATCGGGTTCTGCGCTGGAAGGCGAATGGGCAAT 599

Qy     640 ATTTCCTCACAAATTGCTGTGCCCGGAACATCGGGTTCTGCGCTGGAAGGCGGATGCC 699
           ||||||||||||| |||||||||||||||||||||||  ||||||||||||||||||||
Db     600 ATTTCCTCACAAATTGTTGCCCCGGACGACAATCGGGTTCTGCGCTGGAAGGCGGATGCC 659

Qy     700 TGGTGCCCTGGGGTGCACCGGTTGCACCGGTTGCTGGCCCACTGTATCAGGCGGGTT 759
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     660 TGGTGCCCTGGGGTGCACCGATTGCACCGGTTGCTGGCCCAATGCTGCCACTGTATCAGGCGGGTT 719

Qy     760 TGGCGTGCGGCCTGGCAAGTCCGCGGCCCAGCTCGTGTGGGGAACTGGGGAGCCTGTACG 819
           ||||| ||||||||||||||||||||||||  || ||  ||||||||||||||||| ||||
Db     720 TGGCGTGCGGCCTGGCAAGTCCGCGGCCCAGCTCGTGTGGGGAGCTGGGGAGCCTGTACG 779

Db     720 TGGCTGTGCGGCCTGGCAAGTCCGCGGCCCAACTGTGGGGGAGCTGGGGAGCTGGGTAGCCTATACG 779
           | || |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Qy     820 GGCCCTTGTCGGTCCGGCTTACGTAGCCGCCTATGTGCGGATCCTGGGGATCCTCGGGCTGGGCGAGGTTTACTCCG 879

Db     780 GGCCCCGTCGTCCGGCTCGGGGATCTGGGCCTGGGACGGTGAGGTGTACTCGG 839
           |||||  |||||||||||||||||||||||||||||||||| ||||||||||||
Qy     880 GGGTCCTGACAGTTGCTGTTCGCTTGAGGCGCGGCGCCGGTCTACCTGATCGCCCAACCTGAAGT 939

Db     840 GTGTCCTAACCGTGGACGTCGCGTTGACGCGCCGGATCTACCCGGTGCTAACCTGACGT 899
           | |||| ||||| ||||||||||||||||||||||| ||||||||||||||||||| |||
Qy     940 GTGCAGTAGAATGTGACGTTAAGTGGGAAGGTGGAAGTGAGTTTGGAGATGGACTGAGCAGTTGG 999

Db     900 GTGCAGTGCGTGTGAGTAAAGTGGGAAAGTGGAAGTGAGTTTGGAGATGGACTGAACAGCTGG 959
           ||||||| |  |||  |||||||||||| ||||||||||||||||||||||| ||| ||||||
Qy    1000 CCTCCAATTACTGGATTTTGGAATACCTTGAAGTCCCATTTGAATTTGGAGAGGAG 1059

Db     960 CCTCCAACTACTGGATTCTGGAATACCTCTGAAGGTCCCATTTGATTTTCTGGAGAGGCG 1019
           |||||||| ||||||||| |||||||||| ||||| |||||||||| ||||||||||| |
Qy    1060 TGATGAGCCTGACCCCTCTGTTGGTTGGGCGCCATGGGGGGATGTTCGCAAGGCGCCCCGCCTCCG 1119

Db    1020 TGATAAGCCTGACCCCTTGTTGGTTGGTTTGCGTGGCCGCATGGTGGCCGCATTGCTGCTTGACAACGGG 1079
           |||| |||||||||||| ||||||||| || ||| |||||||| |||||||  |||||||||||||||
Qy    1120 TTGTCATGGTTTTCCTTGCTGGTGACCATGGCGGGGGATGTTGCAAGGCGCCCCCGCCTCCG 1179

Db    1080 TTGTCATGGTCTTCCTCGTGTTGGTGGTGACGATGGTCGCGGATGCCGCAAGGCGCCCCTGCCTCCG 1139
           ||||||||||| ||||| ||||||||| |||||||| ||| ||||||||||||||||  |||||||
Qy    1180 TTTTGGGGTCCGGCCCTTTGACTACGGTTGAAGTGCAGTCATCGTCCGCAGGGCTA 1239

Db    1140 TTTTGGGGTCACGCCCTTTGACTACGGTTGACTTGCAGACCTGCTTCTTGCAGGCCA 1199
           ||||||||| ||||||||||||||||||||  ||||  |||||||||||||||||||
Qy    1240 ACGGGTCGCGTATTCCCACTCGGGAGGAGGGTGTGGGATCGGAGGAATGTCACGCGTCTTGT 1299

Db    1200 ACGGTTCGCGGTTTTTGACTGGGAGGAAGGTGTGGACCGTGGACCGTTACGGTTCAGT 1259
           |||| ||||| | |||| |||||||| |||||||||| ||||| ||||||| ||||||
Qy    1300 GTGACTGCCCAACGGCCCCTGGTTTGGGTGTGGGCTTTTGCCAGGCGGTTGGGTGGG 1359

Db    1260 GTGACTGCCCTAACGGCCCCTGGGTGTTGGTTGCCAGCCTTTTGCCAAGCAATCGGCTGGG 1319
           ||||||||||| |||||||||||| | ||| |||||||||||||||| ||||||| |||||
Qy    1360 GCGACCCCCATTGAGCCACGGCACCAGTGGCAAAAACCAGTGGCCCCTATCATGCCCCCAAT 1419

Db    1320 GTGACCCCATCTATTGGAGCCCACGGCACCTATTAGTGGCCCCCTTTCATGCCCCCAGT 1379
           |||||||| ||| | ||  ||| ||||||| |||  ||||||||| ||||| |||||||
Qy    1420 ATGTCTATGGGTCGTGTCCGGTAACGTGCGTGGGGTTCCGTGCCTGTTGGTTTGCCTCGA 1479

Db    1380 ATGTCTATGGGTGTCGTCTGTACAGTGCACTTGCGTGTGGGTTCCGTTCTTGGTATGCCTCCA 1439
           ||||||||||||| |||| ||  ||||| |||||||  ||||||||| | ||| |||||| ||
Qy    1480 CCGGGCGGTCGTGATTCGAAGATCGATGTGTGTCGGTTTGGTGCCCGGTTGGATCTGCCAGCT 1539
           || |||| ||||| |||||||| ||| ||||| ||||||| ||||||||| |||||||||
Db    1440 CCAGTGCGCGGCGACTCGAAGATAGAGTGTGGTGAGTTTAGTCCGAGTTTAGTGCCAGTTGGCTCTGCCACCT 1499

Qy    1540 GCACCATAGCCGCTCTAGGGTCATCCGACTCGGTCGTTAGAGTTCGGT 1599
           ||||||||||||||||||||||||||||| || |||||||| |||
Db    1500 GCACCATAGCCGCACTTGGATCATCGGATCGGTCGCTTCCGACACGGTGCTCCGAGTGGGG 1559

Qy    1600 GAGTCCCGTGCTAACGTGATTCGGTATTCTGACCGTGGCACCTGTGC 1659
           || |||||||||| ||||| ||| ||| ||||||||||||||||||
Db    1560 GAATCCCGTGCCTGCGACGTGTCGTTCTGCGGTCCGACCGGTTCATGGCGGCCACCACCTGTGTGA 1619

Qy    1660 GGGACTGCTGCGCCCAGAAACCGGGTCGATTCCTTCCATCCGTCGTCCGGCACGGGGC 1719
           ||||||||||||||||||| ||||||||| ||||||||||||||||||||
Db    1620 GGGACTGCTGCGCCCGGGTAGGTTCGGTTAGTTCCCTTGTCGTCGTCCGGCGTGGGGC 1679

Qy    1720 CTCGCTGACAAAGGACTTGGAAGCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCA 1779
           |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    1680 CTCGGCTGACAAAGGACTTGGAAGCTGTCCCTTAGTTCGTCGTCAATAGGACAACTCCCTTCACCA 1739

Qy    1780 TAAGGGGCCCCTGGGAGAGGCAACCCGGTCGCGGTCGCCCCCTGGGTTTTG 1839
           | ||||| ||||||||||||||||||||||| |||||||| || ||||||||
Db    1740 TTAGGGGGCCCCTGGGGCAACCCGGTCGCGGTCGCCCCCCTTGGGTTTTG 1799

Qy    1840 GGTCCTACACCATGACCAAGATCCGGGGAATTCCCTGCATTTGTGAAAAGTCCCACACCAG 1899
           |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db    1800 GGTCCTACACGCATGACCATGACCAGGATCCGAGATACCCTACATCGTCGTGAGTGTCCACCACCAG 1859
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Qy  2980  GCGCAAGAGGGGCCTACCTGTTCACCACATGGGCTCTTCTCCGCGGCCTGTCGTCAAGGAGC  3039
                | ||| |||| |||  | | |||  |||||  || || ||| |||||| |||||| |||||||
Db  2940  GTGCGGAGGAGGAGCTTATTTGTTGTTGCGATCATATGGGGCTCATTTTCCGTGCTGTCAAGGAGC  2999

Qy  3040  GCTTGTTGGAATGGCACGGCCTTGGAGCCCTTGTCATTCACTAGGACGGACTGTCGCA  3099
                ||||||||  |||| ||| |||||| ||||| |||||||||||||| | |||||||||
Db  3000  GCCTGTTGGAATGGGACGGCGCTCTTGAACCTCTGTCATTCACTAGGACGGACTGTCGCA  3059

Qy  3100  TCATCAGAGATGCGCGGAGGACCCTGTCTCGCGGACAGTGCGTCATGGTGTTACCCGTGG  3159
                |||| | ||  |||||| ||| ||||| |||  ||  ||  ||  ||||||  |||||||
Db  3060  TCATACGGGATGCCGCGAGGACTTTGTCCTCGCGGGCAATGCGTCATGGGTTCATGGGTTGTC  3119

Qy  3160  TAGCACGGCGCGTGATGAGGTTCTCATCGGCGTTCTTCAGGATGTGAATCATTGCCTC  3219
                | ||| |||| | |  | ||||| |||||||||||||  |||| ||||||||| ||||
Db  3120  TTGCGGCCCGTGGTGATGAGGTTCTCATCGGCGTTCTTCCAGGATGTGAATCATTTGCCTC  3179

Qy  3220  CCGGGTTGTCCCGACTGCACCAGTTGTCATCCGTGGTGCGGAAGGGCTTCCTGGGGG  3279
                |||||| |||| |||||||  ||||   | |||||||  || ||||  | | ||||||
Db  3180  CCGGGTTTGTTCCGACCGCGCTGTGTCAGGTCGGGATCCTGTGCGGAAAGGGCTTCTTGGGGG  3239

Qy  3280  TCACGAAGGCAGCCTGACAGGTAGGGAGTCCTGACTTACATCCGTGGTGCGACGTCATGGTGT  3339
                |||||  ||||| |||||  ||||  || ||  ||||  ||||||| |  |||||||||| |
Db  3240  TCACAAAGGCTGCCTTGACAGGTCGGGATCCTGACTTACATCCAGGGACGTGCGTCATGGTGT  3299

Qy  3340  TGGGGACGGCTACGTCACGAAGCATGGCACATGTCTGAATGGCCGTCGTGTTCACAACTT  3399
                |||||  |||||| |||| ||   |||| |||||||| || ||||| || || |||| ||
Db  3300  TGGGGACGGCTACGTCTCGCAAGCATGGCACATGTCTGAACGGCCGTCGTGTTCACGACCT  3359

Qy  3400  TCCATGGGCTTCATCCCGCAACCATCGCCACGCCCGTGGGGGCCCTTAATCCCAGGTGTGT  3459
                |||||||||||||||||| |||||| ||||| ||||| ||  | | |||| |||| || |
Db  3360  TCCATGGGCTTCATCCCGCAACCATCGCCACGCCCGTGGGGGCCCTTAATCCCAGGATGT  3419

Qy  3460  GGTCAGCCAGTGATGACGTCACGGTGTACCCGTTCCAGATGGGGCAACTTCGTTGACGC  3519
                |||||||  |||||  ||||  ||||  |||||| || || |||||| |||| || |||
Db  3420  GGTCAGCCAGTGATGATGATGTCACGGTGTATCCCGTTCCAGTTATTGATCCGACGGGGCTTTGTTAACGC  3479

Qy  3520  CCTGCACTTGCCAGGCGGAGTCCTTGTTGGGTTTATTGATGTCGACGGGCTTTGTGCCATG  3579
                |||| |||||||| |||| ||| |||| ||||| |  |  || | |||  | ||||||||
Db  3480  CTTGTTACTTGCCAGGCTGATGTCCTTGTTGGGGTCATCAGATGTCGACGGGCCTATGCCATG  3539

Qy  3580  GCTTGAGCAAGGGACAAGGTTGAGCTGGACTGGCATGTGGCCATGGTCTCTCGACTTCCGTG  3639
                |||||||||||| |||||||| |||||||||||||||| ||||||  || ||| || ||||
Db  3540  GCTTGAGCAAGGGACAAGGTGGAGCTGGACTGGCATGTGGCCATGGTCCCTGATTTCCGTG  3599

Qy  3640  GTTCGTCTGGTTCCTTTGCGACAAAGGGCACGCAGTAAGAAATGCTCGTGTCAG  3699
                ||| | | |||| | | ||||   ||||||| || ||||| | || || ||||
Db  3600  GCTCGTCTGCTCCTTTGCGACGAGTGTGCACGGCACCGAGTAGGAATGCTCGTGTCTG  3659

Qy  3700  TGCTCCACTCTGCGGCAGGGTTACTGCGGCCTTTGTGTGCCATG  3759
                |||||||| |||||| |||||||||| |  || ||| ||||||||
Db  3660  TGCTTCACTCCCGGTGGTCACCGGCCGTTCACTAGGCCGGTTGCGGCCGGTGGTTACTAGGCCAAGTGG  3719

Qy  3760  CAACAGATGCCAAGACTACCACAGACAACCCCTCCGGCGGCAAAAGGAGTTTCAAGG  3819
                |||||||| | ||| | | |||||| |  || |||| ||||| |||| |||||| ||
Db  3720  CAACAGATGCCAAAACCACCACTGAACCCCACTGAACCCCGTGCGCGGCCAAAGGAGTTTCAAAG  3779

Qy  3820  AGGGCCCGTTGTTTATGCCTACGGCGGCGGGAAAGGACACCCGGTACCGTTGGAGTACG  3879
                |||||||| ||||| |||||| |||||| |||| |||| ||  ||  | |||||||| |
Db  3780  AGGGCCCGTTGTTTATGCCTACGGCGGCGGGAAAGAGCACTCGCGTCCGTCCGGTTGGAGTACG  3839

Qy  3880  GCAACATGGCCACAAGGTCTTGATCTTGAACCCGTCGGTAGTCCGTGAGGGCCATGG  3939
                |||||||||  | |||| ||  ||||| |||||| || | |||| |||||||||| ||
Db  3840  GCAACATGGGCACAAGGTCTTGTTGTCTTAGTCTTGAACCCCTCAGTGCGCCGTGTGGGCGGCCAATGGGG  3899

Qy  3940  GCCCATACATGAGCGGCTGGCGGTGGACTACCAGAATTACTTGTGCCATGACACCA  3999
                ||||| | | |||||| |||||| |||||||  |||  | | | |||| | ||| |
Db  3900  GCCCGTACACTGAGCGGCTGGCGGTAAACATCCAGTATATACTGTGGGGCATGGCATGGCATGTC  3959

Qy  4000  CTGCTTTCACAAGGATCACTGACCTCGCCCCCTTTACCTGTGTCTCCAAGATGT  4059
                ||||||||||| ||||||||||| ||||| | || ||| |  |||||| |||||
Db  3960  CTGCTTTCACAAGGATCACTGACCTCCCCCCCGACGTATTCAACCTATGGAGGTTTTGG  4019

Qy  4060  TTGAGTGCGTGTGTGATGGCGGTGAGAGGGGGTGTGTCGGTGGTCATTTGTGACGAGTGCCACAGTC  4119
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Qy  1900  CCATAGAGCCTTCCGACTGGAACGTTCGGGTTCTTCCCGGAGTCCCCATTAACAACT  1959
                || ||| ||||||  |||||| |||| ||| ||||| ||||||||  | |||||||||
Db  1860  CCATCGAGCCCTCCCACCGGACGTTTGGGTTCTTCCCGGACGCCCGCTCAAACAACT  1919

Qy  1960  GCATGCCGCTAGGCACGGAAGTGTCTCGAGGTGTTCGGAGCTGTTGGAGCCGGA  2019
                |||  || ||||  || ||   | || || ||  || |||||| |||| |||||||||
Db  1920  GCATGTCCTTGGGCACCGAAGTGTCTCGAGGTGTTGGGAGCTGGTGGAGCCGGTGG  1979

Qy  2020  TCTACGAGCCTCTGGTTCGCAGGTGTTCGGAGCTGGAGCCGATGGGAACCCGGAAATCCGGTTGCC  2079
                | ||| ||||| || ||  |||||||||| |||| | | |||  | | ||  |  ||||||| | |
Db  1980  TCATACGGGGATGCCGCGGAGGACTTTGTCCTGCGGGCAATCGTCATGGGTTTGTC  2039

Qy  2080  CGGGGTACGGCTGCTCCTCTGCGTAGACCTGACGTTCATACACGTCAGGGCACC  2139
                ||||| || ||| |   | | ||  ||| |  |||||||||||||| ||||||| |
Db  2040  CGGGGTTTGCATGGCTCTCTTGCGGCCAGGCTGTTTATACATGTCACT  2099

Qy  2140  TGCAGGAGGTGATGCGGGCAACTTCATCCCTCCTCACGCTGGTTGCTCTTGGATTTTG  2199
                |||||||| ||| |  ||||||||||||||||| | |  |||| | |||||| ||| ||
Db  2100  TGCAGGAGGTGGATGCGGGCAACTTCATCCCCCGTTGCTCTGGTTCCCGGTTCCTGGACTTTG  2159

Qy  2200  TATTTGTCCTGTCTTATACCGTGATGAGTGGGGTCAGCCTGAGGCACGTTGGTTCCGTTGATCTTGC  2259
                || ||||||| ||| |||||| || ||  |||| ||||| |||||||| |||| || || ||||||
Db  2160  TATTTGTCCTGTCTTATACCGTGATGAGTGGGGTCAGCCTGAGGCACGGTTGGTCCCGGTGATCCTGC  2219

Qy  2260  TTCTGCTGTGGTGGGTGAACCAGTTGGCCGTTCTAGGACTGGCGTCTGGGACGCTG  2319
                | | |  ||| | | ||| |||| || |||  ||||| |||||||| ||| ||| ||
Db  2220  TGCTTGCTATGGTGGTGAACCAGCTCCTAGGCACGCTAGGGCGCTGCTAGGCGTGGAAGCCG  2279

Qy  2320  CCGTGCGGGGTGAAGTTTTGCGGCCCTGCCTTGTCATGGTGTTTGGGCTTTCGGCCTTCCCACTG  2379
                ||||| | ||||| ||  |  ||||||||||||||| | ||| | || |  | | | | ||||  |
Db  2280  CCGTGGCGGGGTGAGGTGTCCATCCCTGCGTCCTGTGTCTGGGTCTGGGACTCCGTCCCCGTCG  2339

Qy  2380  TCAGTATGATACTAGGTCTAGCAAACTGGTTGTTGTTACTTTCGGTGGATGGGGCCCTTCAGC  2439
                |||| | | || | | |||| || |||||| |||| | ||||||  ||| |||| | |||||||
Db  2340  TCAGTATGATATTGGGTTGCAAACCTGGTTTCTGTTACTTTAGATGTTGGAGCCGTTAACCC  2399

Qy  2440  GCCTCAATGTTCCTCGTGTTGGTGGAAGCTTCGCTCGGGAGCTTTCCCGGAGCTCACTTTTGA  2499
                |||  |  |||| ||||||| |||||| |||||| | |  |||| ||||| | ||| |  ||||
Db  2400  GCCTTGACTGTTCCTCGTGTTGGTGGAAGCTTGCTCGGGCGCTTCCCGGAGCTCCTCTTTGA  2459

Qy  2500  TGGGATTCGGCGACCCCGGGGCGCCACTCGTGCTCGGGGCCAGTTCTTCGATG  2559
                ||||| ||||| | ||||| |  | ||||| | | |||||| | | | |||||
Db  2460  TGGGATTTCGGCGACCCCGGGGCGCCACCGCTGCTCGGGGCCCAGTCTGCTTCTTCGATG  2519

Qy  2560  TCACATTCGAGGTGGACACTTCTGACGTTCGGCTGGTTGGGCTGGTGGCTTGGG  2619
                ||| | | ||| ||| |||  |||| || |||||| |||| | ||| ||| |||
Db  2520  CTACATTCGAGGTGGACACTTCGGTTGCCAATGGTGTGGTAGCTTGGG  2579

Qy  2620  CCATAGCGGCCTCCTGAGCTCAATGAGCGGCAGCCTTGAAGCACACAAGCCGTGATCTATA  2679
                |||| || | |  | | |||||||| |||| ||||| |||||| ||||| |||| ||||||
Db  2580  CCATTGCGCTCCTGAGCTCGATGAGCGGCAGGCAGGGGGTGGAGGCACAAGCCGTGATCTATA  2639

Qy  2680  GGACGTGTGTAAGGGTACCAGGCTGTGCGCAGGGTGTGTCGGACGCGGTGG  2739
                |||| ||  ||  | | |||||  ||| || || | | | |||| || |||
Db  2640  GGACGTGTGTAAGGGTACCAGGCAATCCGTCAAAGGGTGTCGAAGGTGTGAGGTGGGG  2699

Qy  2740  AGGGGCGTCCTACCAAGCTTCTGACGTTCGCCTGGTTCGCGTGGTGGCCGG  2799
                |||||||| | || | |||| | || |||| || ||||| | || | ||||
Db  2700  AGGGGCCGGCGCCCAAAACCCTGACCTTTGTTGCCTTTGGTCCTTTATGTCTTACATCCTGGCCAG  2759

Qy  2800  ATGCTGTGATGATGGGTGGTGGCGCCTTGTCGGCCTTCGGCCTTCGACGCACTGG  2859
                |  | || |  || |||| ||||  | |||  ||||| || || ||||||| | ||
Db  2760  ATGCTGTGATGATGGGTGGTGGCGCCTTGGCCTTTGGCCTTTCGACGCCGTGG  2819

Qy  2860  ACTGGGCCCTGAGGAGACTCCTCGTTACGGCGACTGGCACGGACGGGTGG  2919
                | | ||||| | |||| | |  | ||||| |||| |||| | || ||||||
Db  2820  ATTGGGCCTTGGAGGAGATCTTGGTGTCCCGGGCAATCGGCCGTTGGCGCTTGGCGGGTGG  2879

Qy  2920  TTGAGTGCGTGTGTGATGGCGGTGAGAGGGGGTGTGTCGGTGGTCATTTGTGACGAGTGCCACAGTGT  2979
                ||||||||||| ||||||| ||||| |||||| ||||| ||| || |||| ||| || | || | ||
Db  2880  TTGAGTGCGTGTGTGATGGCGGTGAGAGGGGGTGTGTCGGTGGTCATTTTGGTGACGAGTGCCCACAGTC
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Db  5100  GTCTAGCTATCGCGGGGAATGATCTACGCGTCGTACACCGGTCGCTAGTGGTGGTGA  5159
          |||||||||||||||||||||||||||||||||  |||| ||| ||||| |||||||
Qy  5200  CAGACTGGGATGTGAAGGGGGTGAAGGGGGTGCATCGGCATGGAGACGAGGACCACGC  5259
          |||||||||||| || |||| |||||||||| |||| ||||||| |||| |||||||
Db  5160  CAGACTGGGATGTGAAGGGGGTGCATGGGCATGGAGACGAGGACCAGGCCACGC      5219

Qy  5260  CCCAGCCGGTTGTGCAGGTCGCTGGGGGAGTCTGCCCCAT  5319
          ||||||||||||||| |||||||||||||||||||||||||
Db  5220  CTCAGCCGGTTGTGCGTGCAGGTGCTCCTGCGGTGAATCAGCAGCCAT  5279

Qy  5320  CGGATGCCAACACAGTGACAGATGCGGTGCGGCCATCCAGGTGGATTGCGATTGGTCAG  5379
          |||||||||||||||||||||| | |||| ||||||||| ||||| |||||||||||||
Db  5280  CGGATGCCAAGACAGTGACAGCGGCGTGCAGCGCGATCCAGGTGGACTGCGCATTGGACTA  5339

Qy  5380  TCATGACCCTGCGATCGGGGAAGTGCGTGTCTTGCGCTACAGGGGACGCCGAGGCCT  5439
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  5340  TCATGACTCTGTCGATCGGAGAAGTGTTGTCCTTGGCTCAGGCTAAGACGGCCGAGGCCT  5399

Qy  5440  ACGCAGCTACCACCAAGTGGCTTGCGTGCGCTACACGGGGACGCCGGCCGCCTCCCCACTG  5499
          | | ||||||||||||||||||| |||| ||||||| || || ||||| |||||||||||
Db  5400  ACACAGCAGCCACCAGTTGCTCGCTGCGTTACGGGGGACGACGCCGTTCCCCACTG  5459

Qy  5500  TTTCAATTGTTGACAAGCTCTTCGCCGGGGCTGGCGTGGTGGAGGCCATTGCCACA  5559
          ||||| ||||| |||||||| |||||||||||| |||||||||||||||||||||||
Db  5460  TATCCATTGTTGACAAGCTCTTCGCCGGGCGTGTGGGCCACTTCCAGTTGACCATGG  5519

Qy  5560  GTGTAATAGCCTGTCGCAGTGCGGGCGCCTATGGGCTTCTAGGAGCCTCCG  5619
          ||||||||| || ||| |||||| |||| |||| || ||||||||||||||||
Db  5520  ACGTGATTGCTGCGGCGGTGCGGCCCAGTGTCTCCCCGCTCCCGTTGGCCAGCCG  5579

Qy  5620  CCGGTTCCTACCTCATGGGGTTGGGCGTCGGAGGCAACGCCAAACCCGCTTAGCCTCCG  5679
          |||||||||||| |||||| |||||||||||||| |||||| |||||||||||||||||
Db  5580  CGGCTTCCTACCTGATGGGGTTGGGCGTTGGAGGCAACGCGTCGTCTGGCCATCTG  5639

Qy  5680  CCTCCTACTAGGGCGCCTGGGACCGCTCTGGGCACGCCTGTCCTGTGGGTTAACCATGG  5739
          |||||||||  |||| |||||||||||  ||||||  ||||||||| ||||||||||||
Db  5640  CCCTCCTATTGGGGGCTGCTGGAACCGCCCTGGGCACTCCTCGTGTGGGCTGACCATGG  5699

Qy  5740  CGGGGCCGTTCATGGGAAGTGCTAGCGTCTTGTACTCTCCGTCCCCCCTCCTTGGTCACCATTTTACTTGGGGG  5799
          ||| |||||| |||||||||| |||| | ||| |||||||||||||||||||| ||||||||||| ||| |||||
Db  5700  CAGGTGCGTTCATGGGGATCGCTCTCGGGTTGGTTGTATTTCAGTCACCATTTTATTGGGG  5759

Qy  5800  CCGTGGGGCGCTGGGAGGGCGCTGGTGAATGCGCTAGCCTTGTCTTGTATCGCGG  5859
          |||||||||| ||||||| |||||| |||| ||| ||||| ||||||||||||||||
Db  5760  GCCTTGGGCCTCGCGCCCAGTTTGGTTTGTATTCAGTCAACAACTCTGGCCACTACCA  5819

Qy  5860  GGAAACTATCAGAAGATCTGTGTATGCCATCCCAGTGCTAACCAGTCCGGGGCAG  5919
          ||||||||||||||| || |  |||||| ||||||||||||||||||||||||||||
Db  5820  GGAAACTTTCATCAGAGATCTGTATGCCATCCCGGGTACTGACCACCCGGGGGCGG  5879

Qy  5920  GACTTGCGGGGGATCCCCTCGGGTTGGTGTTGTACTCAGCTAAACAACTCTGGCACTACCA  5979
          |||||||| ||||| ||||| |||||||||||  |||||||||||||||||||||||||||
Db  5880  GCCTTGGGGACTTGGTTGCCCTCGGGGTTGGTTTGTATTTCAGTCAACAACTCTGGCACTACCA  5939

Qy  5980  CTTGGTTGAACCGTCTGCTGCTGACTACATTGCCAAGGTCCTCGACTACAGTTACT  6039
          |||||||||||||||||||||| |||||||| ||||||||| |||||||||||||||
Db  5940  CTTGGTTGAACCGTCTGCTGCTGACTACGTTGCCAAGGTCTTCATGGCACCGTAGTTACT  5999

Qy  6040  TTCAGCAGGCCGATTACTGTGACAAGGTCTCAGCTGCTCGACCTGAGCCTGCTC  6099
          |||||||||||| ||||||||||||||||||| ||||||||||||||||||||||
Db  6000  TTCAGCAAGTTGACTATTGCGACAAGGTCTCAGCTCTCCGGCCTCGAGCCTCCCC  6059

Qy  6100  GCACCGTGGTTGCCCTGGTCAACAGGAGCCTAAGGTTCAGGTGGGTACG  6159
          |||||||||||||| || ||||||||||||||||||||||||||||||||
Db  6060  GCACAGTGGTTGCCCTTGCTCAACAGGAGCCTAAGGTGATGAGGTGGGGGTATG  6119

Qy  6160  TCTGGGACTTGTGGGAGTGGATCATGCGTCAAGTGCCATGGTAGTTCGGG  6219
          ||| |||||||||||| |||||||||||||||||||||||||||||||||
Db  6120  TCTGGGACCTGTGGGAGTGGATGATCATGCGTGGTCATGCGACTGGTCAGGG  6179

Qy  6220  CCCTCTGCCCCGTGGTCCCCGTGGTCATTATCTGGCCTTATCCCTTGTGTTGTGGCACTCGGGGAGAAT  6279
          |||||||||||||| |||| ||| ||||||| ||||||||||||||||||||||||||||||||||||||
Db  6180  CCCTCTGCCCCGTGGTGTTCATTATTCACTCCCTGTGTTGTGGCACTCGGGGAGGGTGTCGCGGGGAAT  6239
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Db  4020  ||||||||||||||||||||    ||||| |  || ||||||||||||||||||||
          CCAACCCTAGGCAGATGCTACGGGCGTTTCGGTGGTCATTGTGATGAGTGCCACAGTT  4079

Qy  4120  ATGACTCAACTGTGTTGTTGGGCATTGGGCGTGTCAGGGAGCTGCGCGGATGTGGAG  4179
          ||||||||||| || ||| |   |||  ||| ||||||||| || | |||
Db  4080  ATGACTCAACCGTGCTGTTAGGCATTGGGAGGGTTCGGGAGCTGGCCGTGGTGCGGAG  4139

Qy  4180  TGCAATTGGTGCTCTACGGCCACTGCCACCCTCCGATCCCCGATGACCCAGCACCCAT  4239
          |||||||||||| ||| |||||||||||||| ||||| || ||||||||||| || |||
Db  4140  TGCAACTAGTGCTCTACGGCCACCGCACCGCCTCCCGATCCCCGATGACGCAGCACCCTT  4199

Qy  4240  CAATCATTGAGACAAAACTGGACCTGGGAGAGAATCCCTTCTATGGGCATGGCCATACCTC  4299
          | ||| || ||||||||| ||||||||||||||  ||| || | ||||| ||||| |||||
Db  4200  CCATAATTGAGACAAAATTGGACGTGGGCGCAGAATTCCCTTTATGGGACGGAATACCCC  4259

Qy  4300  TTGAGCGGATGCGGACCGGAAGGCATTCCTATTCTGCCACTCCAAGGCTGAGTGCGAGC  4359
          | | ||| ||| |||| ||||| ||| |||||||||||||  |||||| ||||| ||||||
Db  4260  TCGAACGGGATGCGGAACCGGAAGGCACCTCTGTCTGCCATTCTCAAGGCTGAGTGCGAGC  4319

Qy  4360  GCCTGGCGGGCCAGTTTCGGCTAGGGGGTAAATGCCATTCGCCTATTACAGGGGGAAAG  4419
          ||||||||||||||| ||| || || ||||| |||||||||| || || |||||||||||
Db  4320  GCCTTGCTGGCCCAGTTCTCCGCTAGGGGGTCAATGCCATTCGCCTATTATAGGGGTAAAG  4379

Qy  4420  ACAGTTCTATCATCAAAGATGGAGCACGTGGTGTGTCTACGACCACTATCCCACTG  4479
          |||||||||||||||||  |||| |||||||| || | ||||||||| || ||||||
Db  4380  ACAGTTCTATCATCAAGAATGGAGCACGTGGTGCTGTCTCCGGGACGCCGCTTTCCACTG  4439

Qy  4480  GGTACACTGGGAACTTCGATTCGTCACCGATTGTGGGTTAGTGCGTGGGAGGTCGTCG  4539
          |||||||||| ||  ||| ||||||||| || || |||||  ||||||||||||||||||
Db  4440  GGTACACTGGGAAATTTCGAACTCCCGTCACCGACTGTGATTAGTGCGTGGGAGGTCGTTG  4499

Qy  4540  AGGTGACCCTTGATCCCACCATTACCATCTCCCTGCGACGTCCCGCTCGGCTGAAC  4599
          |||| |||||| |||||| | ||||  ||||| || ||| || |||| ||||||||||
Db  4500  CGGTCGACCCTTGATCCTGCTACCATTACCATCTCCCTGCTCGGCTGAAC  4559

Qy  4600  TGTCGATGCAGCGGCGGAGGACGCACGGGTAGGGCGAGGCTGCGGCGCTACTACGCGG  4659
          |||||| | ||||  ||||||| |||| |||| |||||| |||||| ||||||||||||
Db  4560  TGTCCATGCAAAGACGAGGACGCACGGGTAGGGCGAGGCTCAGTGTCTGACGCTACTACGCGG  4619

Qy  4660  GGGGGCCAAGGCCCCTGCTGGTGTGCGCTCAGGTGCGGCGGTGGAAG  4719
          |||| |||| |||||||| ||| ||| |||||| ||||| ||||||||
Db  4620  GGGTGGGCAAAGCCCCGTGGGTGTGCGCTCAGTGTCCGGTGGCGGTGGAAG  4679

Qy  4720  CCGGTGTGACCTGGTACGGAATGAACTGACCTGACAGCAAACTACTGAGACTTTACG  4779
          |||||  |||| ||| |||||||| ||| ||||| || |||||||||| |||||||||
Db  4680  CTGGAGTGACCTGGTGCGGAATGAACCGACTACTGACTGCTAACCTACTGAGACTTTACG  4739

Qy  4780  ACAACTGCCCTTCAGCCGAGCACATTGGGGAAGCCCGGTTGGGTGTGTCTTTT  4839
          | |||||||| |  | ||||| |||| | |  ||||||| ||||| ||||||||
Db  4740  ACGACTGCCCTTTACACCGGAGCACGCCTCGCGGCTCGATATCCGGAGAGCCCGGTGTTGTTCTTCT  4799

Qy  4840  CCGGTGTGACCTTGAGGTACGGCGCATCGGGATGGTTAGCTGCGCAAAAGTTCGCGCGTCA  4899
          |||||||||||||||  ||||| |||| |||| ||||||| |||| |||||||||||||||
Db  4800  CTGGGGCTCGCGCCAATTGAGGTACGACTTCGGCGTGGCAGTTCGGCAAAAGTTCGCGCGTCA  4859

Qy  4900  ACTGCCCTTCCTGGTGTTCAGCCGGACCATGTGCCGGAAAACACTGTCTCCGGCC  4959
          |||||||  || ||| || |||||| ||||||||||||||||||||||||||||||
Db  4860  ACTGCCCTTCCTGGTGTCCAGCCGGACCATGTGCCGGAAAACACTGTCTCCCGGCC  4919

Qy  4960  CATCGGATGACCCCCAGTGGGCAGGTCTGAAGGGCCGAATCCTGTCCCACTCCTGCTGA  5019
          |||||||||||||||  |||||||| ||| ||| |||||| || || |||||||||| ||
Db  4920  CATCGGATGACCCCCAATGGGCAGGTCTGAAAGGCCCAAATCCTGTCCCACTCCTGCTGA  4979

Qy  5020  GGTGGGGCAATGATTTACCATCTAAAGTGCCGGCCATCCACATCGTGGACGACCTGGTCC  5079
          |||| |||||||| |||||||| ||||||||||||||||||| ||| |||||||||||||
Db  4980  GGTGGGGCAATGATTTACCATCTAAAGTGCCGGCCACCACATAGTGGACGACCTGGTCC  5039

Qy  5080  GTAGGCTCGGGGTGCCGGAGGGTCACGTCGCGCTGCCGATGCTCGCTGCTGATGGTGG  5139
          | ||||||||||||| | |||  |||| || |||||||||||||||| |||||| |||
Db  5040  GGAGACTCGGTGTGCGGGGAGGGTTACGCCCTGCGCACGCTGCGCGATCTTGATGATCG  5099

Qy  5140  GCCTCGCTATTGCGGGGGGCATGATCTATGCGGTCATACACCGGGTCTCTCGTGTGGTTA  5199
          |  || ||||| |||||||  ||||||| ||||||  ||||| ||||||||| || |||||
Db  5100  ...
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Qy   6280 GGTTGTTGGACGGCCATGTTGAGAGTCGTTGTCTTTGTGGTTGGCGTGATCACCGGTGATG 6339
          ||||| ||||| || |||||||||||| | || ||| | || || ||||||||| ||||||
Db   6240 GGTTGCTTGACCGTCATGTTGAGAGTGCTGCTCGTGCGTCGCGCGATCACTGGTGACG 6299

Qy   6340 TTTGAATGGGCAACTCAAAGATCCAGTTTACTCTACCAAGCTGTGCAGGCATTATTGGA 6399
          | ||||| ||||||||||||||| || ||||||||||||||||| |||||| |||||||
Db   6300 TTCTGAATGGGCAACTCAAAGAACCAGTTTACTCTACCAAGCTGTGCCGCCACTATTGGA 6359

Qy   6400 TGGGACAGTCCCTGTGAACATGCTGGGCTATGGCGAGACGTCGCCTTGCTCGCCTCAG 6459
          ||||||| ||||||||||||| ||| || ||| || ||| ||||||||| | |||||
Db   6360 TGGGGACTGTCCCTGTGAACATGCTGGGTTACGGTGAAACCTCGCCTCCTCCTGGCCTCCG 6419

Qy   6460 ACACCCGAAGGTGGTACCATTCGGGACGTCTGGGTGGGCTGAGGTGGTGCACCCCTA 6519
          ||||||||||||||| ||||| |||||||||||| |||||||||||||||||| || |
Db   6420 ACACCCGAAGGTTGTGCCCCTCCGGGACGTCTGGGCTGGCTGAGGTGGTGCACCACTA 6479

Qy   6520 CCCACGTGTGATCAGGCGGAACATCCGCCGCTACAAACTGCGCGCCAGCAAATCCTGTCGG 6579
          ||| ||||||| || ||||| ||||| | |||| ||||||||||||||||| ||| ||||
Db   6480 CCCACGTGGTAATCAGGAGAACTCCGCCTATAAGCTGCTGCGCGCCAGCAAATCCTATCGG 6539

Qy   6580 CTGCTGTTGCTGAGCCTATTACGTCGACGGCATACCGGTCTCATGGGACGCGGACCGCGC 6639
          ||||| |||||||||| |||||| || ||||||| |||||| |||||| || ||| |||||
Db   6540 CTGCTGTAGCTGAGCCCTACTACGTCGACGGCCATTCCGGTCTCATGGGACCGCGGACGCTC 6599

Qy   6640 GAGCCGCTGCCATGGTCTATGGCCCTGGGCAAAGTGTCACCATTGACGGGGAACCGCTACA 6699
          |||| |||||||||||| ||||||||||||| ||||| |||||||||||||||||||||||
Db   6600 GTGCCGCCGCCATGGTCTATGGCCCTGGGCAAAGTGTTACCATTGACGGGGAGCCGCTACA 6659

Qy   6700 CCCTTCCGCATCAACTGCGGCTTAGGAATGTGGCGCCCTGCGAGGTGTCATCCGAGGTGT 6759
          |||||||||||||| |||| || |||||||||||||| || ||||||||||| |||||||
Db   6660 CCCTGCCTCATCAACTGAGGCTCAGGAATGTGGCGCCCTGCGAGGTTTCATCCGAGGTGT 6719

Qy   6760 CCATTGACATTGGGACGGAGACTCAGAACTTCAGCCAGCAACTTGACTGAGGCCGCAGCC 6819
          ||||||||||||||||||||||||||||| || |||||||||||||||||||||||||||
Db   6720 CCATTGACATTGGGACGGAGACTCAGAACTTCAGGCAGCAACTTGACTGAGGCCGCAGCT 6779

Qy   6820 CGGCTCCAGGCTCATCGAGAATGCTGCGAGAATTCTTGAACCTCACATAGATG 6879
          |||||||||||| || ||||| ||||||||| |||||||||||||||||||||
Db   6780 CGGCTCGCTGCCTCAAGCGATCGAGAATGCTGCGAGGATTCTTGAACCGCACATTGATG 6839

Qy   6880 TCATCATGGAAGATTGCAGTACACCCCTCTTTGTGGGAGTAGCCGAGAGATGCCTGTGT 6939
          |||||| |||||| ||||||||||||||| | || |||| |||||||||||||||||||
Db   6840 CCATCATGGAGGACTCCAGTGTCCAGTACACCCCTCTCTGTGTAGTAGCCGAGAGATGCCTGTGT 6899

Qy   6940 GGGGGAGAAGACATACCCGACTCACCCTCCATCCGGTTACTGGTTACGGGCAGCAGCC 6999
          |||||||||| || || ||||| || ||||||||||||||||||||||||||||||||
Db   6900 GGGGGAGAAGACAATCCCGACCACTCCATCCGGTTACTGGTTACTGAGAGCCAGCT 6959

Qy   7000 CAGATGAGAAGACCCCGTCGGTGTCTTCCTGCAGGAGGATACCCCGTCTTGACTCAT 7059
          ||||||||||||||||||| || ||||||| | ||||||||||||| |||| ||||||
Db   6960 CAGATGAGAAGACCCCGTCGGTGTCTTCCTGGCCTCTGGATACCCCGTCTTCCTGACTCAT 7019

Qy   7060 TCGAGGTCATCCAAGAGTCCAGAACGCGCTTCAACGTGCTC 7119
          ||||||||||||||||||||||||||||| || |||||||||
Db   7020 TCGAGGTCATCCAAGAGTCCCAGAACGTCCCGAACGTGCTC 7079

Qy   7120 TTTCCGTACTAAAAGCCTTGTTTCCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGA 7179
          ||| |||| ||||||||||||| ||||||||| || ||||||||||| || |||||||
Db   7080 TTTCCGTATTAGAAGCCTCATTTCCACAGAGCGACCGCCACAACTAGCCTCACCGTTCAAGA 7139

Qy   7180 TGTCATGCTGTTGTTGAGAAGAGCTGAACACGCTTCATTGGGATTGGACGGTCGCTG 7239
          |||||||||||||||| ||||||||| ||||| || ||||||||||||||||||||||
Db   7140 TGTCGTGCTGCGTTGAATAGCGTGAAAGAGCTTGCATTGGGGTTACAGAGCCAGTGCTG 7199

Qy   7240 ACGTGGCAAGCCGTCGTGAGATGGCGCTATTGTGACAAGGTGC 7299
          || ||||||||| | || ||| |||||||||||||||||||||
Db   7200 ATGTTGCTAGCCGTGTGGAGATGGAAATCCAGAACCATAGACAGCCTATTGTGACAAGGTGC 7259

Qy   7300 GCACTCCGTTGAATTGCAGGTTGGGTGCTTGGTGGCAATGAACCTTTGAATGTG 7359
          |||||||| ||||||||||||||| |||||||||||||||||| ||||||||||
Db   7260 GCACTCCGTTGAATTGCAGGTTGGGTGCTTGGTGGCAATGAACCTTTGAATGTG 7319
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Qy   7360 ACAAGTGTGAGGCTAGGCAAGAGACCTTGGCTTCCTTCTCTTACATTTGGTCTGGGGTGC 7419
          |||||||||||||||||||||||||| ||||||| ||||| || |||| ||||| ||||
Db   7320 ACAAGTGTGAGGCTAGGCAAGAAAACCTTGGCTTCCTTCTTCTTACATTTGGTCTGGAGTGC 7379

Qy   7420 CACTGACGAGAGGGCACTCCGGCCAAGCCCCCCTGTGGTAGGAGGTTGGCTTCCTTGCTGG 7479
          | ||||| ||||||||| ||||| ||||||||||||||||| || ||||||| ||||| ||
Db   7380 CGGTGACTAGGGGCACGTAGGGGCACGCCGGCCAAGCCCCGTGGTGAGGCGTGGGTTCTTTATTAG 7439

Qy   7480 TGGCCGACCACCAAGGTGTATGTCACCAACCCGGACAATGTGGGAGAAGAGTTGACA 7539
          |||||||||| || ||||||| ||||||||| |||||||||||||||||||||||||
Db   7440 TGGCCGACACTACTAAGGTGTATGTTACCAATCCAGACAATGTGGGACGGAGGTGGACA 7499

Qy   7540 AGGTTACCTTCTGCGTGCCCCTAGGGTTCATGACAAATTCCTCGTGGACAAATCCATAGAGC 7599
          || | ||||||||||| ||||||| ||||||||| ||||| || ||||||||||||||||||
Db   7500 AGGTGACCTTCTGGCGTCCCTCCTAGGGTTCATGACTCGTGGACTCCGTCATTGAGC 7559

Qy   7600 GGCTAAGAGGGCAGCTCAAGCCTGCTGCCCATGGGCTGCACTTATGGAGGAGCCAATAA 7659
          |||||||||||| |||| |||||||||||||||||||| |||||| ||||||||||||||
Db   7560 GGCCTAAGAGGGGCCGCTCAAGCCTGCTGCCCATGGGCTGCACTTATGGAGGAAGCCAATAA 7619

Qy   7660 GGACTGTAAGGCCACCAATGCTGCCAATGGGCTGCGGGATCGGGACTTCGGTCAAGGACCTCG 7719
          ||||||| ||||||||||||||||||| ||||| ||||||| || ||||||||||||||||
Db   7620 GGACTGTGAAGGCCACCAATGCTGCCATGGGCTGGGATCGGGACTTCGGTTAAGGACTTAG 7679

Qy   7720 CCACCCCTGCGGGGAAGATGGCTGTCCATGACCCGCTCCAGGAGACACTCGAAGGGACGC 7779
          ||||||| |||||||||| ||||||||||| |||||||||||||||| |||||||||||||
Db   7680 CCACCCCGCGGGGAAGATGGCCGTCCATGACCCGCTCCAGGAGACACTCGAAGGGACTC 7739

Qy   7780 CAGTCCCTTTACTCTTACTGTGAAAAAGGAAGTGTTCTTCAAAGACCGAAAGAAGAGA 7839
          ||||||||| |||| |||||||||||||||||||| |||| |||||||||||||||||
Db   7740 CGGTCCCCTTTACTCTTACTGTGAAAAAGGAGTGTTCTTCAAAGACCGGAAGAAGGAGG 7799

Qy   7800 AGGCCCCCCCGCTTCCCCGCCATTGTGTCCGGACTTCCGGATAGCTGAAAAGCTTATTC 7899
          |||||||||||||| |||||| ||||||||||| |||| ||||||||||||||||| |||
Db   7800 AGGCCCCCCCGCTCATTGTGTCCGGACTTCCGGATAGCTGAAAAGCTCATCT 7859

Qy   7900 TGGGAGACCCCGACGCGTTATGCCCTTCAGACCTTCAGAACCATCCAGAGGGGGGCCTACACA 7959
          ||||||| |||| |||||| ||||||||||||| ||| || ||||||| || ||||||||||
Db   7860 TGGGAGACCCCAGACGCGTTACGCGCTCTCTGGCCTTCAGAACCATCCAGAGGGGGCCTACACA 7919

Qy   7960 CCCAAATCAGCGAATTAGGAGGATGCTCAAACTGTGGGAATCAAAGAAGAGACACCATCCG 8019
          |||||||||||||||| || ||| || |||||||||||||| |||||||||||||||||||
Db   7920 CCCAAATCAGCGAGTCAGGAGTCTCAAGCTATGGGAGTCTAAGGAGTCTATGGGGGACCCCTTCG 7979

Qy   8020 CCATCTGTGTGGAGCCGCCACATGCTTCGACAGTAGCATAACTGAAGAGGACGTGGCGCTGG 8079
          ||||||||||||| |||||| || || || ||||||| |||| |||||||||| |||||||
Db   7980 CCATCTGTGTGGACGTCCCACCTGCTCGTTGTGACAGTAGCATAACTGAAGAGGACGTGCTTTGG 8039

Qy   8080 AGACAGAGCTTATGCCCTCAGACCTTCTTGAACCTCCGTCTTGACTCAT 8139
          ||||||||||| ||| ||||||||||||| ||||| |||||||||||||
Db   8040 AGACAGAGCTTATGGCTTCTGACCTCTGGCCTTCTGCCTCCAGATGGGTGGAAAT 8099

Qy   8140 ACTATGCCTCTGGCACAATGGTAACCCCCGGAGGGGTGCCCAGTGAGAGTGATTGTA 8199
          |||| |||||||||| ||||||| | ||||| || ||||||||| ||||| ||||||
Db   8100 ACTATGCCTCAGGCACCATGGTCACCCCGGAGGGGTGCCCGGGTGAGAGTGATTGCA 8159

Qy   8200 GATCCTGTGTGGGGTCTGACTTTGTTCCACAGCGATGCCACAAGAAAGCTTTACCGTTAAGA 8259
          |||||||||||| || ||| | |||||||| ||||| || ||||||||||||||||||||||
Db   8160 GATCCTGGGTGTCTTGACTTTGTCCTAACAACTAGCGCAGCAACTGCTTGACCGTCATCAAGGTGA 8219

Qy   8260 AAGCCGCCTGTGAGAGGGTGGGGCTGAAAAATGTCTCGCTCCTCGCCGATGACT 8319
          ||||||||| ||||||||||||| ||||| |||||||||| || || ||||||||
Db   8220 AAGCCGCCCGTGAGAGGGTGGGGCTGAAGAATGTCTCTCTCATAGCCGGCCGATGACT 8279

Qy   8320 GTTTGATCATATGCGAACGCGTGTGCGATGCATGGGCAGAGCCCTGG 8379
          ||| ||||| |||||| || ||| ||||||| || |||| |||||| |
Db   8280 GCTTGATCATATGGGAGCGCTGCGCGATGCATGGTACGCTTGGGACACCCTAG 8339

Qy   8380 CGAGCTACGGGTACGCCGATGCCATGGCATCACTGGACTGCAATCCTTTGGCAAGGTGC 8439
          |||||| ||||||| ||| ||| |||| | |||||||| ||||| || ||| |||||||
Db   8340 CGAGCTATGGGTACGCCGTGTGCGCAGCCCTCCATATCATGTGGGACACGGCCCCCTTCT 8399

Qy   8440 GCTCCACTTGGCTAGCTGAGTGCAATGCAGTGAGTGCGATGGGAACGCGCCATTTCTTCCTTCGACCACGG 8499
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XX
KW   Hepatitis; HGV; diagnosis; vaccine; antigen; ds.
XX
OS   Hepatitis G virus variant PNF2161.
XX
PN   US5849532-A.
XX
PD   15-DEC-1998.
XX
PF   06-JUN-1995;    95US-0464134.
XX
PR   19-MAY-1995;    95US-0444733;
PR   20-MAY-1994;    94US-0246985.
PR   03-AUG-1994;    94US-0285543.
PR   03-AUG-1994;    94US-0285558.
PR   03-AUG-1994;    94US-0285561.
PR   26-OCT-1994;    94US-0329729.
PR   23-NOV-1994;    94US-0344271.
PR   16-DEC-1994;    94US-0357509.
PR   15-FEB-1995;    95US-0389886.
PR   06-JUN-1995;    95US-0464134.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fry KE,  Kim JP,  Linnen JM,  Wages J,  Young LM;
XX
DR   WPI; 1999-069731/06.
XX
PT   Vector containing hepatitis G virus nucleic acid - and transformed
PT   cells for producing recombinant HGV polypeptide
XX
PS   Example 18; Column 337-346; 204pp; English.
XX
CC   This is the nucleotide sequence of clone 3Z-HGV94-6, a near
CC   full-length hepatitis G virus (HGV) genome produced by PCR
CC   amplification (see AAV82242-47) of 3 overlapping segments of the
CC   HGV variant PNF 2161 genome (see AAV82093) and cloning of PCR
CC   products into vector pGEM32.  This clone can be used to map the
CC   various regions of the viral genome, study its replication, and
CC   examine the mechanisms of HGV pathogenicity in human cells.  The
CC   invention provides a claimed vector that includes HGV-PNF 2161
CC   nucleic acid and a method for the production of recombinant HGV
CC   polypeptides (see AAW89452).  These polypeptides can be used as
CC   antigens (i) in diagnostic methods for detecting the presence of
CC   HGV in test subjects, (ii) in vaccines, and (iii) in the
CC   preparation of anti-HGV antibody.
XX
SQ   Sequence 9327 BP; 1682 A; 2532 C; 2984 G; 2129 T; 0 other;

Query Match             83.9%;  Score 7885.6;  DB 20;  Length 9327;
Best Local Similarity   90.4%;
Matches 8433;      Conservative    0;  Mismatches  894;  Indels    1;  Gaps    1;

Qy     40 GCAAGCCCCATAAACCGACGCCTATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCG   99
          ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAAGCCCCAGAAACCGACGCCTATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCG   60

Qy    100 ACCGGCCAAAAGTGGTGCGATGGGTGGTGCAGGGTTGGTGCAGGGTTGGTGCAGGGTCAT  159
          |||||||||||| || ||||||||||||||| ||||||||||| |||||||||||||
Db     61 ACCGGCCAAAAGTGGTGATGGGTGGTGATGCAGGGTTGGTGCAGGGTTGGTGCAGGGTCAC  120

Qy    160 CCTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTCAGACTCCTCTTGTGCCTGCGGC  219
          ||||||||||||||||||||| ||||||||||||  |||| ||||||||||||||||||
Db    121 CTTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTTAAGATTCCTCTTGTGCCTGCGGC  180

Qy    220 GAGACCGGCCACGGTCCACAGGTGCTGCCCTACCGGTGTGAATAAGGGCCCGACGTCAG  279
          ||||||||||||||||||||||  ||||||||||||  ||||||||||||||||||||||
Db    181 GAGACCGGCCACGGTCCACAGGTGTTGGCCCTACCGGTGGGAATAAGGGCCCGACGTCAG  240

Qy    280 GCTCGTCGTTAAACCGAGCCCGTCACCCACCTCGGCAAACGACGACCCACGTACGGTCCAC  339
          |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    241 GCTCGTCGTTAAACCGAGCCCGTTACCCACCTCGGCAAACGACGACCCACGTACGGTCCAC  300
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Db   8400 GCTCCACTTGGCTTGCTGAGTGCAATGGACGATGCAGACGGGAAGCGCCATTCTTCCTGACCACGG   8459
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   8500 ACTTTCGGAGGCCCCTCGCTCGCATGTCCAGTACAGTGAGTACGAGAGTCCGCATGTGACCCAATGGCTTCGGCCA   8559
          |||| |||||||||||||||||||  ||||||| |||||||||||||||||||||||||
Db   8460 ACTTCCGGAGGAGCCGGCCGCTCGCTCGCATGTCGAGTGAGTAGTATGTGACCCGATGGCTTCGGCCGA   8519

Qy   8560 TCGGTTACATCCTCTATCACCGGTGGCATCCTATCACACGGTGGTCATCATCCCTCACG   8619
          |||||||||||||||  |||||| ||||| |||||||||||||||||||||||||||||
Db   8520 TCGGTTACATCCTCCTTTATCCTGGCACCCCATCACACGGTGGTCATCATCCCTCATG   8579

Qy   8620 TGCCTCACCTCGGCGTTAGGGGTGGTGGCACACGCCTCTGATCCTGTGTGGTGCCAGGTAC   8679
          |||| ||||| || ||||||||||| |||||| |||| ||||||||| ||||||||||||
Db   8580 TGCTAACGTGCGCATTCAGGGGTGGAGGCCACACGTTTGTGTGCCCAGGTAC   8639

Qy   8680 ATGGTAATTACTACAAGTTCCACTGGACAAACTGCCTAACATCATCGTGGCCCTCCACG   8739
          |||||||  ||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   8640 ATGGTAACTACTACAAGTTCCACTGGACAAACTGCCTAACATCATCGTGGCCCTCCACG   8699

Qy   8740 GACCAGCAGCGTTGAGGGTTACCGCAGACACAACTAAGACAAAAATGAGAGGGTTGGCAAGG   8799
          |||||||||||||||||||||| |||||||||||||| |||| |||||||||| ||| ||||
Db   8700 GACCAGCAGCGTTGAGGGTTACCCGCAGACACAACTAAAACAAGATGAGAGGGCTGGTAAGG   8759

Qy   8800 TGCTGAGCGACCTCAAGCTCCCTGCCCTAGCAGTCCACCGGAGAAGCCGGGGCCATTGC   8859
          | |||||||||||||||||||||||  |||||||||||||  |||||||||||||||||
Db   8760 TTCTGAGCGACCTCAAGCTCCCTGCTTAGCAGTCCACCGAAAGAAGCCGGGGCGTTGC   8819

Qy   8860 GAACCGTATGCTCCGGTCGCGGCCGGTTGGCTAGGGGCGTGTTGTTGGCGTC   8919
          |||| ||| |||||||  | | ||||||||||||||||||||  |||| ||||| |
Db   8820 GAACACGCATGCTCCGCGCTCGCGGCCGGTTGGCTAGGGGCGTTGTTGTGTGGCCATC   8879

Qy   8920 CAGGGCCTGCGCGGCTTCCCCCCTCCGGAGATTGCTGCTGGTATCCCCGGGGGTTTCCCCTTTCCC   8979
          |||||||| ||| |||||||||||||| |||||||||||||||||||||||||||  ||||| ||||||
Db   8880 CAGGGCCTACGGCTTCCCCCCTCCCGAGATTGCTGCTGGTATCCCCGGGGGGTTTCCCCTCTCCC   8939

Qy   8980 CCCCTATATGGGGGTGGTGTCATCAATTGGATTTCACAGACCAGGAGTCGCTGGCCGT   9039
          ||||||||||||||||||||  | |||||||||||||| | ||||| |||||||||||||
Db   8940 CCCCTATATGGGGGTGGTGTACACCAATTGGATTTTACAAGCCAGGAGTCGCTGGCCGT   8999

Qy   9040 GGTTGGGGTTCTTAGCCCCTGCTCATCGTGAGCCCTGAACTAAATTCATCTGTT   9099
          ||||||||||||||||||||||||||||||||||| | ||| |||||||||||||
Db   9000 GGTTGGGGTTCTTAGCCCCTGCTCATCGTGAGCCCTTCGGTGAACTAAAATTCATCTGTT   9059

Qy   9100 GCGGCAAGGTCCGGTGACTGATCATCACTGGAGGAGGTTCCCGCCCTCCCCGCCCAGGG   9159
          |||| |||| | ||||||||||| |||| ||||||||||||||||||||||||||||||
Db   9060 GCGGCGAGTCGTGTGACTGATCGTCACCGGAGGAGGAGGTTCCCGCCCTCCCCGCCCAGGG   9119

Qy   9160 GTCTCCCCGCTGGGTAAAAAGGGCCCGGCCTTGGGAGGCATGGTTACTAACCCCCTG   9219
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   9120 GTCTCCCCGCTGGGTAAAAAGGGCCCGGCCTTGGGAGGCATGGTTGGTTACTAACCCCCTG   9179

Qy   9220 GCAGGGTCAAAGCCTGATGTGTCTAATGCCACTGCCACTTCGGTGGCGGGTCGCTACCTTA   9279
          |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9180 GCAGGGTTAAAGCCTGATGTGTCTAATGCCACTGCCACTTCGGTGGCGGGTCGCTACCTTA   9239

Qy   9280 TAGCGGTAATCCGTGACTACGGGCCCTCCAGAGCCCTCCCAGAGCCCTCGATGGGGACAGTGCAC   9339
          ||||||||||||||||||||||||| | ||||||||||||||||||||||||||  ||||||||
Db   9240 TAGCGGTAATCCGTGACTACGGGCCTCGCCAGAGCCCTCCCAGAGCCCTCGATGGGGCACAGTGCAC   9299

Qy   9340 TGTGATCTGAAGGGGTGCACCCGGTAA   9367
          || ||||||||||||||||||||| ||
Db   9300 TGAGATCTGAAGGGGTGCACCCGGGAA   9327
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RESULT 14
AAV82248
ID   AAV82248 standard; cDNA; 9327 BP.
XX
AC   AAV82248;
XX
DT   29-MAR-1999  (first entry)
XX
DE   Hepatitis G virus clone 3ZHGV-6.
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Qy    340  GTCGCCCTTCAAATGTCTCTGTTGACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAGT  399
           ||||||||||||||||||||||| || ||||||||  | |  ||||||||||||||||||||
Db    301  GTCGCCCTTCAAATGTCTCTGTTGACCAATAGGCGCTAGCCGGCGAGTTGACAAGGACCAGT  360

Qy    400  GGGGCCGGGGGTTATGGGAAGACCCCAAACCCTGCCCTTCCCGGTGGCCGGGAAAT       459
           |||||||||||||  ||  | ||  |||  ||||||| ||||||||||||||||||
Db    361  GGGGGCCGGGGGCT-TGGAGAGGGACTCCAGTCCCGCGCCCTTCCCGGTGGCCGGGAAAT    419

Qy    460  GCATGGGGCCACCCAGCTCGCCGCCGGCCTCGCAGCGCGGGGTAGCCCAAGAATCCTTCGGG  519
           |||||||||||||||||||| | |||||  | ||||||||||  |||||||||||||||||
Db    420  GCATGGGGCCACCCAGCTCCGCGCCGGCCTCGCAGCGCGGGGTAGCCCAAGAATCCTTCGGG  479

Qy    520  TGAGGGCGGTGGCATTTCTCTTTCTATACCATCATGGCAGTCCTTCTCTGCTCCTCCTTCTCG  579
           |||||||||||||||||     ||||||||||||||||||||||||||||||||||||||||
Db    480  TGAGGGCGGTGGCATTTCCTTTTCTATACCATCATGGCAGTCCTTCTCTGCTCCTCCTTCTCG  539

Qy    580  TGGTTGAGGCCGGGGCCATTCTGCCCCGGCCACCACCGTTGTCGAGCGAATGGGCAAT      639
           |||||||||||||||||||||||  | |||||||||||||||||||||||||||||||
Db    540  TGGTTGAGGCCGGGGCCATTCTGCCCCGGCCACCACCGTTGTCGAGCGAATGGGCAAT      599

Qy    640  ATTTCCTCACAAATTGCTGCGTGCCCCGGAAGACATCGGGTTCTGCCTGGGAAGGCGGATGCC  699
           |||||||||||||| |||||||||||||||||||| ||||||||||||| | ||||||||||
Db    600  ATTTCCTCACAAATTGTGCCCTGGGCAACCAGGAGAGCAACCCGGTGTGCCCTTCGTCAACAT  659

Qy    700  TGGTGGCCCTGGGGTGCACGGTTTGCACCGACCGTTGCCCACTGTATCAGGCGGGTT      759
           |||||||||||||||||||||||| |||||  ||||||||||||||||| ||||||||
Db    660  TGGCTGGCCCTGGGGTGCACGATTTGCACTGACCAATGCTGGCCCACTGTATCAGGCGGGTT  719

Qy    760  TGGCTGTGCGGCCTGGCAAGTCCCGGCCCCAGCTCGTTGGGGACTGGGAGCCTGTACG      819
           |||||||||||||||||||||  | ||||  ||| ||||||||||||||||||  ||||
Db    720  TGGCTGTGCGGCCTGGCAAGTCCCGGCCCCAGCTCGTTGGGGACTGGGAGCCTATACG      779

Qy    820  GGGCCCTTCGGTCGGCTTACGTAGCCCGGGATCCTCGGGCTGGTTCTTCGGCGAGGTTTACTCCG  879
           |||||||||||||||||||   |  ||| ||||||||||||||||||||||||  ||||||||||
Db    780  GGCCCCCTTGGTCGGCTCGGCTGGTGTGGGGATCCTCGGGCTGGTGAGGGTGACTGGTTACTCCG  839

Qy    880  GGGTCCTGACAGTTGGGTTGCGTTGGAGGCGCCCGGTCTACCTGATGCCCAACCTGAAGT   939
           |||||||||||| |||| || |||  | |  || ||||| ||||  | ||||||||||||
Db    840  GTGTCCTGACGGTTGGGTTGCGTTGAGCGGCGCCCGGTCTACCTGTATCGGGCCTAACCTGACGT  899

Qy    940  GTGCAGTAGAATGTACGTTAAGTGGGAAGGTTGAGTTTTTGGAGATGGGGAAGTGGGG      999
           |||||||||||||||  | || |||||||||||||||||||||||||||||||||||
Db    900  GTGCAGTAGGTGTGACGTGTAAAGTGGGGAAAGTGAGTTTTTGGAGATGGGGAACAGCTGG      959

Qy   1000  CCTCCAAATTACTGGATTTTGGAATACCTTTGGAAAGTCCCATTTGAATTTTTGGAGAGGAG  1059
           ||| ||||||||||||||||| ||||||||||  || ||||||||  ||| |||||||||||
Db    960  CCTCCAACTACTGGATTCTGGAATACCTTTGGATTTGCTCCCATTTGAATTTGATTTCTGGAGAGGCG  1019

Qy   1060  TGATGAGCTGACCCCTCTGTTGGTTGCGTTTGGTGGCCGACAACGGA            1119
           |||| ||  ||||| |||| |||| |||||||| |||||||||||||
Db   1020  TGATAAGCCTGACCCCTCTGTTGTGCCTGCGTTTGGTGGCCGACAACGGG       1079

Qy   1120  TTGTCATGGTTTTCCTGCTGTGGTGACGATGGCGGGGGATGTTGCAAGGCGCCCCGCCTCCG  1179
           ||||| | |||| |||| | ||||| |||||||| |||||| ||||||  || |||||||||
Db   1080  TTGTCATGGTTCTCCTGCTGTGGTGACGATGGCGGGGGATGTTGCAAGGCGCAGGCGCCCCTCCG  1139

Qy   1180  TTTTGGGGTCCCCGCCCTTGACTACGGGTTGAACGTGGCAGTGCAGTCCTCCTGCCAGGGCTA  1239
           ||| ||||| |||||||||||||||| || |   |  ||||||| |||||||| ||||||||
Db   1140  TTTTGGGGTCACGGGTCCCCGCCCTTGACTACGGGTCGGCAGAAGGTGCCAGTTCCTGCAGGGCCA  1199

Qy   1240  ACGGGTGCGCGTATTCCCACTGGGGAGAGGGTTGGGATCGAGGGAAATGTCACGCTCTTGT   1299
           |||| | |||||  | ||||| |||||||||||| ||| ||  ||  ||  || ||||||||
Db   1200  ACGGTTCGGCGTTTTTGACTGGGGAGAGAGGTTGGGGTGTGTTTGTTGGCCAAGCGTTACGGTTCAGT  1259

Qy   1300  GTGACTGCCCAACGGGTTTTTTCGGCCGCTTTTGTTGCCAGGCGCGTTGGGTGGG       1359
           |||||||||||| ||||||   ||  | |||| | |||||||| || |||||||||
Db   1260  GTGACTGCCCTAACGGGTCCTGGTGTGTTTGCCAAGGCCTTTGCCAAGTCGGCTGGG      1319

Qy   1360  GCGACCCCATCACCCATTGGAGCCACGGCACGACAAAACCAGTGCCCTATCATGCCCCAAT  1419
           |||||| ||| | ||||||  |||||| | | |  ||| |||||||||||||||  |||||
Db   1320  GTGACCCCATCACTATTGGAGCCACCAGGCACGGCAAAATCAGTGGCCCCCTTTCATGCGCCCTTGA  1379

Qy   1420  ATGTCTATGGGTCTGTGTCCGTAACGTCGGTGGGTTTCCGTGTCTCTTGGTTTGCCTCGA  1479
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1380  ATGTCTATGGGTCTGTGTCCGTAACGTCGGTGGGTTTCCGTGTCTCTTGGTTTGCCTCCA  1439
           |||||||||||||||||||| | ||||||||| || |||||||||||||||||||||||
Qy   1480  CCGGCGTCGTTGGATTCGAAGATCGATGTGTGCCAGCT                        1539
           || | ||||| |  | ||  | || |||| ||||  | |  ||||||||||||||||||||
Db   1440  CCAGTGGTCGCGCACTCGAAGATAGATGTGTGGCAGTTTGGAGTTGCCTGCCCACCT     1499

Qy   1540  GCACCATAGCCGCTCTAGGGTCATCGGATCGCACACGGTGTTGACACGTGCCGGGTCTCCGAGTGGG  1599
           |||||||||||||| || ||||| |  |||||  | | |||||| ||||||||||||||||||||||
Db   1500  GCACCATAGCCGCTCTAGGGGTAGCCGTGCACGCGCCGGCGTTGACACGTGCCGGGTCTCCGAGTGGG  1559

Qy   1600  GAGTCCCGTGCTAACGTGTATTCTCGGACCGTCGGCCTCGCCGCTGCTCATGTGACCGTGTGC  1659
           |||||||||||||||| | ||||| |||||| ||||||||||| | ||||| ||||||||||
Db   1560  GAATCCCGTCGTGACGTGGTGTTCCATTCCATCCGGTGGTTGGTTTGTTGTTGTTGGGTGTGA  1619

Qy   1660  GGGACTGCTGCCCGAAACCGGTCGGTTAGATTCCTTTTCATCGTGTGCGCACGGGGC    1719
           |||||||||||||| |||||||| | || |||||  ||||  |||||||| |||||||
Db   1620  GGGACTGCTGCCCGGAACCGGTCGGTTAGTTTCCATTCCATTCGTGTGGTGGTGGGGC  1679

Qy   1720  CTCGGCTGACAAAGACTTGAAGCTGTGCCCTTGCTCAACAGGACAACTCCCTTCACCA  1779
           |||||||||||| | ||||||||||||| |||| ||||||| | || |||||||||||
Db   1680  CTCGGCTGACAAAGGACTTGGAAGCTGTGCCCTTTGTCAATAGGACAACTCCCTTCACCA  1739

Qy   1780  TAAGGGCCCCCTGCCCCAGGAGCAACCCGGTGTGCGTCGCCCGTCGGGTTTG       1839
           | ||||| ||||||||||||||| |||||||||||| | ||||||| |||||||
Db   1740  TTAGGGGCCCCCTGCCCCAGGAGCCAACCGGTGTGCGTCGCCCGTCGGTGTTTTG     1799

Qy   1840  GGTCCTACACCATGACCAAGATCCGGGATCCGGGATTTGGTGAAATGTCCCACCAG  1899
           |||| ||||| |||| |||| ||||| ||| |||| |||||||||||||||||||||
Db   1800  GGTCCTACACGGCCATGCCATCCGGGATCCGAGATCCTGGTGAGTGTCGTCCCACCAG  1859

Qy   1900  CCATAGAGCCTCGACTGGACAACGTTCGGGGTTCTTCCCCGAGTCCCCGCCATTAACAACT  1959
           |||| |||||||| |||  ||||||| || |||| |||  | ||||||| ||||||||||
Db   1860  CCATCGAGCCTTCCCACCGGGACGCGTTTGGGGTTCTTCCCCGAGCGAGTCCTCAACAACT  1919

Qy   1960  GCATGCCGCTAGGCACGGAAGTGTCTCAGGTTCGAGGTCGTGATGGACGCCGAAATCCGGTTGCC  2019
           |||| | ||| |||||||||||||| | ||| | ||||| |||||| ||| ||||||||| |||
Db   1920  GCATCGTCTCTTGGGCACGGAAGTGTCCCAGGTGTCCGAGGCACTTGGGGGGCTGCCTCACGCGGGGGT  1979

Qy   2020  TCTACGAGCCTCTGGTTCGGTGTTCGCAGGTGTTCGAGACGTCGATGGACTGACCAGTTGC  2079
           |||| ||||||| | | |||| |||| |||||||  ||| |   ||| ||| ||||||| |
Db   1980  TCTATGAACCCCCTGGTTTATATACCTGGGCCAGGTGCGAGCTGTATAAGCCCGGTTGTC   2039

Qy   2080  CGGGTACGGACGATGGCGTGTCTCTGTAGACCTGACGGGTTCATACACGTCCAGGGGCACC  2139
           | ||||  |  ||||||| | |  ||  || ||||  ||| ||| |||| | |  ||||||
Db   2040  CGGGGTTTGCATGGTTGGCTCTCTTCGCGGCAGGCCTGATGGTTTATACATGTTCCAGGGTCACT  2099

Qy   2140  TGCAGGAGGTGGATGCGGGCAACTTCATCCCTCCTCCTGGTTGCTTTTGGATTTTG  2199
           |||||||||||| ||| |||||||||| | |||  | |||| |||||||||||||||
Db   2100  TGCAGGAGGTGGATGCGGGCAACTTCATCCCGCCCCCGGTGGTTGGTTGCTTTTGGACTTTG  2159

Qy   2200  TATTTGTCCTCTCTATCTGATGAAGCTGGCTGTGGTTGGTCCGTTGATCTTGC      2259
           ||||||||||| |||||||||||||||| ||||||||||| |||||| ||||||
Db   2160  TATTTGTCCTGTTATACCTGATGAAGCTGGCTGTGGTTGGTCCGTTGATCTTGC     2219

Qy   2260  TTCTGCTGTGGTGGGTGGGTGAACCAGTTGGCCGGCTGTGCGGACGCTG       2319
           |||| ||||||||||| ||| ||||||||||  ||||| ||| ||||| ||
Db   2220  TGCTGTATGGTGGTGGGTGGGTGAACCAGCAGCAGCTGGCAGTCCTGGTGCGGCCG     2279

Qy   2320  CCGTGGCGGGTGAAGTTTTTGTCCGGGATCGTGTTGCCCTTCATCCCCCACTG  2379
           |||| ||||||||||||||    |||| | |||||| | |||||||||||||| 
Db   2280  TGCTGGCAGTGGAGGTGAGGTCTTGCGGGTTGAACCAGCAGCTGGGCCCCGGTCG    2339

Qy   2380  TCAGTATGATACTAGGTCTAGCAAAACGTGTTGTTACTTTCGAGATGGGGCCCTTCAGC  2439
           |||| |||||| ||| |  ||| ||| ||  ||| ||| |   ||  |||| ||||  ||
Db   2340  TCAGTATGATATTGGGTTTGGCAAAACCGGTTACGGTTACTTTAGATGTTGGGACCCCAAC  2399

Qy   2440  GCCTCATGTTCCTCGTTGTGGAAGCTCCGCTGGCCACTTTGA              2499
           |||| || |||| |||||||||||||| | || ||  |||||| |  ||||||||||||||
Db   2400  GCCTGATGTTCCTCGTTGTGGAAGCTTGGCTGCTTGTCGGGGCCCTGCTTCTCCTTGA  2459

Qy   2500  TGGGGATTTCGGCGACCCGCGGGCCCACCTCGTGTGCTGCCGAGTTCTCGTTCGATG  2559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         5760 CCGTCGGAGGTTGGGAGGGGTTGTTGTCAACGGCGGCAGCCTAGTCTTTGACTTCATGGCGG 5819
                ||||| |||||||| ||||| |||||||||||||||||||||||||||| |||| ||||| |||

Qy         5860 GGAAACTATCATCAGAAGATCTGTGTATGCCATCCCCAGTGCTAACCAGTCCGGGGCCAG 5919
                |||||||| |||||| |||||||||||||||||||||||||||||||| |||||||||||||
Db         5820 GGAAACTTCATCAGAAGATCTGTGGTATGCCATCCCGTACTGACCAGCCGACCAGTTACT 5879

Qy         5920 GACTTGCGGGATCGCCCTCCGGTTGCGTGGTTGTACTCAGCTAACAACTCTGGCACTACCA 5979
                | |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         5880 GCCTTGCGGGATCGCTCCGGTTGCGTGGTTTGTATTCAGCTAACAACTCTGGCACTACCA 5939

Qy         5980 CTTGGTTGAACCGTCGCTGCTGACTACATTGCCAAGGTCCTCATGCATCCCTGACAGTTACT 6039
                |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         5940 CTTGGTTGAACCGTCGCTGCTGACTACGTTACCAAGGTCTTCATGTATCCCGGACAGTTACT 5999

Qy         6040 TTCAGCAGGCCGATTACTGTGACAAGGTCTCAGCTGTCCGACCTTGAGCCTCACTC 6099
                |||||| | ||||| || ||||||||||||||||||||||||||||| |||||||||||
Db         6000 TTCAGCAAGTGACTATTGCCGACAAGGTCTCAACAGGAGCCTAAGGTCGCCTGAGCCTCACCC 6059

Qy         6100 GCACCCTGGTTGCCCTGGTCAACAGGAGCCTAAGGTGGATGAGGTTCAGGTGGGGTACG 6159
                ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db         6060 GCACAGTGGTTGCCCTGGTCAACAGGAGCCTAAGGTGGATGAGGTACAGGTGGGGTATG 6119

Qy         6160 TCTGGGACTTGTGGGAGTGGATCATGCGTCCAAGTGCCAGACTTCGGG 6219
                || ||||||||| ||||||||||| |||||||||||||||||||||||||
Db         6120 TCTGGGACCTGTGGGAGTGGATCATCGCCGTGTCATGGCCCAGACTCAGGG 6179

Qy         6220 CCCTCTGCCCCGTGGTCATTACCCTTATGGCACTCGGGGAGGGTGGTCCGGAGAAT 6279
                |||||||||||||||||| ||||||||| |||||||||||| |||||||||| | |||
Db         6180 CCCTCTGCCCCGTGGTCATTACCCTTGTGTCATTACCCTTGTGTCGTTACGGTGAACATGGTGGTCCGGGAAT 6239

Qy         6280 GGTTGTTGGACGGCCATGTGTTGAGAGTCGTTGTCTTTGTGGTTGCGTGATCACCGGTGATG 6339
                ||||| |||||||||||||| ||||||||| ||||||||||| |||| |||||||||||||
Db         6240 GGTTGCTTGACGGTCATGTGTTGAGAGTCATGTTGGTGGCTCGGCTCGTGCGCGATCACTGGTGACG 6299

Qy         6340 TTTGAATGGGCAACTCAAAGATCCAGTTTACTCTACCAAGCTGTGCAGGCATTATTGGA 6399
                || ||||||||||||||||||| |||| ||||||||||||||||||||||||||||||||
Db         6300 TTCTGAATGGGCAACTCAAAGAACCAGTTTACTCTACCAAGCTGTGCCGGCACTATTGGA 6359

Qy         6400 TGGGGACAGTCCTGTGAACATGCTGGGCTATGGCGAGACGTCGCCCTTGCTCGCCCAG 6459
                |||||| |||||||||||||| |||||||||||| ||||||||||||||||||||||||
Db         6360 TGGGGACGTCCCTGTGAACATGCTGGGCTTACGGTGGTGAAACGTCGCCTCTCCTGGCCTCCG 6419

Qy         6460 ACACCCCGAAGGTGGTACCATTCGGGACGTCTGGGCTGAGGTGGTTGGTGACCCCTA 6519
                ||||||| |||||||||||||||||||||||| ||||||||||||||||| |||||||||
Db         6420 ACACCCCGAAGGTTGTCCCCTTCGGGACGTCTGGCCTGGGCTGGGCTGTGGTGACCACTA 6479

Qy         6520 CCCACCTTGTGATCAGGGCGAACATCCGCCTACAAAACTGCTGCGCAAATCCTGTGG 6579
                |||||||| ||| |||||||| ||||| |||||||| || ||||||||||||||||||||
Db         6480 CCCACGTTGGTAATCAGGAGAACAACTCCGCCTATAAGCTGTCGCCGCACTATCCTATCGG 6539

Qy         6580 CTGCTGTTGCTGAGCCTGTTGCTGAGCCCGTCTCATGGGACGGCGGACCGCGGC 6639
                ||| || ||||| ||||||| |||||||||||||||||||||||||||||||||||
Db         6540 CTGCTGTAGCTGAGCCCGTTGCTGAGCCCGTCTCATGGGACGGCGGACCGCGACCGCTC 6599

Qy         6640 GAGCGCCTGCCATGGTCTATGGCCCTGGGCAAAGTGTCCACCATTGACGGGGAACGCTACA 6699
                ||| ||||||||||| ||||||||||||||| |||||||||||| |||||||||| |||||
Db         6600 GTGCGCCTGCCATGGTCTATGGCCCTGGGCAAAGTGTTACCATTGACGGGGAGCGCGTACA 6659

Qy         6700 CCCTTCCGCATCAACTGCGGCTTAGGAATGTGGCGCCCTCTGAGGTGTCATCCGAGGTGT 6759
                |||| ||| |||| || ||||| || |||||||| |||||| |||||||||| ||||||||
Db         6660 CCCTGCCTCATCAACTGAGGCTCAGGAATGTGGCGCCCTCTCGAGGTTTCATCCGAGGTGT 6719

Qy         6760 CCATTGACATTGGGACCGGAGGCCCGTCTGACTGAGGCCGCGACCTGCCGCCGGG 6819
                ||| |||||||||||||||||||||||| || |||||| |||||||||| |||||||
Db         6720 CCATTGACATTGGGACGACGGAGACTCGAGGCCGATCGCGAGGCCGACGCGCCGCCG 6779

Qy         6820 GGCTGCAGCCCTTCAGGCTATCGCAGGTCTATCGAGAATGCTGCGAGAATTCTTGACACCTCACATAGATG 6879
                ||||| |||||| ||||| ||||| |||||| || |||||||| || |||||||||||||||||
Db         6780 CGGCTGCTGCTCTCCAAGCGATCTGCTGCGAGGAGAATGCTGCGACACCGCACACCATTGATG 6839

Qy         6880 TCATCATGGAAGATTGCAGTGACTACCACCCTCTCTTCTTGTGTGGAGTAGCCGAGAGATGCCTGTGT 6939
                |||||||||| || |||||||||||||||||||||||||||| |||||| |||||||||||||||||
Db
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Qy         4720 CCGGTGTGACCTGGTACGGAATGGAAGTGAACCTGACCTGACAGCAGCAAACCTACTGAGACTTTACG 4779
                | ||||| ||||||||||||||||||||||||| |||||| ||||||||||||||||||||||||||||
Db         4680 CTGGAGTGACCTGTACGGAATGGAAGTGAACCTGACCTGACAGCTAACTACTACTGAGACTTTACG 4739

Qy         4780 ACAACTGCCCTTCACACCGGACGCCGCAGCTCGCAGCATTGGGGAGCCCGGTGTGTTCTTTT 4839
                ||||||||| ||||||| ||||||||||||||||||||||| ||||| | |||||||||| |||
Db         4740 ACGACTGCCCTTCACACCGGACGCCGCAGCTCGCGGCTGCTGATATCCGATGATCGG 4799

Qy         4840 CGGGGCGTTGCCCCCGTTGAGGATGCATCCGATGTTAGCTGGCAAAAGTTCGCCGCGTCA 4899
                | ||||||||| |||||||||||| ||||| |||| |||| ||||||||||||||||||||
Db         4800 CTGGGCGTTCGCCCCATTGAGGATGCACCCTGATGTCAGCTGGCAAAAGTTCGCCGCGTCA 4859

Qy         4900 ACTGGCCCTTCCTCGTGTTCAGCGGACCATGTGCCGGACAACACTGTCTCCCGGCC 4959
                |||||||| ||||||| ||||||||||||||||||||| |||||||||||||||||||||
Db         4860 ACTTGGCCCCTTCGGTGTTCAGCGGACCATGTGCCGGACAACACTGTCTCCCGGCC 4919

Qy         4960 CATCGGATGACCCCAGTGGCCAGGTCTGAAGGGCCCGAATCCTGTCCCACTCCTGCTGA 5019
                |||||||||||||||| |||||||||||||||||||||||||||| ||||||||||||||
Db         4920 CATCGGATGACCCCCAATGGGCCCAAATCCTGTGCCCCAAATCCTGTCCCACTCCTGCTGA 4979

Qy         5020 GGTGGGGCAATGATTACCATCTAAAGTGCGGCGCCCATCACATCGTGGACGACCTGGTCC 5079
                |||||||||||||||||||||||||||| | |||| ||||| ||||||||||||||||||
Db         4980 GGTGGGGCAATGATTACCATCTAAAGTGGCGGCCACCAGTGGACGACCTGGTCC 5039

Qy         5080 GTAGGCTCCGGGTGTCGCAGGGTTACGTCCGCGATGCGGGACCCATCTTGATGGTGG 5139
                | |||| |||||||| ||||| |||||||||||| |||||||||||| |||||||||||
Db         5040 GGAGACTCCGTGTCGGTCAGGGTTACGTCGGCCGATCTTGATGATCG 5099

Qy         5140 GCCTCGCTATTGCCCCGTGAGGGGCATGAATCTATGCGTCATACACCGGTCTCTCGTGTGGTTA 5199
                ||||||||||||| |||||| || |||||||| || ||||||||||||||||| |||||||
Db         5100 GTCTAGCTATCGCGGGGGAATGATCTACGCGTCGTACACCGGTCGCGTTAGTGGTGGTGACTA 5159

Qy         5200 CAGATGCTGGGATGTGAAGGGGTGGCAGCCCCCCTTATGGCCACCAGGAGACCACCAGCC 5259
                |||||||||||||||||||||||||||| || ||||||||| ||||||||| ||||||||
Db         5160 CAGACTGGGATGTGAAGGGGTGGCAGCCTGGCCATGCCATCGAGACCAGGAGACCACCAGCC 5219

Qy         5260 CCCAGCCGGTGTGCAGTCCCCCGGTAGGACCATCGGCGCGGGGAGAGTCTCGCGCCAT 5319
                ||||||||| ||||||||| |||| |||| ||||| || |||| ||||||||||||||||
Db         5220 CTCAGCCGGTGTGTCAGTCCTCCGGTAGACCATCGGCGCGGGGGTGAATCAGCACCAT 5279

Qy         5320 CGGATGCCAACAGTGACACAGTGCGGATGCGGCCATCCAGGTTGGCGATTGGTCAG 5379
                | |||||||||||||| |||||| ||||| ||||||||||||||||| ||||| |||||
Db         5280 CGGATGCCAGCTGGACAGTGCGGATGCGGCCATCCAGGTTGGCGATTGGACTA 5339

Qy         5380 TCATGACCCTGTCGATCGGGGAAGTGCTGTCCTTGCGCTCCTTCAGGGCCTAAGACGGCCGGAGGCCT 5439
                ||||||||||||| ||||||| |||||| ||||| ||||||||| ||| |||||||||||||||||||
Db         5340 TCATGACTTCTGTCGATCGGAGAAGTGTTGTCCTTGTTCCTGCTCAGGGCTAAGACGGCCGGAGGCCT 5399

Qy         5440 ACGCAGCTACCCAAGTGCTTGCTGGCGTTGGCGTTCGCGAGGCAACGCGGGCCGTCCCCACTG 5499
                || |||||| ||||||||||| || || ||||||||||||||| |||||||| ||||||||||
Db         5400 ACACAGCAGCCACCAAGTGCTTGGTGGGTTGGCGTTGGCTATTACGGGGACCCGTTCCCACTG 5459

Qy         5500 TTTCAATTGTTGACAAGCTCTTCCGCGGCGCTGGCGCGGGTGTAGGCCATTGCCACA 5559
                ||| ||||| ||||||||| | |||| ||||||||| || ||||||||||||||| |||
Db         5460 TATCCATTGTTGACAAGCTCTTCCGCGGCGCTGGCGCGGTGTGTGGCCATTGCCACA 5519

Qy         5560 GTGTAATAGCTGCGGCAGTGCGGCAGTCTCAGGAGGGCTTCAGGGCTGCTG 5619
                || | |||| || |||||| ||||||||| ||||| |||| ||| |||| |||
Db         5520 ACGTGATTGCTGCGGCGGCGGCTACGGGGGCTTCAAAGAGCCCCGGCCCGTTGGCAGCCG 5579

Qy         5620 CGCGCTTCCTACCTCATGGGTTGGGGCGTCGGAGGCAACGCGCAAACCCGCTTAGCCTCCG 5679
                ||||| || | |||||||||| ||||| ||||| ||||| || |||||||||||| |||||
Db         5580 CGGCTTCCTCGATGATGGGGCCCCGTGATGGGGCGCCAACCTCAGACGCGTCCGCATCTG 5639

Qy         5680 CTCTCCTACTAGGGGGCCCGTCTGGGCGGCACGCGTCTGTGGGTTAACCATGG 5739
                | |||||||| ||||||| || | ||||||||||| |||| |||||||||| |||
Db         5640 CCCTCCTATTGGGGCCCTGTGTCGTGGGCCTTGTCGTCTCCTGTTGGGCCTTGACCATGG 5699

Qy         5740 CGGGGCCGGTTCATGGGAAGTGCTAGCGTCTC ||| || ||||||||||| ||||||||||||||||||||||||||||||||||||||||| 5799
Db         5700 CAGGTGCGGTTCATGGGGCGCCAGTGTTGCTGCCCAGTGTGCTGTGAATGCGGAGGATGTGGCGG 5759

Qy         5800 CCGTGGGGGCGGGGCTGGGAGGGCGTGGTGAATCGGCGGCCTTGTCTGCTTCGAATGGCGG
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Db   6840 CCATCATGGAGGACTGCAGTACACCCTCTCTTTGTGGTAGTAGCCGAGAGATGCCTGTAT 6899

Qy   6940 GGGGAGAAGACATACCCCGCACTCCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCC 6999
           ||||||||||||| ||||| |||||||||||||||||||||||||||||||||||||||
Db   6900 GGGGAGAAGACATCCCCCGTACTCCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCT 6959

Qy   7000 CAGATGAGAAGACCCCGTCGGTGTCTTCCTCGCAGGAGGATACCCCGTCTTCTGACTCAT 7059
           ||||||||||||||||||||||||| ||||||||||||||||||||||| ||||||||||
Db   6960 CAGATGAGAAGACCCCGTCGGTGTCCTCCTCGCAGGAGGATACCCCGTCCTCTGACTCAT 7019

Qy   7060 TCGAGGTCATCCAAGAGTCCGAGACAGCCGAAGGGGAGGAAAGCGTCTTCAACGTGGCTC 7119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7020 TCGAGGTCATCCAAGAGTCCGAGACAGCCGAAGGGGAGGAAAGCGTCTTCAACGTGGCTC 7079

Qy   7120 TTTCCGTACTAAAAGCCTTGTTTCCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGA 7179
           |||||||| || |||||| |||||||||||||| || || || ||||||||||| ||||
Db   7080 TTTCCGTATTAGAAGCCTCATTTCCACAGAGCGACGCGACCAGGAAGCTTACCGTCAAGA 7139

Qy   7180 TGTCATGCTGTGTTGAGAAGAGCGTAACACGCTTCTTTTCATTGGGATTGACGGTCGCTG 7239
           |||| ||||| ||||| |||||||| || ||||| || |||||||| |||||||| ||||
Db   7140 TGTCGTGCTGCGTTGAAAAGAGCGTCACGCGCTTTTTCTCATTGGGGTTGACGGTGGCTG 7199

Qy   7240 ACGTGGCAAGCCTGTGTGAGATGGAAATCCAGAACCATACAGCCTATTGTGACAAGGTGC 7299
           | || || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7200 ATGTTGCTAGCCTGTGTGAGATGGAAATCCAGAACCATACAGCCTATTGTGACAAGGTGC 7259

Qy   7300 GCACTCCGCTTGAATTGCAGGTTGGGTGCTTGGTGGGCAATGAACTTACCTTTGAATGTG 7359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7260 GCACTCCGCTTGAATTGCAGGTTGGGTGCTTGGTGGGCAATGAACTTACCTTTGAATGTG 7319

Qy   7360 ACAAGTGTGAGGCTAGGCAAGAGACCTTGGCTTCCTTCTCTTACATTTGGTCTGGGGTGC 7419
           |||||||||||||||||||||| |||||||| ||||||||||||||||||||||| ||||
Db   7320 ACAAGTGTGAGGCTAGGCAAGAAACCTTGGCCTCCTTCTCTTACATTTGGTCTGGAGTGC 7379

Qy   7420 CACTGACGAGGGCCACTCCGGCCAAGCCCCCTGTGGTGAGGCCGGTTGGCTCCTTGCTGG 7479
           | ||||| |||||||| ||||||||||| || |||||||||||||||||||| || | |
Db   7380 CGCTGACTAGGGCCACGCCGGCCAAGCCTCCCGTGGTGAGGCCGGTTGGCTCTTTATTAG 7439

Qy   7480 TGGCCGACACCACCAAGGTGTATGTCACCAACCCGGACAATGTTGGGAGAAGAGTTGACA 7539
           |||||||||| || ||||||||||| ||||| || |||||||| || | || || ||||
Db   7440 TGGCCGACACTACTAAGGTGTATGTTACCAATCCAGACAATGTGGGACGGAGGGTGGACA 7499

Qy   7540 AGGTTACCTTCTGGCGTGCCCCTAGGGTTCATGACAAATTCCTCGTGGACTCCATAGAGC 7599
           |||| |||||||||||||| |||||||||||||| || | |||||||||||| || ||||
Db   7500 AGGTGACCTTCTGGCGTGCTCCTAGGGTTCATGATAAGTACCTCGTGGACTCTATTGAGC 7559

Qy   7600 GCGCTAAGAGGGCAGCTCAAGCCTGCCTAAGCATGGGTTACACTTATGAGGAGGCAATAA 7659
           ||||||||||||| |||||||||||||||||||||||||||||||||||||| |||||||
Db   7560 GCGCTAAGAGGGCCGCTCAAGCCTGCCTAAGCATGGGTTACACTTATGAGGAAGCAATAA 7619

Qy   7660 GGACTGTAAGGCCACATGCTGCCATGGGCTGGGGATCTAAGGTGTCGGTCAAGGACCTCG 7719
           ||||||||||||||||||||||||||||||||||||||||||||||||| |||||| | |
Db   7620 GGACTGTAAGGCCACATGCTGCCATGGGCTGGGGATCTAAGGTGTCGGTTAAGGACTTAG 7679

Qy   7720 CCACCCCTGCGGGGAAGATGGCTGTCCATGACCGGCTCCAGGAGATACTTGAAGGGACGC 7779
           ||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||| |
Db   7680 CCACCCCCGCGGGGAAGATGGCCGTCCATGACCGGCTCCAGGAGATACTTGAAGGGACTC 7739

Qy   7780 CAGTCCCCTTTACTCTTACTGTGAAAAAGGAAGTGTTCTTCAAAGACCGAAAGGAAGAGA 7839
           | ||||||||||||||||||||||||||||| ||||||||||||||||| ||||| |||
Db   7740 CGGTCCCCTTTACTCTTACTGTGAAAAAGGAGGTGTTCTTCAAAGACCGGAAGGAGGAGG 7799

Qy   7840 AGGCCCCCCGCCTCATTGTGTTCCCCCCCCTGGACTTCCGGATAGCTGAAAAGCTTATTC 7899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   7800 AGGCCCCCCGCCTCATTGTGTTCCCCCCCCTGGACTTCCGGATAGCTGAAAAGCTCATCT 7859

Qy   7900 TGGGAGACCCTGGACGGGTAGCCAAGGCGGTGTTGGGGGGGGCCTACGCCTTCCAGTACA 7959
           |||||||||| | ||||||||||||||||||||||||||||||||||||||||||||||
Db   7860 TGGGAGACCCAGACCGGGTAGCCAAGGCGGTGTTGGGGGGGGCCTACGCCTTCCAGTACA 7919

Qy   7960 CCCCAAATCAGCGAATTAGGGAGATGCTCAAACTGTGGGAATCAAAGAAGACACCATGCG 8019
           |||||||||||||| ||| |||||||||||| || ||||| || |||||||| || ||||
Db   7920 CCCCAAATCAGCGAGTTAAGGAGATGCTCAAGCTATGGGAGTCTAAGAAGACCCCTTGCG 7979

Qy   8020 CCATCTGTGTGGACGCCACATGCTTCGACAGTAGCATAACTGAAGAGGACGTGGCGCTGG 8079
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||| |||
Db   7980 CCATCTGTGTGGACGCCACCTGCTTCGACAGTAGCATAACTGAAGAGGACGTGGCTTTGG 8039

Qy   8080 AGACAGAGCTTTATGCCCTGGCTTCAGACCATCCAGAATGGGTGCGTGCCCTGGGGAAAT 8139
           |||||||||| || || ||||| || |||||||||||||||||||| || || |||||||
Db   8040 AGACAGAGCTGTACGCTCTGGCCTCTGACCATCCAGAATGGGTGCGGGCACTTGGGAAAT 8099

Qy   8140 ACTATGCCTCTGGCACAATGGTAACCCCCGAGGGGGTGCCAGTGGGTGAGAGGTATTGTA 8199
           |||||||||| ||||| ||||| ||||| ||||| || |||||||| || |||||||||||||| |
Db   8100 ACTATGCCTCAGGCACCATGGTCACCCCGGAAGGGGTGCCCGTCGGTGAGAGGTATTGCA 8159

Qy   8200 GATCCTCAGGGGTCTTGACCACCAGTGCGAGCAACTGCTTGACTTGCTATATCAAGGTGA 8259
           ||||||| || ||| | || || || ||||||||||||||||| ||||| ||||||||||
Db   8160 GATCCTCGGGTGTCCTAACAACTAGCGCGAGCAACTGCTTGACCTGCTACATCAAGGTGA 8219

Qy   8260 AAGCCGCCTGTGAGAGGGTGGGGCTGAAAAATGTCTCGCTCCTCATCGCTGGCGATGACT 8319
           |||||||||||||||||||||||||||| |||||||| || ||||| || ||||||||||
Db   8220 AAGCCGCCTGTGAGAGGGTGGGGCTGAAGAATGTCTCTCTTCTCATAGCCGGCGATGACT 8279

Qy   8320 GTTTGATCATATGCGAACGGCCTGTGTGCGATCCTAGCGACGCTTTGGGCAGAGCCCTGG 8379
           | ||||||||||| || ||||| |||||||| || ||||||||||||||||||||||| |
Db   8280 GCTTGATCATATGTGAGCGGCCAGTGTGCGACCCAAGCGACGCTTTGGGCAGAGCCCTAG 8339

Qy   8380 CGAGCTACGGGTACGCATGCGAGCCTTCGTATCATGCATCACTGGACACGGCCCCCTTCT 8439
           ||||||| |||||||| |||||||| || ||||||||||| ||||||||||||||||||
Db   8340 CGAGCTATGGGTACGCGTGCGAGCCCTCATATCATGCATCCTTGGACACGGCCCCCTTCT 8399

Qy   8440 GCTCCACTTGGCTAGCTGAGTGCAATGCAGATGGGAAACGCCATTTCTTCCTGACCACGG 8499
           ||||||||||||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db   8400 GCTCCACTTGGCTTGCTGAGTGCAATGCAGATGGGAAGCGCCATTTCTTCCTGACCACGG 8459

Qy   8500 ACTTTCGGAGGCCCCTCGCTCGCATGTCGAGCGAGTACAGTGACCCAATGGCTTCGGCCA 8559
           |||| |||||||| ||||||||||||||||| ||||| |||||||| ||||||||||| |
Db   8460 ACTTCCGGAGGCCGCTCGCTCGCATGTCGAGTGAGTATAGTGACCCGATGGCTTCGGCGA 8519

Qy   8560 TCGGTTACATCCTCCTATACCCTTGGCATCCTATCACACGGTGGGTCATCATCCCTCACG 8619
           |||||||||||||||| || |||||||| || |||||||||||||||||||||||||| |
Db   8520 TCGGTTACATCCTCCTTTATCCTTGGCACCCCATCACACGGTGGGTCATCATCCCTCATG 8579

Qy   8620 TGCTCACCTGCGCGTTTAGGGGTGGTGGCACACCGTCTGATCCTGTGTGGTGCCAGGTAC 8679
           |||| || ||||| || |||||||| ||||||||||||||||| || |||||||||||||
Db   8580 TGCTAACGTGCGCATTCAGGGGTGGAGGCACACCGTCTGATCCGGTTTGGTGCCAGGTAC 8639

Qy   8680 ATGGTAATTACTACAAGTTTCCACTGGACAAACTGCCTAACATCATCGTGGCCCTCCACG 8739
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8640 ATGGTAACTACTACAAGTTTCCACTGGACAAACTGCCTAACATCATCGTGGCCCTCCACG 8699

Qy   8740 GACCAGCAGCGTTGAGGGTTACCGCAGACACAACTAAGACAAAAATGGAGGCTGGCAAGG 8799
           ||||||||||||||||||||||||||||||||||||| ||||| ||||||||||| ||||
Db   8700 GACCAGCAGCGTTGAGGGTTACCGCAGACACAACTAAAACAAAGATGGAGGCTGGTAAGG 8759

Qy   8800 TGCTGAGCGACCTCAAGCTCCCTGGCCTAGCAGTCCACCGGAAGAAGGCCGGGGCATTGC 8859
           | |||||||||||||||||||||||| ||||||||||||| |||||||||||||| ||||
Db   8760 TTCTGAGCGACCTCAAGCTCCCTGGCTTAGCAGTCCACCGAAAGAAGGCCGGGGCGTTGC 8819

Qy   8860 GAACGCGTATGCTCCGGTCGCGCGGTTGGGCTGAGTTGGCTAGGGGGCTGTTGTGGCGTC 8919
           |||| || |||||||| ||||||||||||||||||||||||||||| ||||||||| ||
Db   8820 GAACACGCATGCTCCGCTCGCGCGGTTGGGCTGAGTTGGCTAGGGGCTTGTTGTGGCATC 8879

Qy   8920 CAGGCCTGCGGCTTCCCCCTCCGGAGATTGCTGGTATCCCCGGGGGTTTCCCCCTTTCCC 8979
           ||||||| |||||||| || || ||||||||||||||||| ||||||||||| || ||||
Db   8880 CAGGCCTACGGCTTCCTCCCCCTGAGATTGCTGGTATCCCGGGGGGTTTCCCTCTCTCCC 8939

Qy   8980 CCCCCTATATGGGGGTGGTTCATCAATTGGATTTCACAAGCCAGAGGAGTCGCTGGCGGT 9039
           ||||||||||||||||||| || ||||||||||| |||||||||||||||||||||||||
Db   8940 CCCCCTATATGGGGGTGGTACACCAATTGGATTTTACAAGCCAGAGGAGTCGCTGGCGGT 8999

Qy   9040 GGTTGGGGTTCTTAGCCCTGCTCATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTT 9099
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9000 GGTTGGGGTTCTTAGCCCTGCTCATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTT 9059
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CC   HGV clones (such as this sequence). The protein expressed from the
CC   vector, can then be used to create antibodies specifically reactive with
CC   HGV or a HGV epitope. The antibodies can be used to detect the presence
CC   of HGV in a sample, as with the probe sequences. The purified protein
XX   sequence can also be used in vaccines.
SQ   Sequence 9327 BP; 1682 A; 2531 C; 2985 G; 2129 T; 0 other;

            Query Match   83.9%; Score 7884; DB 17; Length 9327;
            Best Local Similarity   90.4%; Pred. NO. 0;
            Matches 8432; Conservative   0; Mismatches 895; Indels 1; Gaps   1;

Qy   40   GCAAGCCCCATAAACCACGCCTATCTAAGTAGACGCAATGACTCGGCGCCGCGACTCAG   99
            |||||||| ||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   1   GCAAGCCCCAGAAACCGACCGCCTATCTAAGTAGACGCAATGACTCGGCGCCGCGACTCAG   60

Qy   100   ACCGGCCAAAAGGTGGTGACAGGGTTGGTAGGTCGTAAATCCCGGTCAT   159
            || ||||||||||||||||||||||||| | |||||||||||||||||||
Db   61   ACCGGCCAAAAGGTGTGGATGGGTGGTGACAGGGTTGGTAGGTCGTAAATCCCGGTCAC   120

Qy   160   CCTGGTAGCCACTATAGGTTGGTGTTCTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTGCGGC   219
            |||||||||||||||||||||||| ||| ||||||||||||||||| || ||||||||||||
Db   121   CCTGGTAGCCACTATAGGTTGGTGTTCTTAAGAGAAGGTTAAGATTCCTCTGTGCCTGCGGC   180

Qy   220   GAGACCGGCGACGGTCCACAGGTGCTGGCCCTACCGGTGTGAATAGGGCCGACGTCAG   279
            |||||||||||||||||||||||||||||| ||||||||||||||| |||||||||||||
Db   181   GAGACCGGCGACGGTCCACAGGTGTTGGCCCTACCGGTGGGAATAAGGGCCGACGTCAG   240

Qy   280   GCTCGTCGTTAAACCGAGCCCGGCCAAACGACGCCCACGTACGGTCCAC   339
            |||||||||||||||||||| | |||||||||||||||||||||||||||
Db   241   GCTCGTCGTTAAACCGAGCCCGGCCAAACGACGCCCACGTACGGTCCAC   300

Qy   340   GTCGCCCTTCAATGCTCTCTTGACCAATAGGTTTATCCGGCCGAGTTGACAAGGACCAGT   399
            |||||||||||||||||||||||||||||||||| | |||||||||||||||||||||||
Db   301   GTCGCCCTTCAATGTCTCTCTTGACCAATAGGCGTAGCCGGCCGAGTTGACAAGGACCAGT   360

Qy   400   GGGGGCGGGGTTATGGGAAGGACCCCAAACCCTGCCCTTCCCGTGGCCGCGGGAAAT   459
            ||||||||||||| |||| | |||| || ||||||||||||||||||||||||||||||
Db   361   GGGGGCGGGGGCT-TGGAGAGGGACTCCAAGTCCCGGCCCGCGGGTAGCCCAAGAATCCTTCGGG   419

Qy   460   GCATGGGCCACCCAGCTCCGCGGCGGCCCTGCAGCCGGGGTAGCCCAAGAATCCTTCGGG   519
            |||||||||||||||||||||||||||||| || || ||||||||||||||||||||||||
Db   420   GCATGGGCCACCCAGCTCCGCGGCGGCCCTCAGCCGGGGTAGCCCAAGAATCCTTCGGG   479

Qy   520   TGAGGGCGGTGGCATTCCTTTTCTATACCATCATGGCAGTCCTTCTGCGCTTCCTCCTCTCG   579
            |||||||||||||||||||| ||| ||||||||||||| ||||||||||||||||||||||
Db   480   TGAGGGCGGTGGCATTTCCTTTTCTATACCATCATGGCAGTCCTTCTGCGCTTCCTCCTCTCG   539

Qy   580   TGGTTGAGGGCGGGGCCATTCCGGGCCACCCAGCGCTTGTCGAGCGAATGGGCAAT   639
            |||||||||||||||||||||||||||||| || ||||||||||||||||||||||||
Db   540   TGGTTGAGGGCGGGGCCATTCCGGGCCACCCACACGTGTGGGGGAGCGAATGGGCAAT   599

Qy   640   ATTTCCTCACAAATTGCTGTGCCCGGAAGACATCGGGTTCTCGCCTGGAAGGCGGATGCC   699
            ||||||||||||||||||||||||||||| |||||||||||||||||| |||||||||||
Db   600   ATTTCCTCACAAATTGTTGTGCCCGGAGGACATCGGGTTCTCGCCTGGAGGGTGGATGCC   659

Qy   700   TGGTGGCCCTGGGGGTGCACGGTTGCACGGCCACCGTTGCTGCTGGCCACTGTATCAGGCGGGTT   759
            ||||||||||||||||||||||||| | ||| || |||||||||||||||||||||||||||
Db   660   TGGTGGCCCTGGGGGTGCACGATTTGCACTGACCAATGCTGCTGGCCACTGTATCAGGCGGGTT   719

Qy   760   TGGCTGTGCGCGGCCTGGCCAAGTCCGCGGCCCCAGCTCCTTGGGGAACTGGGAGCCTGTACG   819
            ||||||||||||||||||||||||||||| || ||| | |||||||||||||||||||||||
Db   720   TGGCTGTGCGCGGCCTGGCCAAGTCCGCGGCCCCAACTGGTGGGGGAGCTGGTAGCCTATACG   779

Qy   820   GGGCCCTTGTCTGGTCTCGGCTTACGTAGCCCGGATCCGGATCCTGGGCGGTTCGGGCGAGGTTACTCCG   879
            |||| ||||| || ||||||||||||| ||||| ||| ||| ||||||||||||||||||||||||||
Db   780   GGGCCCCGTCGTCGGCTCGGCCCCATGTGGCTGGGATCGCTGACATCCCGGTGACCGGTGAGGTGACTCGG   839

Qy   880   GGGTCCTGCGACAGTTGGTGTTGCGTTGAGGGCCGCCGGGTCTACCTGACTGCCCAACCTGAAGT   939
            | ||||||| || ||| || ||| ||||||| |||||||||||||||||||||||||||||||||
Db   840   GTGTCCTAACGGTGGGAGTCCGGTTGACGCCCGGATCCGATCTACCCGGTGCCTAACCTGACGT   899

Qy   940   GTGCAGTAGAATGTGACGTTAAGTGGGAAGTGAGTTTGGAGATGGACTGAGCAGTTGG   999
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Qy   9100   GCGGCAAGGTCCGTGACTGATCATCACTGGAGGAGGTTCCCGGCCTCCCGCCCAGGG   9159
            |||| ||||| |||||||||||| |||| ||||||||||||||||||||||||||||||
Db   9060   GCGGCGAGGTCGTCGTGACTGATCGTCACCGGAGGAGGTTCCCGCCCTCCCGCCCCAGGG   9119

Qy   9160   GTCTCCCCGCTGGGTAAAAAGGGCCCGCCTTGGGAGGCATGGTGGTTACTAACCCCTG   9219
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   9120   GTCTCCCCGCTGGGTAAAAAGGGCCCGCCTTGGGAGGCATGGTGGTTACTAACCCCTG   9179

Qy   9220   GCAGGGTCAAAGCCTGATGGTGCTAATGCACTTCGGTCGGCGGTCGCTAACTTTA   9279
            ||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   9180   GCAGGGTTAAAGCCTGATGGTGCTAATGCACTTCGCCACTTCGGTCGGCGGTCGCTAACTTTA   9239

Qy   9280   TAGCGTAATCCGTGACTACGGGCTGTCTCGCAGAGCCCTCCCCGGTGCACAGTGCAC   9339
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   9240   TAGCGTAATCCGTGACTACGGGCTGTCTCGCAGAGCCCTCCCCGGTGCACAGTGCAC   9299

Qy   9340   TGTGATCTGAAGGGGTGCACCCCGGTAA   9367
            || |||||||||||||||||||||||| |
Db   9300   TGAGATCTGAAGGGGTGCACCCCGGGAA   9327
```

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RESULT 15
AAT08958
ID     AAT08958 standard; cDNA; 9327 BP.
XX
AC     AAT08958;
XX
DT     20-AUG-1996 (first entry)
XX
DE     Hepatitis G virus clone 3Z-HGV94-6.
XX
KW     Hepatitis G virus; HGV; Flaviviridae; viral capsid protein; probe;
KW     viral envelope protein; non-structural protein; RNA helicase; antibody;
KW     chymotrypsin like serine protease; RNA dependent RNA polymerase; clone;
KW     HGV genome; ss.
XX
OS     Synthetic.
XX
PN     WO953229l-A2.
XX
PD     30-NOV-1995.
XX
PF     19-MAY-1995;  95WO-US06l69.
XX
PR     15-FEB-1995;  95US-0389886.
PR     20-MAY-1994;  94US-0246985.
PR     03-AUG-1994;  94US-0285543.
PR     03-AUG-1994;  94US-0285558.
PR     26-OCT-1994;  94US-0329729.
PR     23-NOV-1994;  94US-0344271.
PR     16-DEC-1994;  94US-0357509.
PR     03-AUG-1994;  94US-0285561.
XX
PA     (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI     Fry KE,  Kim JP,  Linnen JM,  Wages J,  Young LM;
XX
DR     WPI; 1996-049299/05.
XX
PT     Hepatitis G virus isolates, polypeptide(s) and related nucleic acids
PT     - useful for antibody prodn., vaccines and screening sera
XX
PS     Example 18; Page 389-396; 452pp; English.
XX
CC     This sequence represents the hepatitis G virus (HGV) clone 3Z-HGV94-6.
CC     This sequence was constructed from the sequences amplified by the
CC     primers shown in AAT08952-T08957. The amplified fragments were digested
CC     and cloned into a pGEM32 vector to give this sequence. The full length
CC     HGV sequence (see AAT08812) can be used to create probes for the HGV
CC     genome, giving a means of detecting HGV in a sample (especially a serum).
CC     The full length genomic sequence (or fragments of it) can be cloned into
CC     a vector, which can be used to express the encoded protein in a host cell
CC     for isolation and purification. The fragments can also be used to create
```

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Db        |||||||  ||||||  |||||||||||||||||||||||||||||||| |||
          GTGCAGTCGCGTGTGAGTTAAAGTGGAAAGTGAGTTTTGGAGATGGACTGAACAGCTGG  959

Qy  1000  CCTCCAATTACTGGATTTTGGAATACCTTGGAAAGTGAGATTTTGGAGAGGAG  1059
          ||||||||| ||||||||||||||||||||  ||||||||| |||||||
Db   960  CCTCCAACTACTGGATTCTGGAAGTCCCATTTGATTTCTGGAGGAGGCG  1019

Qy  1060  TGATGGAGGTGATGCGGCCGCAACTTCATCCTCCTCCCCAGCGTGGTTGCTCTTTTG  1119
          |||||||| ||||| ||||||||||||||||  ||||||||||||||||||
Db  1020  TGATAAGCCTGACCCCCTGTTGGTTTGCTGGCGCCGCCATTGCTTTGCTGCTCTGAGCAACGGG  1079

Qy  1120  TTGTCGTGATGGTTTCCTGCTGCTGTGACGATGGCGGGGATGTTGCAAGGCGGCCCCGCCTCCG  1179
          ||||||||| |||||||||||||||||||||  |||||||||||||||||||||
Db  1080  TTGTCATGTGCTTCCTGTTGGTGACGATGGCCGGGATGTCGCAAGGCGGCCCCTGCCTCCG  1139

Qy  1180  TTTTGGGGTCCCGCCCCCTTTGACTACGGGTTGAAGTGGCAGTCATGCTCCTGCGAGGGCTA  1239
          ||||||||||||| ||||||||||||||||| ||||||||||||||||||||||||
Db  1140  TTTTGGGGTCACGCCCCCTTTGACTACGGGTTGGCCAGACCCTGCTCCTTGCGAGGGCCA  1199

Qy  1240  ACGGGTCGCGTATTCCCACTGGGGAGAGGGTGTGGATCGAGGAATGTCACGCGTCTTGT  1299
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  1200  ACGGGTCGCGTTTTTCCACTGGGGAGAGGGTGTGGGACCGTGTGGGAACGTTACGCGTTCAGT  1259

Qy  1300  GTGACTGCCCCAACGGCCCCTGGGTTTGGGTCCCGCCGTTTGCCAGGCGGGGTTGGGTGGG  1359
          ||||||||||||||||||||||||| |||||||||||| | ||||
Db  1260  GTGACTGCCCCTAACGGCGTGGGTGTTTGCCAGCCCTTTTTGCCAAGCAATCGGCCTGGG  1319

Qy  1360  GCGACCCCATCACCCATTGGAGACCCACGGACAAAACCAGTGCCCCTATCCATGCCCCAAT  1419
          | ||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  1320  GTGACCCCATCACCTTATTGGAGACCCACGGACGCGGCAAAATCAGTGCCCCTTTCCATGCCCCCAGT  1379

Qy  1420  ATGTCTATGGGTCTCTGTCTGTGGGTTCCGTGTCTTGTTTCCGTGTTCCTCGA  1479
          ||||||||||||| |||||||||||  | ||| |||||||||||||||||
Db  1380  ATGTCTATGGGTCTGCTACAGTCACTTGCCGTGTTTCGCTTCCGTGTATGCCTCCA  1439

Qy  1480  CCGGGCGTCGTGATTCGAAGCAATGCGATGGGTGGAGTCGTTGGTGCCGGTGGATCTGCCAGCT  1539
          ||| || |||||||||||||||||| || ||||||||||||||||||||||||
Db  1440  CCAGTGGTCCGCGACTCGAAGAATAGTGTGGAGTTTAGTGCCACGTTGGGCTCTGCCCACCT  1499

Qy  1540  GCACCATAGCCGCTCTAGGGTCATCGGACACGTGGGTTGAGCTCTCCGAGTGGG  1599
          |||||||||||| || ||||||||||||||| ||||||||||||||||||||||
Db  1500  GCACCATAGCCGCTGGATCATCGGACACGTGCCCTGGGCTCTCCGAGTGGG  1559

Qy  1600  GAGTCCGTGCGTAACGTGTATTCTGGACCGTCGGCCTTCATGGCACCTGTGTGC  1659
          ||| |||||||| ||||||||||||||||||||||||||||||||||||||
Db  1560  GAATCCCGTGCGGTGTGTTCTGCGGCCGTCGGCCTTCATGCGGCACCTGTGTGA  1619

Qy  1660  GGGACTGCTGGCCCCCAAACCGGTCGTTTAGATTCCCTTTCCATCCGGTGCGGCCACGGGGGC  1719
          |||||||||||||| ||||||||| |||||||||| |||||||||||||||||||
Db  1620  GGGACTGCTGGCCCCAGAACCGGGTCGTTTAGGTGGAGTTTAGTGCCCATCCGTGCGGGCGTGGGGC  1679

Qy  1720  CTCCGGCTGACAAAGGACCTGAAGCTTGCCCTTCGTCAACAGGACAACTCCCTTCACCA  1779
          |||||||||| |||| ||||||||||||||||||||||||||||||||||||||
Db  1680  CTCCGGCTGACAAAGGACTTGAAGCTTGCCCTTCGTCAATAGGACAACTCCCTTCACCA  1739

Qy  1780  TAAGGGGCCCTAGGCACGGAGAGTGCTGAGGCAACCAGGGAGAGGCAACCCGGTCGGT TTTTG  1839
          ||||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||
Db  1740  TTAGGGGCCTTGGCACGGAGAGTGCTGAGGCAACCAGGGCCGAGCGCAACCCGGTCGGT TTTTG  1799

Qy  1840  GGTCCTACACCATGACCAAGAGTCCGGGATTCCCTGCATTTGGTGAAATGTCCCACACCAG  1899
          ||||||||||||||  |||| |||||||||| ||| |||| || ||||||||||||||||
Db  1800  GGTCCTTACGCCATGACCATGACCGGGATCCCGAGATACCCTACAT CTGGTGACATCCGGTCCCACCAG  1859

Qy  1900  CCATAGAGCCTCCGACTGGAACGTTCGGGTTCTTCCCCGGAGTCCCCATTAAACAACT  1959
          |||| ||||||| ||||||||| ||| ||| |||| |||||||||||| |||||||
Db  1860  CCATCGAGCCTCCACCGGGGACCGTTTGGGTTCTTCCCCGGGACCGCCTTCTCAACAACT  1919

Qy  1960  GCATGCGGCTAGGCACGGAGAGTGCTGAGGCGTTGGCCGGAGCTGGGCTTGGCCTTGCGGGGGT  2019
          |||||||||||||| ||||||||||| |||||||||||||| |||||||||||||||||||||
Db  1920  GCATGCTCTTGGGCACGGAGAGTGCTGAGGCCTGGGCTTGGCCTTGCACGCGGGGGGT  1979

Qy  2020  TCTACCAGCCTCTGGTTCGCAGGTTGCGATGCGGCCGCTGATGGACGCCGAAATCCGGTTGCC  2079
          |||| || ||||||||  ||| |||||||||||||||||||||||||||||
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Db  1980  TCTATGAACCCCTGTGCGCCAGTCGTTCGGAGCTGTTGATGGGAAGCCGAAATCCGGTTTGTC  2039

Qy  2080  CGGGGTACGCATGGCTGTCCTCTGTAGACCTGGTTCATCACGCGTTCAGGGCCACC  2139
          ||| |||  |||||||| ||||| || ||||| | |||||||||||  |||||||
Db  2040  CGGGGTTGCATGGCTTCTCTCGGCAGGCCTGATGGGTTTATACATGTCCAGGGTCACT  2099

Qy  2140  TGCAGGAGGTGATGCGGCCGCCAACTTCATCCTCCTCCTCCCCAGCGTGGTTGCTCTTTTG  2199
          |||||||||| ||||| |||||||||||||  |||||||||||||| | ||| |||||||
Db  2100  TGCAGGAGGTGGATGCAGCAGGCAACTTCATCCCCGCCGCCGCCGGTCGTTGCTCTTGTGGACTTTG  2159

Qy  2200  TATTTGTCCTGCTCTATCTGATGAGCTGATGAAGCTGATGAAGCGTTGGTCCGTTGATCTTGC  2259
          |||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db  2160  TATTTGTCCTGTTATACCTGATGAAGCTGATGAAGCGTTGGTGGTCCCGTGATCTTGC  2219

Qy  2260  TTCTGCTGTGGTGGTTGTGGACCAGTTGGACCTGTGCCGGCGTGCCGGCTGTGGACGCGTG  2319
          |||| ||| |||||||||| || ||||||| ||||||||||||  || |||||||||||
Db  2220  TGCTCCTATGTGGTGGTGGTGAACCAGCTGACTGGGTGAACCTGGGAGCCC  2279

Qy  2320  CCGTGCGGGTGAAGTTTTTCGGGAGTTGCTGCTGTTTGGGGCTTCCTCCCACTG  2379
          |||| | || |||||| | || ||||||||||||||||||| ||||||
Db  2280  CCGTGCCAGTGGAGGTTCTTCGGGGGCTCCGTGTCCTGGTGTCGGGACTCCCCGGTCG  2339

Qy  2380  TCAGTATGATACTAGCTCTAGCAAACCTGGTTGTTGTACTTTCGGTGTGGATGGGCCCTCAGC  2439
          ||||||| |||| || |||||||||||||||||  |||| |||||||| ||||||||||
Db  2340  TCAGTATGATATTGGGGTTGGCAAACCTGGTTGCTGTACTTTAGATGTTGGGACCCCCAAAC  2399

Qy  2440  GCCTCATGTTCCTCGTGTTGGAAGCTCGCTCGGGGAGCTTCCCGGCCGGCCCTTTGA  2499
          ||||| |||  || |||||||||||||||  ||||||||||| ||  ||||| ||||
Db  2400  GCCTGATGTTCCTCGCGTGTTGCGGAAGCTTGCTCGGGGAGCTTTCCCGGCCCTCTTGA  2459

Qy  2500  TGGGGATTTCGGCGACCCGGCGCACCTCGTGCTCCGGGCCGAGTTCTCGTCGGATG  2559
          ||||| |||||||| |||||||| |||||||||||||||||||||||||||||||
Db  2460  TGGGGATTTCGGCGACCCGGCGCACCTCAGTGCTCGGGGCCGAGTTCTCGTGCTCGATG  2519

Qy  2560  TCACATTCGAGTGACACTTCGGTGTTGGTGCCGGCCAGCGTGGTGGTTGGG  2619
          |||| ||||||||| |||||||||||||||||||  |||  ||||||||||
Db  2520  CTACATTCGAGTGACACTTCGGTGTTGGCTGGTGCCAATGTGTTGGTAGCTTGGG  2579

Qy  2620  CCATAGCGCTCCTGAGCTCAATGAGCGCAGGGGGTGGAAGCACAAGGCCGTGATCTATA  2679
          |||||| ||||||| |||||||||||  ||||||| ||| || ||||  ||||||||||
Db  2580  CCATTGCGCTCCTGAGCTCGATGAGCGCAGGGGGTGAGCGCACACACCGTGATCTATA  2639

Qy  2680  TGGGGGTGGTAAAGGGTACCAGGTTCGGGCGCCAGAGGGTGGTCGGCACCTGTGTGC  2739
          ||||| ||||| ||||||||||||| ||||||||||||||| |||||||||||||||
Db  2640  GGGGGTGGTGGTAAGGGGTACCAGGGTACGGCGCAATCCGTCAAAGGTGTGAGGAGCCTCGGGG  2699

Qy  2740  AGGGGCGTCTACCAAGCTTCTGACGTTCGCGTGGTCTTGGCCTCATACATCTGGCCGG  2799
          ||||| |||||||||||||||||| |||||||||||||||||| ||||||||  ||||
Db  2700  AGGGGCGCCTGCCAAACCCCTGACCTTTGCCTTGGTGCTTTGGCCTACATCTGGCCAG  2759

Qy  2800  ATGCTGTGATGAGTGGTGGTGCCGGCCACTGG  2859
          ||||| ||||||| ||||||  |||||||||| ||
Db  2760  ATGCTGTGATGAGTGGTGGTGGAGCCCACAAGCGCGTGG  2819

Qy  2860  ACTGGCCCCTGGAGGAGCGCCTGGTCTCGGTCGTCCCGCTGCGCTGGGACTGGCACGGGTGG  2919
          | ||||| |||||| ||||||| || || ||||||||||| || |||||||| |||||||
Db  2820  ATTGGGCCTTGGAATGGGACGCGGCTCTTCATTCACTCAGTCGTTCATTCACTACTAGGACGGAACTGTCGCA  2879

Qy  2920  TTGAGTGCTGTGATGGCGGGGCGAGGAAGGCCACCACCGACTGGTCTTCCAAGATGT  2979
          ||||||||||||||||||||||||  ||||||||  |||| ||||||||||||||||
Db  2880  TTGAGTGCTGTGATGGCGGGGTGAGAAGGCCACAACCGTCCGGCTGGTCGTCTCCAAGATGT  2939

Qy  2980  GCGCAAGAGGGGCCTACCTGTTTGACCACATGGGCTCTTTCGCGCGCTGTCAAGGAGC  3039
          |||| ||| || ||||| |||||||||||||| || ||||| || |||||||||||||
Db  2940  GTGCGAGAGGAGCTTATTTGTTCGACGATCATATGGGCTCATTTCGCGTGCTGTCAAGGAGC  2999

Qy  3040  GCTTGTTGGAATGGCGACGCGGCTTTGGAGCCCTTGCATTCATTCACTACCTGTCGCAGACTGTCGCA  3099
          ||| ||||||||| |||  ||| ||||||||||  |||| |||||||||| ||||||
Db  3000  GCCTGTTGGAATGGGACGCGGCTCTTGTGAACCTCTCTGTCATTCATTCACTACCGGGACTGTCGCGA  3059

Qy  3100  TCATCAGAGATGCCGGCGAGGACCCGTCCTGCGGGCAGCAGTCCCTCATGGGTTCATGGGATGT  3159
          ||| || |||||||  || ||||||||||||||||||  ||||| |||||||||||||||||
Db  3060  TCATACGGGATGCCGGGATCGCCGAGGACTTTGTCCTTGCGGGCAATGCGCAGTTTGTTTACCCGTGG  3119
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Qy 3160 TAGCACGGCGCGGTGATGAGGTTCTCATCGGCGTCTTTCAGGATGTGAATCATTTGCCTC 3219
        -||-||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db 3120 TTGCGCGGCGTGGTGATGAGGTTCTCATCGGCGTCTTTCAGGATGTGAATCATTTGCCTC 3179

Qy 3220 CCGGGTTTGTTGTCCCGACTGTCACCAGTTGCATCGGCGTTGTCATCCGACGGTGCGGAAAGGGCTTCCTGGGGG 3279
        ||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db 3180 CCGGGTTTGTTGTCCGACCGCGTGTTGTCATCGGCGTTGTCATCCGACGGTGCGGAAAGGGCTTCCTGGGGG 3239

Qy 3280 TCACGAAGGCAGCCTTGACAGGTAGGATCCTGACTTACATCCAGGAACGTCATGGTGT 3339
        ||||| ||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db 3240 TCCAAAGGCTGCCTTGACAGGTCCGGGATCCTTGACTTACATCCAGGGAACGTCATGGTGT 3299

Qy 3340 TGGGGACGGCTACGTCACGAAGCATGGGCACATGTCTGAATGCCTGCTGTTCACAACTT 3399
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3300 TGGGGACGGCTACGTCGCGAAGCATGGGAACATGTCTTGAACGCGTCCTGCTGTTCACGACCT 3359

Qy 3400 TCCATGGGGCTTCATCCCGAACCATCGCCACACCCCTTAATCCCAGGTGGT 3459
        |||||||||||||||||||||||||  |||||||||||||||||||||||
Db 3360 TCCATGGGGCTTCATCCCGAACCATCGCCACACCCGTGGGGGCCCTTAATCCCAGATGGT 3419

Qy 3460 GGTCAGCCAGTGATGACGTCACGGTGTACCCGCTTCCAGATGGGCAACTTCGTTGACGC 3519
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db 3420 GGTCAGCCAGTGATGATGTCACGGTGTATCCGCTTCCACTCCCGGATGGGCTACTTCGTTAACGC 3479

Qy 3520 CCTGCACTTGCCAGGCGGAGGTTCTGTTGGGTTATTAGATCCGACGGGGCTTTGTGCCATG 3579
        |||||||||||||||||||  |||||||||||||||||||||||||||||||||||||
Db 3480 CTTGTACTTGCCAGGCGGTGAGGTCGTCAGTGTGGGATGTGCCGCCATGCAGATCGGCCCCTATGCCATG 3539

Qy 3580 GCTTGAGCAAGGGGACAAGGTTGAGCTGGATGTGGCCATGGACGCACGCAGTCTCTGACTTCCGTG 3639
        ||||||||||||||||||||||||  ||||||||||||||||||||  |||||||||||||||||
Db 3540 CTTGTGAGCAAGGGGACAAGGTGAGCTGGATGTGGCCATGGGCACGCAGCAGTGGTCCCTGATTTCCGTG 3599

Qy 3640 GTTCGTCTGGTTCACCGGTCCTTTGCGACAAAGGGCACGCAGTTAAGAATGCTCGTGTCAG 3699
        ||||||||||||||||||||| |||||||||||||||||  |||||||||||||||||
Db 3600 GCTCGTCTGGTTCACCGGTCCTATGTGACACTGGTAGAGGCACGCAGCAGTGGAATGCTCGTGTCTG 3659

Qy 3700 TGTCCCACTCTGCGCAGGGTTACTGCCGGCGGTTGATCTTGAACCCGTCGGACTTCACTCACAGTAC 3759
        ||||||||||||||||||||  ||||||||||||||||||||||||||||||||  ||||||||
Db 3660 TGTTCACTCTGCGCAGGGTGTAGGTCGTTCACTCAGGCCGGTTCACTCAGGCCGGTTGACCCCAAGTGC 3719

Qy 3760 CAACAGATGCCAAGACCACCAGAACCCCTCCGGTGCCGGCAAAAGGAGTTTTCAAGG 3819
        ||||| ||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db 3720 CAACAGATGCCAAAACCACCACTGAACCCCTCCGGTGCCGGCAAAAGGAGTTTTCAAAG 3779

Qy 3820 AGGCCCCGTTGTTTATGCCTACGGGGGCGGAAAGAGCACCCGCGGGTACCGTTGGAGTACG 3879
        ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3780 AGGCCCCGTTGTTTATGCCTACGGGGGCGGAAAGAGCACCCGCGGGTTGGGGCCGTTGGAGTACG 3839

Qy 3880 GCAAACATGGGCCACAAGGTCTTGAATCTTGAACCCGTCGGAGCTACCGTGAGGGCCATGG 3939
        |||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db 3840 GCAACAGTGGGGCACAAGGTCTTGAATCTTGAACCCGTCAGTGGCCACTGTGCCGGCCATGG 3899

Qy 3940 GCCCATACATGACAGAGCGGCGCTGGGCGGGAAACACCCCAGTATTACTGTGGCCATGACACCA 3999
        ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db 3900 GCCCATACATGACAGAGCGGCGCTGGGCGGGATAAACCAGTATATACTGTGGGCATGATGACAA 3959

Qy 4000 CTGCTTCACAAGGATCACTGACTCGCGCCCTTACGTATTCCACTTACGGAAGGTTTTTGG 4059
        ||||||||||||||||||||||||||||  ||||||||||||||  ||||||||||||||
Db 3960 CTGCTTCACAAGGATCACTGACTCGTTTTAGCGCATTGGGAGAGGTTCGGGGTTTTTGG 4019

Qy 4060 CCAACCCTAGGCAGATGCTGAGGGGTGTGTCCGGTGGTCATTTGTGACGAGTGCCACAGTC 4119
        |||||||||||||||||||||||||||||  |||||||||||||||||||||||||  ||
Db 4020 CCAACCCTAGGCAGATGCCGGGTTTTCGGTGGTCATTTGTGATGAGTGCCACAGTT 4079

Qy 4120 ATGACTCAACTGTGTTGGGAGTCTGGGCGGTCAGGGAGCTGGCCGAGGATGTGGAG 4179
        ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db 4080 ATGACTCAACTGTGTTGGGAGTCTGGGCGGTCAGTGGGAGCTGGCGGCGGTGCCGGAG 4139

Qy 4180 TGCAATTGGTGCTCTACGCCCTCCCACCCTTCCTCCCGGATCCCCGATGACCCAGCCCCAT 4239
        ||||| |||||||||||||||||||||  |||||||||||||||||||||||||||||| |
Db 4140 TGCAACTAGTGCTCTACGCCCTCCCACCCCTATGACGCAGCACCCCCTATGACGCAGCACCCTT 4199
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Qy 4240 CAATCATTGAGACAAAACTGACGCGTGGGAGAGATCCCTTCTCATGGCATGGCATACCTC 4299
        -||-||||||||||||||||||  ||||||||||||||||||||||  ||||||||||||
Db 4200 CCATAATTGAGACAAAAATTGACGTGGGCGGAGATTCCCTTTTATGGCACGGCGAATACCCC 4259

Qy 4300 TTGAGCGGATGCGGACCGAAGGCATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGC 4359
        ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db 4260 TCGAGCGGATGCGGACCGGAGGGCACCGTGTTCTCGTGTTCTGCCCATTCTAAGGCTGAGTGCGGTTG 4319

Qy 4360 GCCTGGCGGCGGCCAGTTTCGGCGGGGGTAAATGCCATTACGCCGCCTTATTACAGGGGGAAAG 4419
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4320 GCCTTGCTGGCCAGTTCTCCGCTAGGGGGTCAATGCCATTTATTATAGGGGTAAAG 4379

Qy 4420 ACAGTTCTATCATCAAAGATGAGACCTGGTGGTGTGTGCTACAGACGCACTATCCACTG 4479
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4380 ACAGTTCTATCATCAAGGATGGGACCTGGTGGTCGTGTGCCACAGCGCGCTTTCCACTG 4439

Qy 4480 GGTACACTGGGAACTTCGATTCTGTCACCGATTGTGGTTAGTGTGGAGGAGGTCGTCG 4539
        ||||||||||||||||||||  |||||||||||||||||||||||||||||||||||||
Db 4440 GGTACACTGGAAATTTCGACTCCGTCACCGACGTGGATTAGTAGTGGTGGAGGAGGTCGTTG 4499

Qy 4540 AGGTGACCCTTGATCCACCATTACCCATCTCCCTGCCCGCACGGTGCCCGCGTCGGCGTGAAC 4599
        |||||||||||||||  ||||||||||||||  |||||||||||||||||||||||||||||
Db 4500 AGGTGACCCTTGATCCTACCATTACCCATCTCCCTGCGACAGTGCCTGCTGCCCGCGTCGGCGTGAAC 4559

Qy 4600 TGTCGATGCAGCGGCGGAGGACGCACGGCAGGTCTGGGCGCCTACTACGCGG 4659
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4560 TGTCGATGCAAAGACGGAGGACGCACGGCAGGTCTGGACGCCTACTACTACGCGG 4619

Qy 4660 GGGTCGGCAAGGCCCCCTGCTGGTGGTGCGCGCTCAGGTCCTGTCTTGGTCGGCGGTGGAAG 4719
        ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db 4620 GGGTGGGCAAGGCCCCCTGCTGGTGGTGCGGTGGCCTCAGGTCCTCGTGTCGGCGGTGGAAG 4679

Qy 4720 CCGGTGTGACCTGGTACGGAATGAACCTGACCGACAGCAGACAAACCTACTGAGACTTTACG 4779
        ||||||||||||||||  |||||||||||||||||||||||||||||||||||||||||
Db 4680 CTGAGTGACCTGGTACGGAATGAACCTGACACTTGACCAGTCTAACCTACTGAGACTTTACG 4739

Qy 4780 ACAACTGCCCTTACACCGCAGCCGCGTGACATTGGGAAGCCGGCGGTGTCTTTTT 4839
        ||-||||||||||||||||||||||||||||||||||||||||||||||||  |
Db 4740 ACGACTGCCCTTACACCACCAGCCGCGTGATATGGGCGTGATATCGGCGGCCCAAATCTGTCCCACTCCGTGTCTCT 4799

Qy 4840 CGGGGCTTGCCCCGTTGAGGATGAGTAGCTGGCAAATCCCGGCGCGTCA 4899
        ||||||||||||||||||  |||||||||||||||||||||||||||||
Db 4800 CTGGGCTCGCCCCCATTGAGGATGCCGGCTGGGCCGGCAAAAGTCGCGGGGTCA 4859

Qy 4900 ACTGGCCCTTCCTGGTGTTCAGCGGACCATGTGCCGGAAAACACTGCTCTCCCGGCC 4959
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4860 ACTGGCCCTCTTGGTGTTCAGCGGACCATGTGTCGGACCATGTGCCGGAAACACTGTCTCTCCCGGCC 4919

Qy 4960 CATCCGATGACCCCCAGTGGGCAGGGCCTGAAGGGCCGGAATCCTGTCCCACTCCTGCTGA 5019
        ||||||||||||||||||||||||||  ||||||||||  |||||||||||||||||||||
Db 4920 CATCCGATGACCCCCAAATGGGCAGGGCCCAAATCCTGTCCCACTCCTGCTGA 4979

Qy 5020 GGTGGGGCAATGATTTACCATCTAAAGTGCCCGGCCATCACCATCGTGGACGACCTGGTCC 5079
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4980 GGTGGGGCAATGATTTACCATCTAAAGTGGCCGGCCACCATCACCACCATAGTGGACACCTGGTCC 5039

Qy 5080 GTAGGCTCGGGTCGCGAGGGTTACGGCCGGCGGGACCCATCTTGATGGTGG 5139
        ||||||||||  |||||||||||||||||||||||||||  ||||||||||||
Db 5040 GGAGACTCGGTGTGTCGGAGGGTTACGCCGTGCGGGACGCTGGCGGCCATCTTGATGATCG 5099

Qy 5140 GCCTCGCTATTGCGGGGGGGCATGATCCATCTGTCTCGGGTCTCTCGGTTGGTGTTA 5199
        ||-|||||||||||  ||||||||||||||||||||||||||||||  ||||||||||
Db 5100 GTCTCAGCTATCGCGGGGGATCTACGCCGTCGGTCACCGGTCACCGGTGTCGCTAGTGGTGGTGA 5159

Qy 5200 CAGACTGGGATGTGAAGGGGGTGGCCCGGAGCTGGCACCCCCTTTATCGGCATGGAGACCACCACGC 5259
        ||||||||||||||  ||||||||||||||||||||||||||||  ||||||||||||||||||||
Db 5160 CAGACTGGGGCAATGTGTGAAGGGGGTGGCGCAGTCGCCATGCATGGGAGGATCTTTATCGGCATGATGGAGACCAGGCCACGC 5219

Qy 5260 CCCAGCCGGTTGTGCAGGTGTCCCCCGATGACCCAGCCCCAT 5319
        ||-||||||||||||||||||||||  |||||||||||||
Db 5220 CTCAGCCGGTTGGTGTCAGGTTCCTCCCGGATCCATCAGTGAATCAGCAGCCAT 5279

Qy 5320 CGGATGCCAACACAGTGACAGATGCCGGCGGCGGCCATCCCAGGTGGATTGCCGATTGGTGTCAG 5379
Db 5320 CGGAACTAGTGCTCTACGCCCTCCTACGCCCTCTATGACGCAGCACCCCCTATGACGCAGCACCTT 5320
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Db  6360  TGGGGACTGTCCCTGTGAACATGCTGGGTTACGGTGAAACGTCGCCCTCCTGGCCTCCG  6419
                |||||||||||||||||||||||||| |||||| ||||||||||||||||
Qy  6460  ACACCCCGAAGGTGGTACCATTCGGACGTCTGGGTTGGGCTGAGGTGGTGAGGTGACCCCTA  6519
                |||||||||||||||||||| ||  |||||||||||| ||||||| ||||||||||||
Db  6420  ACACCCCGAAGGTTGTCCCTTCGGACGTCTGGGCTGGCTGGGTGGTGAGGTGTGACCACTA  6479

Qy  6520  CCCACGTTGTGATCAGGCGAACATCCGGCTACAAACTGCTGCGCCAGCAAATCCTGTCGG  6579
                |||||||| || ||  |||||||||||||| || ||||||||||||||||||||||
Db  6480  CCCACGTTGGTAATCAGGAGAGAACCTCCGCCTATAAGCTGCTGCGCCAGCAAATCCTATCGG  6539

Qy  6580  CTGCTGTTGCTGAGCCCTATTACGTGCACGGCATACCGGTCTCATGGACGCGGACGCGC  6639
                | |||||||||||||||||||| ||||||||||| ||||||||||||||||| ||||
Db  6540  CTGCTGTAGCTGAGCCCTACTACGTGCACGGCATTCCGGTCTCATGGACGCGGACGCGCTC  6599

Qy  6640  GAGCGGCTGCCATGGTCTATGGCCCTCGGGCAAAGTGCACCATTGACGGGGAACGCTACA  6699
                | |||||||||||||||||||||||||||||| ||||| |||||||||||||||||
Db  6600  GTGCGGCCCGCCATGGTCTATGGCCCTGGCCAAAGTGTTACCATTGACGGGGAGCGCTACA  6659

Qy  6700  CCCTTCCGCATCAACTGCGGCTTAGGAATGTGCGCCCCTGAGGTGTCATCCGAGGTGT  6759
                |||| | |||||||||||| |||||||||||||| |||||||||||||||||||| |
Db  6660  CCCTGCCTCATCAACTGAGGCTCAGGAATGTGCGCCCCTGAGGTTTCATCCGAGGTGT  6719

Qy  6760  CCATTGACATTGGACGGAGACTGAAGACTCAGAACTGACTGAGGCCGACCTGCCGCCGG  6819
                || |||||||||||||||||||||||||| ||||||||||||| ||||||||||||
Db  6720  CCATTGACATTGGACGGAGACTGCAGAACTGACTGAGGCCGATCTGCCGCCGG  6779

Qy  6820  CGGCTGCAGCCCTTCAGGCTATCGAGAATTCTTGAACCTCACATAGATG  6879
                |||||||| |  ||| ||||||| |||||  ||||||||||||||  |||
Db  6780  CGGCTGCGCTCCAGCGATCGGAGAATGCGGAGGATTCTTGAACCGCACATTGATG  6839

Qy  6880  TCATCATGGAAGATTGCAGTACACCCTCTCTTGTGGGAGTAGCCGAGAGATGCCTGTGT  6939
                |||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  6840  CCATCATGGAGGACTGCAGTACACCCTCTCTTGTGGTAGTAGCCGAGAGATGCCTGTAT  6899

Qy  6940  GGGGAAGAGACATACCCGCACTCCATCGCCCAGCACTTATCTCGGTTACTGAGACAGCC  6999
                |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  6900  GGGGAGGAAGACATCCCGTACTCCATCCAGCACTTATCTCGGTTACTGAGACAGCT  6959

Qy  7000  CAGATGAGAAGACCCCGTCGGTGTCTCCTGCGGATACCCGCTCTTCTGACTCAT  7059
                |||||||||||||||||||| || | ||||||||||||||  ||||||||||||
Db  6960  CAGATGAGAAGACCCCGTCGTGTCCTCGCAGGAGATACCCGCTCTTCTGACTCAT  7019

Qy  7060  TCGAGGTCATCCAAGAGTCCGAGAGTCCGAGACAGCCGAAAGTCGTCTTCAACGTGGCTC  7119
                |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db  7020  TCGAGGTCATCCAAGAGTCCGAGAGTCCGAGAGGGGAAAGCGTCTTCAACGTGGCTC  7079

Qy  7120  TTTCCGTACTAAAAGCCTTGTTTCCACAGAGCCGATGCCACAGAGAAAGCTTACCGTTAAGA  7179
                ||||||||||| || ||| ||||||||||||||||||||||| ||||||||||||||||
Db  7080  TTTCCGTATTAGAAGCCTCATTTCCACAGAGCCGACGCGACCAGGAAGCTTACCGTCAAGA  7139

Qy  7180  TGTCATGCTGTGTTGAGAAGACGTAACACGCTTCTTTCATTGGATTGACGGTGCGCTG  7239
                ||||| |||| || |||||||||||||||| || ||||||||| |||||||||||
Db  7140  TGTCGTGCTGCGTTGAGAAAGAGCGTACACGGCGTTTTCTCATTGGGTTGACGGTGCTG  7199

Qy  7240  ACGTGCAAGCCTGTGTGAGATGGAAATCCAGAGAATCGGAAATCCAGAACCATACAGCCTATTGTGA  7299
                 | ||||||||||||||||| ||||| |||||| |||| |||||||| |||||||||||
Db  7200  ATGTTGCTGACCTGTGTGAGATGGAAATCCAGAACCATACAGCCTATTGTGACAAGTGC  7259

Qy  7300  GCACTCCGCTGAATTGCAGGTTGGGTGCTTGGGTGGGCAATGAACTTTGAATGTG  7359
                ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  7260  GCACTCCGCTTGAATTGCAGGTTCGGGTGCTTGGGTGGGCAATGAACTTTGAATGTG  7319

Qy  7360  ACAAGTGTGAGGCTAGGCAAGAACCTTGGCTTCTCTACATTGGTCTGGGGTGC  7419
                |||||||||||||||||||||| || |||||||| |||| | |||||||||||
Db  7320  ACAAGTGTGAGGCTAGGCAAGAAAACCTTGGCTTCTCTTACATTGGTCTGGGGTGC  7379

Qy  7420  CACTGACGAGGGCCACTCCGGCCAAGCCCCTGTGTGAGGCGCCATTATTGGA  7479
                |  ||||||||||||||||||| || ||||||||||||||||| ||| |||||
Db  7380  CGCTGACTAGGGCCACCCGCCAAGCTCCCGTGGTGAGGCGCCGGTTGCCTTTATTAG  7439

Qy  7480  TGGGGCAGACCACCAAGGTGTATGTCCACAAGGTGTATGTTACCAATCCAGACAGTTGACA  7539
                |||||| |||||||||||| ||| || ||||||| ||  |||||||||||| |||||||
Db  7440  TGGCCGACACTACTAAGGTGTATGTTACCAATCCAGACAAATGGGACGAGGGTGGACA  7499
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Db  5280  CGGATGCCAAGACAGTGACACAGATGCGGTGCGCAGCCATCCAGGTGCGATTGGACTA  5339
                |||||||| |||||||||| || |||||||| |||||||||||| |  |||||||||
Qy  5380  TCATGACCCTGTCGATCGGGAAGTCGTCTCCTTGGCCCAGCTAAGACGGCCGAGGCCT  5439
                ||||| ||||||||| || || |||| ||||||||| |||| ||||||||||||||||
Db  5340  TCATGACTCTGTCGATCGGAGAAGTGTTGTCCTTGGCCTCAGGCGGCCTAAGACGGCCGAGGCCT  5399

Qy  5440  ACGCAGCTACCACCAAGTGGCTTGTGGCTGCTACACGGGGACGCGGCGGCCGTTCCCACTG  5499
                 ||||| || ||| ||||| |||| || || || |||||| || || |||||||||||||
Db  5400  ACACAGCAGCCACCAAGTGGCTTGTGGCTGCTACACGGGGACGCGGCGGCCGTTCCCACTG  5459

Qy  5500  TTTCAATTGTTGACAAGCTCTTCGCCGGGGCTGGGCGCGTGGTGGTAGGCCATTGCCACA  5559
                  ||| ||||||||||||||||| || | ||||||| |  |||||| ||||||| |||||
Db  5460  TATCCATTGTTGACAAGCTCTTCGCCGGGGCGTGGGTGGTGGTGGGCCATTGCCACA  5519

Qy  5560  GTGTAATAGCTGCGGCAGTGGCAGTGGGCTCTAGGAGCCCTCCATTGGCTGCTG  5619
                || || |||| || |||||||||| ||||||||||  |||||||| ||||||||
Db  5520  ACGTGATTGCTGCGGCGGTGGCAGTGGGGCTTCAAAGAGCAGCCCGTTGGCCAGCCG  5579

Qy  5620  CCGCTTCCTACCTCATGGGGTTGGGCGTCGGAGGCAACGCGCAAACCCGCTTAGCCTCCG  5679
                |||| |||||||||| ||||||||||||||||||||||||||||||  ||||| ||||| |
Db  5580  CGGCTTCCTACCGATGGGGGTTGGGCGTCGGAGGCAACGCGTCAGACGCGTCTGGCATCTG  5639

Qy  5680  CTCTCCTACTAGGGGCCGCTGGGACCGCTGTCGGGGCACGCCGTCTGGGGTTAACCATGG  5739
                |||||  ||||||||||| |||||||| | |||| | || ||||||| |||||||||| |
Db  5640  CCCTCCTATTGGGGCTGCTGGAACCGCCTTGGGGCTTGGCACTGTCTGGGCTTGACCATGG  5699

Qy  5740  CGGGGCCGTTCATGGAAGTCTAGCGTCTCCCCCTTGGTCACCATTTTACTCGGGG  5799
                 || |||||||||||| | ||||| ||||  ||||||||||||||| ||| |||||
Db  5700  CAGGTCGTTCATGGGGCGGCCCAGTGTCTCCCCCTTGGTCACCATTTTATTGGGGG  5759

Qy  5800  CCGTGGGGGCTGGTGGAGGGGCCGTCTGGTGAATGCGGCTAGCCTTTTCGACTTTATGGCGG  5859
                |||||||||||| ||||||||||||| |||||||||||||||| | ||||||||||||||
Db  5760  CCGTGGGGGCTGCTGGGAGGGGTGTTGTCAACGCGGCCTAGTCTTTTGACTTCATGGCG  5819

Qy  5860  GGAAACTATCATCAGAAGATCTGTGTAGTCTGTGTATGCCATCCAGGTACTAACCAGTCCG  5919
                |||||||||||||||||||| | || |||| ||| ||||||||||| |  ||||||||||
Db  5820  GGAAACTTTCATCAGAAGATCTGTGTATGTCTGTATGCCATCCGGGTACTGACCAGCCGGCGG  5879

Qy  5920  GACTTGCGGGGGATCGCCCTCGGGTTGGTTGTACTCAGCTAACAACTCTGGCACTACCA  5979
                 | |||||||| ||||||| || |||||| | |||||| ||||||||||||||||||||
Db  5880  GCCTTGCGGGGGGATCGCCTCGGGTTGGTTTTTGTATTCAGCTAACAACTCTGGCACTACCA  5939

Qy  5980  CTTGGTTGAACCGTCTGCTGACTACATGGCCTCAAGTCATGCATGTCATGCATGCACAGTTACT  6039
                |||| |||||||||| ||||||||||||||  ||||||||||||||||||||||||||||
Db  5940  CTTGGTTGAACCGTCTGCTGACTACGTTCAGCTCCTACCAAGTGGTCATGCATGCACAGTTACT  5999

Qy  6040  TTCAGCAGGCCGATTACTGTGACAAGGTCTCAGCTGCGTCCGACGCCTTGAGCCTCACTC  6099
                ||||||  | ||  | ||  ||||| || |||||  |||| ||||  || |||||||||||
Db  6000  TTCAGCAAGTTGACTATTGCGACACAGGTCGGTCATTGCCATGCTGCCGACCTTGAGCCTCACTC  6059

Qy  6100  GCACCGTGGTTGCCCTGGTCAACAGGGAGCCTAAGGTGGATGAGGTTCAGGTGGGTACG  6159
                ||||||| || ||||||||||||||||||| |||| |||| || |||| |||| || ||
Db  6060  GCACAGTGGTCGCCCTGGTCAACAGGGAGCCTAAGGGTGGATGAGGTTCAGGTGGGTATG  6119

Qy  6160  TCTGGGACTTGTGACGTACTGGGTGAGTGTGATGGCCAGACTTCGGG  6219
                ||||||||||| | |||| || ||||| || ||||||||||||||||
Db  6120  TCTGGGACCTGTGACGTACTGGGTCAGTGTGATGGCCAGACTTCAGGG  6179

Qy  6220  CCCTCTGCCCCGTGGTATTACCCTTATGGCACTGCGGGGAGGGTGTCCGGAGAAT  6279
                |||||||| ||||||| |||| |||||||||||||||||||||| ||||||| |||
Db  6180  CCCTCTGCCCGTGGTATTGACCTTATGCGTGCACTGCGGGGAGGGTGGTGTCCGGGGAAT  6239

Qy  6280  GGTTGTTGGACGGCCATGTTGAGAGTGCTTGTTGTTGGTTGTCGTGATCACCGGTGATG  6339
                |||| ||||  | ||||| ||||| || ||| |   ||||||||||||||||||||||||
Db  6240  GGTTGCTGACGGTCATGTTGAGGCTAGCTGCCGTCGATCACTGGTGCAG  6299

Qy  6340  TTTTGAATGGGCAACTCAAAGATCCCAGTTTTACTCCTACCAGCAGTGTCAGGCATTATTGGA  6399
                 ||| ||||| ||||||||| | | || |||||||| ||| |||| || | ||||| || ||
Db  6300  TTCTGAATGGGCAACTCAAAGAACCAGTTTTACTCCTACCAAGCGTGCCCGGCCACTATTGGA  6359

Qy  6400  TGGGGACAGTCCCTGTGAACATGCTGGCCTATGCCGAGACCCTTCGTGCCGCCTCAG  6459
                ||||| | ||||||||||| ||||||||||||||||||||||||||||| | |||||
Db  6400  TGGCCGACACTACTAAGGTGTATGTTACCAATCCAGACAGATCCAGACAAATGGGACGAGGGTGGACA  7440
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Qy   7540  AGGTTACCTTCTGGGCGTGCCCTAGGGTTCATGACAAATTCCTCGTGGACTCCATAGAGC  7599
                 ||||||||||||||||||||||||  |||||||||||||| || |||| ||||||
Db   7500  AGGTGACCTTCTGGGCGTGCCTAGGGTTCATGATAAGTACCTCGTGGACTCTTATTGAGC  7559

Qy   7600  GCGCTAAGAGGGCAGCTCAAGCTGCCTAAGCATGGGTTACACTTATGGAGGCAATAA  7659
                 |||||||||||||||||||||||||||||||||||||  |||||
Db   7560  GCGCTAAGAGGGCCCGCTCAAGCCTGCCTAAGCATGGGTTACACTTATGGGAAGCAATAA  7619

Qy   7660  GGACTCGTAAGGCCACATGCTGCCATGGGCTGGGATCTAAGGTGTCGGTCAAGGACCTCG  7719
                 |||||||||||||||||||||||||||  |||||||||||||||  |||||| |
Db   7620  GGACTCGTAAGGCCACATGCTGCCATGGGCTGGGATCTAAGGTGTCGGTTAAGGACTTAG  7679

Qy   7720  CCACCCTGGGGGAAGATGGCTGTCCATGACCGGCTCCAGGAGTACTTGAAGGGACGC  7779
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Db   7680  CCACCCCGGGGGAAGATGCCGTCCATGACCGGCTCCAGGAGTACTTGAAGGGACTC  7739

Qy   7780  CAGTCCCCTTTACTCTTACTGTGAAAAAGGAAGTGTCTTCAAAGACCGAAAGGAAGAGA  7839
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Db   7740  CGGTCCCCTTTACTCTTTACTGTGTGAAAAAGGAGTGTTCTTCAAAGACCGGAAGGAGGAG  7799

Qy   7840  AGGCCCCCCGCCTCATTGTGTTCCCCCCCTGGACTTCCGGATAGCTTATTC  7899
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Db   7800  AGGCCCCCCGCCTCATTGTGTTCCCCCCCTGGACTTCCGGATAGCTGAAAAGCTCATCT  7859

Qy   7900  TGGGGAGACCCTGGACGGGTAGCCAAGGCCGTGTTGGGGGGCCTACGCCTTCCAGTACA  7959
                 |||||||||||||||||||||||||||||||
Db   7860  TGGGAGACCCCAGGACGGGTAGCCAAGGCCGTGTTGGGGGGCCTACGCCTTCCAGTACA  7919

Qy   7960  CCCCAAATCAGCGAATTAGGGAGAGATGCTCAAACTGTGGGAATCAAAGAAGACACCATGCG  8019
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Db   7920  CCCCAAATCAGCGAGTTAAGGAGAGATGCTCAAGCTATGGGAGTCTAAGGAAGAAGACCCCCTTGCG  7979

Qy   8020  CCATCTGTGTGGACGCCACATGCTTCGACACCAGTGTAACCCGGTGCCGCTGG  8079
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Db   7980  CCATCTGTGTGGACGCCACCATGCTTCGACACGAGTGTAACCCGGTGCCGCTTTGG  8039

Qy   8080  AGACAGAGCTTTATGCCCTGCTTCAGACCATCCAGAATGGTGCGTGCCGTGGGGAAAT  8139
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Db   8040  AGACAGAGCTACGGTGTGACCATCCAGAATGGTGCCGCGGCACTTGGCC  8099

Qy   8140  ACTATGCCTCTGCACAATGGTAACCCCGAGGGGTGCCAGTGGTGAGAGGTATTGTA  8199
                 |||||||||||||||| ||||||
Db   8100  ACTATGCCTCAGGGCACCATGTCACCCCGAAGGGGTGCCCGTGGTGCGAGAGGTATTGCA  8159

Qy   8200  GATCCCACTTCAGGGGTCTTGACCACCAGTGCGAGCAACTGCTTGACTTGCTATATCAAGGTGA  8259
                 |||| ||||| |||| || |||
Db   8160  GATCCTCGGGTGTCTGACACTAGCGCGGAGCAACTGCTTGACTTGCTACATCAAGGTGA  8219

Qy   8260  AAGCCGCCTGTGAGAGGGTGGGGCTGAAAAATGTCTCGCTCCTCATCGCTTGGCGATGACT  8319
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Db   8220  AAGCCGCCCTGTGAGAGGGTGGGGCTGAGAAGATGTCTCTCTCCATAGCCCGGCGATGACT  8279

Qy   8320  GTTTGATCATATGCGAACGGCCTGTGTGCGACCCCAGTGTGCCACCCAAGCGACAGCCCTGG  8379
                 ||||||||||||| ||
Db   8280  GCTTGATCATATGTGAGGCGGTACGGCCAGTGTGCCGACCCCAGTGTGCCCCAGGAGCCCTAG  8339

Qy   8380  CGAGCTACGGGTACGGCCATGGCGTGCGAGCCCCTCATATCTTGGGACACGGCCCCCCTTCT  8439
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Db   8340  CGAGCTATGGGTACGGCTTGCTGAGCCCCTCATATCATTTGGACACGCCCCCCCTTCT  8399

Qy   8440  GCTCCACTTGGCTACTGCACATTGCAATGCAGATGGGAAAACGCCATTTCTTCCTGACCACACGG  8499
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Db   8400  GCTCCACTTGGCTACTGCAATGCAATGCAGATTGGGAAGCCGCCATTTCTTCCTGACCACACGG  8459

Qy   8500  ACTTTCGGAGGCCCCCTCGCCTCGAGCTGCCATGTGCGAGCGAGTACGGCTTCGGCCA  8559
                 ||| ||||||||||||||||||
Db   8460  ACTTCCGGAGGCCCGCTCGCTGCCATGTCGAGTGTCGAGTAGTGAACCCGAGTGGCTTCGGCGA  8519

Qy   8560  TCGGTTACATCCTCCTATACCCTTGGTCATCCTATCGCACGTGGGTCATCCCCTCACG  8619
                 ||||||||||||||||||||||
Db   8520  TCGGTTACATCCTCCTTTATCCTTGCACCCCATCACACGTGGGTCATCATCCCCCATG  8579
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Qy   8620  TGCTCACCTGCGCGTTTAGGGTGGTGGTGGCACACCGTCTGATCCTCGTGTGGTGCCAGGTAC  8679
                 ||| || ||||||||||||||||||||||||||| |||||| |||| |||||||
Db   8580  TGCTAACGTGCGCATTCAGGGTGGAGGCACACCGTCTGATCCTCGGTTTGGTGCCAGGTAC  8639

Qy   8680  ATGGTAATTACTACAAGTTTCCACTGACAAACTGCCTAACATCATCGTGGCCCTCCACG  8739
                 |||||||||||||||||||||||||||||||||||
Db   8640  ATGGTAACTACTACAAGTTTCCACTGACAAACTGCCTAACATCATCGTGGCCCTCCACG  8699

Qy   8740  GACCAGCAGCGTTGAGGGTTACCGCAGACACAACTAAGCACACAACTAAAAATGAGGCTGGCAAGG  8799
                 ||| ||||||||||||||||||||||||||||||||||||||||||
Db   8700  GACCAGCAGCGTTGAGGGTTACCGCAGACACAACTAAGCACACAACAAAACAAAGATGAGGCTGGTAAGG  8759

Qy   8800  TGCTGAGCGACCTCAAGCTCCCTGGCCTTAGCAGTCCACCGGAGGAGGCCGGGGCATTGC  8859
                 | |||||||||||||||  |||||  |||||||||||||||||||||||||||||||
Db   8760  TTCTGAGCGACCTCAAGCTCCCTGGCCTTAGCAGTCCACCGGAAAGAAGGCCGGGGCGTTGC  8819

Qy   8860  GAACGCGTATGCTCCGGTCGCGCGCGGTCTGAGTTGGCTAGGGGTCTAGTGGGGCTGTTGTCGGGGTC  8919
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Db   8820  GAACACGCATGCTCCGGTTCGCGCGCGGTTGGCTGCGTTGTGTTCGGGGCTGTTGTCGGGCATC  8879

Qy   8920  CAGGCCCTGCGCGGCTTCCCCCCTCCGCCCGGGTTCCCCTTTCCC  8979
                 ||||||||||||||| ||||| || ||||||||||||||||||||
Db   8880  CAGGCCCTACGGCTTCCCCCCTGAGATTGCTGGTATCCGGGGGTTCCCTCTCTCCCC  8939

Qy   8980  CCCCTATATGGGGTGTTCATCAATTGGATTGAATCAATGGATCAAGCCACCAGGAGTCGCTGGCGGT  9039
                 |||||||||||||||||||||  ||||||||||||||||||||||||||
Db   8940  CCCCTATATGGGGTGTTCATCAATTGGATCAATGGATCAAGCCACCAGGAGTCGCTGGCGGT  8999

Qy   9040  GGTTGGGGTTCTTAGCCCTGCTCATCGTGAGCCCTCTTCGGGTGAACTAAAATTCATCTGTT  9099
                 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9000  GGTTGGGGTTCTTAGCCCTGCTCATCGTGAGCCCTCTTCGGGTGAACTAAAATTCATCTGTT  9059

Qy   9100  GCGGCAAGGTCCGGTCGGGTGACTGACTGATCATCACTGGAGGAGGTTCCGCGGCCTGG  9159
                 ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9060  GCGGCGAGGTCGGGTCGGGTGACTGACTGATCGTCACCGGAGGAGGTTCCGCGCCGCCTGG  9119

Qy   9160  GTCTCCCGCTGGGTAAAAAGGGCCGCCTTGGAGGCATGGTGTTACTAACCCCCTG  9219
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Db   9120  GTCTCCCGCTGGGTAAAAAGGGCCGCCTTGGAGGCATGGTGTTACTAACCCCCTG  9179

Qy   9220  GCAGGGTCAAAGCCTGATTGTCACTGCTAATGGCACCAGCTCGTTCGGTGGCGGGTCGCTACCTTA  9279
                 |||||||||||||||||||||||||||||||
Db   9180  GCAGGGTTAAAGCCTGTTAATGCAGTCACTGCCCACTTCGGTGTCGTGGTCGCGGTCGCTACCTTA  9239

Qy   9280  TAGCCGTAATCCGTGACTTGACTACGGCGTCTCCAGAGCCCTCCCCCGGATGGGGCACAGTGCAC  9339
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Db   9240  TAGCCGTAATCCGTGACTTGACTACGGCTGCTCGCCAGAGCCCTCCCCCGGATGGGGCACAGTGCAC  9299

Qy   9340  TGTGATCTGAAGGGGTGCACCCCGGTAA  9367
                 | |||||||| ||||||||||||||| ||
Db   9300  TGAGATCTGAAGGGGTGCACCCCGGGAA  9327
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Search completed: October 9, 2002, 00:19:47
Job time : 905 secs

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                 GenCore version 5.1.3
            Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October  8, 2002, 23:18:15 ; Search time 6372 Seconds
                                         (without alignments)
                                         19900.172 Million cell updates/sec

Title:            US-09-828-498-1
Perfect score:    9395
Sequence:         1 tgacgtggggggttgatcc.........cccaaggccgggtcctact 9395
Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0
Searched:         13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters:          27472414
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
              1:  em_estba:*
              2:  em_esthum:*
              3:  em_estin:*
              4:  em_estmu:*
              5:  em_estov:*
              6:  em_estro:*
              7:  em_htc:*
              8:  gb_est1:*
              9:  gb_est2:*
             10:  gb_htc:*
             11:  gb_gss:*
             12:  em_gss_hum:*
             13:  em_gss_inv:*
             14:  em_gss_pln:*
             15:  em_gss_vrt:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	65.6	0.7	925	12	CNS0091P	AL053013 Drosophil
c 2	56	0.6	1101	12	CNS017SY	AL108460 Drosophil
3	49.6	0.5	895	12	CNS0071A	AL066286 Drosophil
4	49	0.5	1100	12	CNS016KD	AL106855 Drosophil
5	48.6	0.5	934	12	AG080424	AG080424 Pan trogl
6	48.6	0.5	964	12	CNS003WG	AL065254 Drosophil
c 7	48	0.5	910	12	CNS006ON	AL065629 Drosophil
8	48	0.5	922	12	CNS0073W	AL066784 Drosophil
9	47.4	0.5	452	12	AU101413	AU101413 AU101413
c 10	47.4	0.5	615	9	AU069689	AU069689 AU069689
c 11	47.2	0.5	925	12	CNS0091P	AL053013 Drosophil
c 12	47	0.5	1039	12	CNS00JRF	AL076642 Drosophil
c 13	46.2	0.5	755	10	BI329221	BI329221 60298391l
14	45.6	0.5	884	12	CNS006U0	AL065923 Drosophil
15	45.6	0.5	914	12	CNS00CZP	AL059740 Drosophil
16	45.4	0.5	645	12	CNS012I3	AL101589 Drosophil
c 17	45.4	0.5	1101	12	CNS012S8	AL101954 Drosophil
18	45.2	0.5	657	10	BI959738	BI959738 HVSMEn002
c 19	45.2	0.5	997	12	CNS06DN	AL065132 Drosophil
c 20	45	0.5	870	12	CNS06NFU	AL406720 T7 end of
c 21	44.8	0.5	355	10	BI907164	BI907164 603065726
c 22	44.8	0.5	667	12	CNS03VGK	AL266285 Tetraodon
23	44.8	0.5	902	10	CNS006QP	AL065804 Drosophil
24	44.6	0.5	1000	10	BG674928	BG674928 60261094
c 25	44.4	0.5	875	12	CNS02705	AL184982 Tetraodon
c 26	44.2	0.5	936	12	CNS01608	AL106130 Drosophil
c 27	44	9	366	9	AI619629	AI619629 ty5la09.x
c 28	43.8	0.5	518	9	AI259159	AI259159 LP02509.5
29	43.8	0.5	519	9	AI294490	AI294490 LP07873.5
30	43.8	0.5	576	9	AI405974	AI405974 GH26141.5
c 31	43.8	0.5	884	10	BG822842	BG822842 60272783A
32	43.8	0.5	948	12	CNS007HK	AL067579 Drosophil
33	43.8	0.5	1101	12	CNS012GS	AL101542 Drosophil
34	43.6	0.5	572	12	CNS043SN	AL273200 Tetraodon
35	43.6	0.5	764	9	AL547921	AL547921 AL547921
36	43.4	0.5	1159	12	CNS015XR	AL106041 Drosophil
c 37	43.2	0.5	844	12	CNS0052P	AL056652 Drosophil
c 38	43.2	0.5	962	10	BG421857	BG421857 60450890
39	43.2	0.5	983	12	CNS04QNN	AL302828 Tetraodon
40	43.2	0.5	1101	12	CNS00LXJ	AL078875 Drosophil
c 41	43	0.5	634	9	AA567915	AA567915 HL01989.5
42	43	0.5	920	12	AG013041	AG013041 Homo sapi
c 43	43	0.5	935	12	CNS006XK	AL066051 Drosophil
c 44	43	0.5	1201	12	CNS016AG	AL106498 Drosophil
45	43	0.5	1203	12	CNS01SV4	AL106054 Drosophil

ALIGNMENTS

```
RESULT 1
CNS0091P
LOCUS       CNS0091P          925 bp    DNA        linear   GSS  03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL053013
VERSION     AL053013.1  GI:4934461
KEYWORDS    GSS.
SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 925)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp; the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1..925
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
```

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                    /clone="BACR19D16"
                    /note="end : TET3"
BASE COUNT    120 a    61 c    61 g   172 t   511 others
ORIGIN

Query Match               0.7%;  Score 65.6;  DB 12;  Length 925;
Best Local Similarity    16.6%;  Pred. No. 0.00016;
Matches   56;  Conservative  153;  Mismatches  128;  Indels    0;  Gaps    0;

Qy   5525 CGGGGGCTGGGCGGCGGCGGTGGTAGGCCATTGCCACAGTGTAATAGCTGCGGCCAGTGGCGGC 5584
               ::|: :.:|: ::||:::::::::::::::|  |  ||::: :::::::: :|
Db    560 YGKGCSSGGBSCSCCSSSCSSSSCBCCCCSSCSSYCCSSSBSSSKCSSTSBSCSC 619

Qy   5585 CTATGGGGCTTCTAGGAGCCCTCCATTGGCTGCTGCCGCCGCTTCCTACCTCATGGGGTTGGG 5644
               |   | : |:: :::::::::::::::: ::: ::::::::: ||:|:|
Db    620 CCCSKSVCGTSCSSSSSCSSSSSSTSSSSSSTSKSSSGGSSSSSSSYTTSKSTSASG 679

Qy   5645 CGTCGGAGGCAACGCGCCAAACCCGTCTAGCCTCCGCTGCTCCTACTAGGGCCGCTGGGAC 5704
               :|: |: |:|:::::.::|::: | .::::|::: ::::|:::::::: ::::::|:
Db    680 SGSWSAGGGSGGTGSTSSSSSSTSTSSSSVSSGGSKSSTBSSGSBSSSSGGSSSSSSSTSSB 739

Qy   5705 CGCTCTGGGCACGCCTGTCGTGGGGTTAACCATGGCGGCGCGTTCATGGGAAGTGCTAG 5764
               :||::::: ::|::|:: |:: .:: :::|::|||: ::: ::|: :::|:
Db    740 BSCTSTSSSSSSYSSSTSCCCTCCCSYSYSSTSSSSSTSWGSTSCSSSSVGTSSSSD 799

Qy   5765 CGTCTCCCTCCTTGCTCACCATTTTACTGGGGCCGTGGGGGGTGGAGGGCGTGGT 5824
               : |:|||::| |: :::|:: || ::::|:::::: |::|::|:: | ||||
Db    800 STSTCCCSCCYMCTCCSTYBMBCYTSTSCGGSSSSKGVTKCCGCCGCGSSSTNGMBGT 859

Qy   5825 GAATGCGCGCTAGCCTTTGTCTTCGACTTTATGGCGGGG 5861
               :| :::::: ::::: :::|:: ::|:
Db    860 SSACSSSSSSCSSSSVSSSSKKSSASSSSVSSSGGSGGV 896


RESULT 2
CNS017SY/c
LOCUS       CNS017SY                1101 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL108460
VERSION     AL108460.1  GI:5628764
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk ". This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1..1101
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN37L08"
                     /note="end : SP6"
BASE COUNT    254 a   176 c   160 g   152 t   359 others
ORIGIN


Query Match               0.8%;  Score 56;  DB 12;  Length 1101;
Best Local Similarity    17.6%;  Pred. No. 0.034;
Matches   72;  Conservative  177;  Mismatches  157;  Indels    2;  Gaps    1;

Qy   8785 TGGAGGTGGCAAGGTGCTGAGCGACCTCAAGCTCCTGGCCTAGCAGTCCACGGAAGA 8844
               ::|: :.:::|:::::::::::::::::::::.::|.::|:::|::|. .:::|:|
Db   1046 BSGSSSBSSBBSSSTSSSSCSSSSTSSSSSSTSBBTBSTSSSSTTTTTTTTTTSTTBTB 987

Qy   8845 AGGCCGGGCATTGCGAACGCGTATGCYCCGGTCGCGCGGTTGGCGTCGAGTTGGCTAGGG 8904
               ::::::::::|:::::::::::::::::::.:::::::|:::::::::::::
Db    986 BSSBSBSSSSSTSSSBBYSKSBFSBSSBBSTSSSASBSSSSSSSBSSTSTTBSTSBBBSTS 927

Qy   8905 GGCTGTTCTGGGCGTCCAGGCCTGCGCCTTCCCCCTCCGAGATTGCTCGTATCCCGGGG 8964
               ::: .::|::::: :::: .|::::::|:::::::::|::::::::::::
Db    926 SSSSGGSSSSBBBSTBSBSSBBTBPTTTBTKSTSTSSSSTSBBTTSBBSSSSSSSBSSSB 867

Qy   8965 GTTTCCCCTTCCCCCCCTATATGGGGTGGTTCATCAATTGGATTTCACAAGCCAGA 9024
               :||||: ::|::::::::::::::::|:::.:::|: || :::::::::::|:|||
Db    866 STTTSBSS--TBSSYGSSSBTCTSKCSTBTSGSGBTBTSTBMSKBSSTSSTSBTSGSSSBCGG 809

Qy   9025 GGAGTCGCTGGGCGTGGTGTTGGGTTCTTAGCCCTGCTCAGCCCTTCTTCGGGTGAA 9084
               : ::|:. :::::|:::||:|:: ::|:: :||| ::|:|| ||||  |||  |:.:
Db    808 SCGSTSGSSCSSBCGKSTSSGSTSSGGTTCGBCSSTGGCSCCYCSCCCTCSTCGTSTCCS 749

Qy   9085 CTAAATTCATCTGTCGCGCAAGGTCCGTGACTGATCATCACTGAGGAGGTTCCCGCC 9144
               | .. .: ::|::|::: || :::|:: || :: ::::| | | ::::: |  ||||
Db    748 CSCSGTGSSBKCCYSTSSSASTGSSCSSSTSSSGGTKMTGGCCGHTTKGTGSTCCCTGG 689

Qy   9145 CTCCCCGCCCCAGGGGTCTCCCCGCTGGGTAAAAAGGGCCCGGCCTTG 9192
               :|: ||| :::|:::::| ||| :::|::|::::||||||:||:|| |
Db    688 BYCCYBCMTMMCCGGSCCCSCYCCGSSKCTSMGTTGCMYYCCGCTS 641


RESULT 3
CNS0071A
LOCUS       CNS0071A                 895 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC
            BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL066286
VERSION     AL066286.1  GI:4945153
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1..895
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
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```
                    /plasmid="pBeloBAC11"
                    /db_xref="taxon:7227"
                    /clone_lib="DrosBAC"
                    /clone="BACN16D22"
                    /note="end : SP6"

BASE COUNT   132 a   229 c   106 g   220 t   413 others
ORIGIN

Query Match                0.5%;  Score 49;  DB 12;  Length 1100;
Best Local Similarity     22.1%;  Pred. No. 1.6;           Indels   6;  Gaps   1;
Matches  113;  Conservative 170;  Mismatches 222;

Qy  5181  GGGTCTCCGTGGTGGTTACAGACTGGATCTGGATGTGAAGGGGGTGGCAGCCCCCTTATCGG  5240
          ||:|| :  ||  :|| ||        :|:| |: :| :|| : ::.       :|:
Db   579  GGCKGKSGTSGGGSKGTGCGTGCGTGSGGGSGGCCGTGGTYTKKSGCKGYGGCCBCGGSGS   638

Qy  5241  CATGGAGACACCAGGCCACGCCCAGCCGGTTGCAGGTCCCCCGGTAGACCATCGGCCG     5300
          | :|  :| | ::::||| ::: ||:| ::|| |||      | :|||||||||||
Db   639  GCKSTCGGSGSGGGGGVGKSKCSGSCCGGSGGCSGGSGGCGCSCSSSSCGGKCGCSKSGCSC  698

Qy  5301  GGGGAGAGTCGCCATCGGATGCCAACACAGTGACAGATGCGGTGGCGGCCATCCAG       5360
          :::: || ::| | ||: | :| ||| :| | || |||:::|:|::|||| :::
Db   699  CSBBSGGYCBGGSSSCKCCSGBCCGGCSGCCGGSCCCCGCTCCGCKGBGBGGGCSYGYCG   758

Qy  5361  GTGGATTGCGATTGGTCAGTCATGACCCTGTCGATCGGGGAGTGCGTCTTGGCCCAG       5420
          :| : ||: ::| ::| ||||      | | |||:::|||| |: :||:
Db   759  CGSKCCBCTGKTCCCSCYSTCKKSKCGGTGTGCGGSCTTGCKCKCCTGTGCKCBYCKCYCTTCKY  818

Qy  5421  GCTAAGACGGCCGAGCCTACGCAGCTACCACCAAGTGGCTTGCTTGGCTG------CTAC    5474
          :| | ||:||| ::|  | |  |||||||| :| |||| |::| ||:|:        ::||
Db   819  SYCKCBCYKCGCGCGCGCSCBKSCCCGSCKCKTCKKCYKKKKKYBKKYKKCCKCTYKCK      878

Qy  5475  ACGGGAGACGGGGCCGTGCCCCACTGTTCAATTGTTGACAAGCTCTTCGCCGGGGCTGG     5534
          :| :|| |:|| || | |  |:|::||: |:| | || | :|:|:|:| ::||| :|:
Db   879  KCBCCKYYKCKBBKCKCCKBKCKCKCKCKCCBBKCBKCBKCKCKCCBKBBCCCB          938

Qy  5535  GCGGGCGTGGTAGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGGCGGGCTATGGGGCT    5594
          :| ::|: ::| || :| :| |||| | :| | | || :| :|: ::| :||:|| :::
Db   939  KCYKCCCKBCCBCKBKYKCKCCKBKKBYKKCBCBKCCCBCBCKBCKCKCCKBBKCCK       998

Qy  5595  TCTAGGAGCCCTCCATTGGCTGCTGCCGCTTCCTACCTCATGGGGTTGGGCGTCCGGAGGC   5654
          :| |   ||| :| | || |: :| ||| :||  |:|||:|| ||::||::|:| |:|::|
Db   999  KCKKKCBKCKBBKCBCKBCKBCKBCKBCKBBCBCKCCCKKYTYTBKKYKKKKKKYKC       1058

Qy  5655  AACGGGCAAACCCGGTTAGCCTCCCGCTCTCC   5685
          ::| ::| ||| |||:|||| |||||| :|||
Db  1059  KCYKCBSCBKKCKKBBKCKCKCBCKCBKCC    1089


RESULT 5
AG080424
LOCUS       AG080424               934 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-076J08.R, genomic survey sequence.
ACCESSION   AG080424
VERSION     AG080424.1  GI:11632226
KEYWORDS    GSS; GSS (genome survey sequence).
SOURCE      Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
            BAC Library clone:PTB-076J08.R.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1 (sites)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 934)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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```
                    /clone="BACR14B09"
                    /note="end : TET3"
BASE COUNT   124 a    80 c   204 g   179 t   308 others
ORIGIN

Query Match                0.5%;  Score 49.6;  DB 12;  Length 895;
Best Local Similarity     19.0%;  Pred. No. 1.1;
Matches   82;  Conservative 148;  Mismatches 202;  Indels   0;  Gaps   0;

Qy  2266  TGTGGTGGTGGGTCAGAACCAGTTGCGGTTCTAGGACTGCCGGCTGTGGACGCTGCCGTGG   2325
          ::::::::::: :| | ::||  :  |::| | :|| ||  ::|  |:::
Db   461  KKTGKKGGTGGTRGKGGGKGKGKGKTTKKTGGKTKKKKKKKGGGGGKGKGKKKKK         520

Qy  2326  CGGGTGAAGTTTTTGCGGGCCCTGCCTTGTCATGGTGTTTGGGCCTTCCCACTGTCAGTA    2385
          ::|::||||| :|| | ::|||  :|:  ::|  :|| || ||:|       :|
Db   521  GGKKKTKKKKKTTKTGGKKGKGTGKTKTGGKTKKKKKKGGTGTKTTKKKKTKGKTKK       580

Qy  2386  TGATACTAGGTCTAGCAAACCTGGTGTTGTACTTTCGGTGGATGGCCCTCAGCGCCCTCA    2445
          | ::||| ::: |:  ::::|  : : ::  ||||||||     |||     | | ::::
Db   581  KTGKGKTKKKKGTGKTGKKGGTGKKTKTKTGKGKKGGGGTGKKKGTGGGKGGKKGKTKKTGT   640

Qy  2446  TGTTCCCTCGTGTTGTGGAAGCTCGCTCGGGGAGCTTTCCCGCTGGCACTTTTGATGGGGA   2505
          |:::  :|| | | :::|::|:   |  :|||||| :::   | |:  | :::::|| :
Db   641  GKKTGGKTKTKTKKKKKGTGTKGGGKGKGTKGKKKKKKKGTKTKKTTTKTTT            700

Qy  2506  TTTCGGACCCCGGCGGGCCACCTCTGTCTCGGGGCCGAGTTCTGCTTCGATGTCACAT     2565
          |:| :| | :|||:||| : ::| | | :|||||  |||   :|::||||  |:|:|:
Db   701  TTKTKTTGKKKTGGKGGGKGKGKCCGAGTTCTGCTTCGATGTCKTKKTTKTGKGKKKKTKTT   760

Qy  2566  TCGAGGTGGACACTTCGGTGTTGGGCGTGGTGGTGGCCAGCGTGGTTGGGCCCATAG       2625
          :| ::|:|: | |:|:|:||:| |:| |::|: ::|:|::| | ::  ::| :: ||
Db   761  KKKTGKTKKKGTKKKKTGTGKGKTKKKGTGKKGKGKGGKKKKKTGKKTTTGTKGGK        820

Qy  2626  CGCTCCTGAGCTCAATGAGCGCAGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACGT    2685
          ::  :::|| ::|  |  :|:||:  ::|::|:| | |  :: |:||:| :| :||:|:
Db   821  KGGGGKTKKKKGGKKKTKKKKGTKKKKKTKKGGKTKKKTTGTKTKKKKKKGKGKK         880

Qy  2686  GGGTGAAAGGGT   2697
          ::|:: |  :||
Db   881  GGKTKKGGGKGT    892


RESULT 4
CNS016KD
LOCUS       CNS016KD              1100 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106855
VERSION     AL106855.1  GI:5524152
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1100)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1..1100
                     /organism="Drosophila melanogaster"
```

```
COMMENT     (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from
            the chimpanzee BAC library PTB This BAC end was generated during
            the R&D process and may have higher chance of clone tracking
            errors.
PRIMERS
            Sequencing: M13Rev
LIBRARY
            Vector   : pKS145
            R.Site 1 : SacI
            R.Site 2 : SacI.
FEATURES             Location/Qualifiers
     source          1..934
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="PTB-076J08.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT       27 a    450 c    306 g    141 t     10 others
ORIGIN

Query Match            0.5%;   Score 48.6;  DB 12;  Length 934;
Best Local Similarity 47.1%;   Pred. No. 1.9;
Matches  132;  Conservative    0;  Mismatches  148;  Indels    0;  Gaps    0;

Qy   2588 GGGCTGGGTGGTGGCCAGCGTGGTGGCTGTGGGCCATAGCGCTCCTGAGCTCAATGAGCGC 2647
            |    ||  ||||  |||   |  ||  ||  | ||      |  | |||
Db      1 GCGTCGGTGGGGGGGGGAGGGGGTCTCTTTNATTTCTACCTCTGGAGCCGGNGGCTCCC 60

Qy   2648 AGGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGTACCAGGCTGT 2707
            | |||||   | ||   | ||| ||    |  |||||||   | ||
Db     61 CTCCTGTTGGAAAGNGANNCCNGTCTTTTGGGGGGGNGGGAAAAACCCCGNGGNGGGGN 120

Qy   2708 GCGCCAGAGAGGTGGTGCGGAGCCCCCTCGGGGAGGGGCGTCCTACCAAGCTTCTGACGTT 2767
            |  |      ||||| | || |||||| |||| || |  |  |||      || |   |
Db    121 GGGAAGGGGGGGGGGGGGGGGGGCCCCCGGGGGCACGCGCCCCAGAGGCCCCCCCGGG 180

Qy   2768 CGCCGTGCTGCCTCATCATCATCCGGATGCTCCGATGCTGATGATGGTGGTGGCCTT 2827
            | ||   |   |  |  | |   ||  ||  ||     | |  |  | | | |||
Db    181 CGCCCGGCCGGCCGGCCGGCCCCCGGCCGGCGGGGGCGCGGGGGGCGCGGGGGCGGG 240

Qy   2828 GGTCCTCCTCTTCGGCCTGTTCGACCGCACTGGACTCGGCC 2867
            || |   |  | | ||  | |  |  | |  || |  |||
Db    241 GGGGCGCGGCCGCCGCCCGCCCGCCGCCGCCCGCCGCCCCGCCC 280

RESULT 6
CNS003WG/c
LOCUS       CNS003WG    964 bp    DNA    linear    GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR09E09 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065254
VERSION     AL065254.1    GI:4942606
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 964)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1..964
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR09E09"
                     /note="end : TET3"
BASE COUNT      234 a    160 c     60 g    105 t    405 others
ORIGIN

Query Match            0.5%;   Score 48.6;  DB 12;  Length 964;
Best Local Similarity 21.6%;   Pred. No. 1.9;
Matches  104;  Conservative  179;  Mismatches  189;  Indels    9;  Gaps    3;

Qy   2301 CTGCCGGCTGTGGACGTGCCGTGGCCGGTGAAGTTTTGCGGGCCCTGCCTTGTCATGG 2360
            |  ||| ::  |  ::||  :: : : :  ||   :  :: :: :: ::
Db    951 CBSCSGCVYKTTTCBSCCGGSGSTBYSCSSTSSCGSCBYGSBGSGSBBGTSGKGSSTSGS 892

Qy   2361 TGTTTGGCCTTCCCACTGTCAGTATGATACTTAGGTCTCAGCAAACCTGGTGTGTTACTTT 2420
            |::|: |: ::  : :  : |: :  : :  :: :: ::: ::   || :  :  ::
Db    891 TSTYBGCSVSGSSSTGSSGSSBGSRCCGSCTCBSSCSGCGSCCSWKCGBTTTTSMSANM 832

Qy   2421 CGGTGATGGGCCCTCAGCGCCTCATGTTCCTCGTGTTGTGGAAGCTCGCTCGGGAGCT 2480
            :::::|::: ::: : ::: :::  ::::: :: :: ::|  |:: :|  ::::: :: :::
Db    831 SGSSGSGSGSGGGSSGGGSVYSSRTRKKRSSGSGBSGGKGSGGGRGAGGGGGGGRGGSSK 772

Qy   2481 TTCCCGCTGCCACTTTTGATGGGGATTTCGGCG---ACCCGCGGCCGACCTCTGCT 2536
            ::  ::| : : ::::::|  :: ::|| ::: |   ::::: ::  :::::|:| |:|
Db    771 SSTSGCGSGSGGRRTTTTKGGSSSSGGSTTGSCSGGGAAASSSSGRGVGABBGKTTGTGST 712

Qy   2537 CGGGGCCGAGTTCTGCTTCGATGTCACATTCGAGG-TGGACACTTCGGTGTTGGGCTGGG 2595
            :::::::|:||  | | |::: : ::: ::: |:|| | ::::: :: ::| ::: ::
Db    711 TGSKVGSKYTTTSGKVNTSSSSRYCRSTSGASARGTTBGSAAAGNSSSAAMSMKCSASS 652

Qy   2596 TGGTGGCCAGCGTGGTGGTGCTTGGGCCATAGCGCTCCTGAGCTCAATGAGCGCCAGGGGGGGT 2655
            ::| ::::: ::: :::: | ::::: ::|| :::: :: ::: :::  :: ::: :::::::|
Db    651 VVGVSCCSMCSASSSCCSSSCMVGCGGKCGTKCGSSSVVSRSGSSRTGCVGVGCCSSGSGBT 592

Qy   2656 GGAAGCACAAGGCCGTGATCYATAGGACGTGGTGTAAAGGTACCAGGCTGTGCGCCAGA 2715
            :: :::| ::| :: : |:: |::::|::|  ::: : :  :::: ::::|:|  :::|
Db    591 TSSGGSVAAAKACSACGCAK---GGSSVSGGCCGYTWSSRADCAAAGMACRRVSSGTVA 536

Qy   2716 GGGTGGTGCGGAGCCCCCTCGGGGAGGGGCGTCCTACCAAGCTTCTGACGTTCGCCTGGT 2775
            :::| :::::: :::::: : :::: ::::: :: :::::: :: :: :::  :: : :|
Db    535 VRBTSHNTSTGSSSSSCSCCCSCSMYSCSTCKTCCSSSSSAAVKTTGGCARWRSGRSSSBT 476

Qy   2776 G 2776
            |
Db    475 G 475

RESULT 7
CNS006ON
LOCUS       CNS006ON    910 bp    DNA    linear    GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACRI4J21 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065629
VERSION     AL065629.1    GI:4944698'
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
```

REFERENCE Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
AUTHORS 1 (bases 1 to 922)
TITLE Genoscope.
JOURNAL Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see http://www.fruitfly.org The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
 source 1..922
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR14D09"
 /note="end : TET3"
BASE COUNT 223 a 95 c 109 g 221 t 274 others
ORIGIN

Query Match Best Local Similarity 22.8%; Score 48; DB 12; Length 922;
 Matches 103; Conservative 128; Mismatches 220; Indels 0; Gaps 0;

Qy 2169 CCTCCTCCACGCTGGTTGCTCTTGGATTTTGTATTTGTCCTGCTCTATCTGATGAAGCTG 2228
Db 470 CCCYCTTGGTGCTTTTTTTTTKTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 529
Qy 2229 GCTGAGGCACGGTTGGTCCCGTTGATCTTGCTTCTGCTGGTGGTGGTGAACCAGTTG 2288
Db 530 TKTTGGGTKGCGTKTTYTTTSTGTKTKGTGTKTKTTKKTTKKTRTKKTTYKBKTG 589
Qy 2289 GCGGTTCTAGGACTGCCGGCGTGTGGACGCTGCCCGTGGCGGGTGAAGTTTTGCGGCCCT 2348
Db 590 TGTSTGKGKGKGKGKTKKTTTGKKTTGKKTKKKKKTKTTKGKKKKTKTTKGKKKGTGKG 649
Qy 2349 GCCTTGTCATGGTGTTTGGGCCTTCCCACTGTCAGTATGATACTAGGTCTAGCAAACCTG 2408
Db 650 KKTGTTGGGKKKKTKTKKKKTGKKKKKKTGKKGKKGTKKTKKTTKTTKGGKGGKKTKKKKKT 709
Qy 2409 GTGTTGTACTTCGGTGGATGGGCCCTCAGCGCCTCATGTTCCTCGTGTTGTGGAAGCTC 2468
Db 710 TKKTTKKTTKTKTKKKKKTKTTKKKKTKTTKKKGTKKKKGKTKGTGTKK 769
Qy 2469 GCTCGGGGAGCTTTCCCGCTGGCACTTTTGATGGGGATTTCGGCGACCCGCCGGGGCACC 2528
Db 770 GTGGKGKKKGKGKGKKKKKKKKKKKGKGTGTKKKKTKGTGKTKKTKKTKTKTKKKG 829
Qy 2529 TCTGTGCTCGGGGCCGAGTTCTGCTTCCGATGTGCACATTCGAGTGTGGACACTTCGGTGTTG 2588
Db 830 TKKGGKTKKGTKKGKKKKGTKKKKNTTKKTKGTGTKKKKKKKGKGKGKKKKKKGKKKK 889
Qy 2589 GGCTGGGTGGTGGCCAGCGTGGTGGCTTGGG 2619
Db 890 GKGGKGKKKGKKKGKKKGGGGKGGKKGKKK 920

RESULT 9
AU101413/c
LOCUS AU101413 452 bp mRNA linear EST 22-AUG-2000

REFERENCE Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
AUTHORS 1 (bases 1 to 910)
TITLE Genoscope.
JOURNAL Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see http://www.fruitfly.org The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
 source 1..910
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR14J21"
 /note="end : T7"
BASE COUNT 202 a 63 c 112 g 198 t 335 others
ORIGIN

Query Match Best Local Similarity 17.8%; Score 48; DB 12; Length 910;
 Matches 63; Conservative 154; Mismatches 135; Indels 2; Gaps 1;

Qy 2582 GGTGTTGGGCTGGGTGGCTGGGTGGCCCAGCGTGGTGGCTTGGGCCATAGCGCTTCCTGAGCTCAAT 2641
Db 519 GSSSKGGCGGCGSSYGGGGGYGGTGSSGGGGSSSSGGGGSSSSSSSSCCSSSBGCBS 578
Qy 2642 GAGCGCAGGGGGGTGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCA 2701
Db 579 SCGCGCSCSYSSSSGTGSCGCGSSSSSSSSSCCSSTSTSSSSTSGCGYSSSSGSBSSSCS 638
Qy 2702 GGCTGTGCGCCAGAGGTGGTGCGGAGCCCCCTCGGCGGAGGGCGTCTACCAAGCTTCT 2761
Db 639 STBTSSSTTBTBTKBTSTYSYSYTTTSTTSTBSBTSYGSBBKSTSSTSSSTSSSTSSSS 698
Qy 2762 GACGTTCGCCTGCTGCTTGGGCCTCATACATCTGGCCCGATGCTG--TGATGATGGTGGTG 2819
Db 699 SSSSTSSCTSTKBYSTSTBSYSBTBTBTTSTSTBBTTSTBBTTBYTKSTTSMTSTY 758
Qy 2820 GTGGCCTTGGTCCTCTTCCGCCTGTTCGACGCACTGGACCTGGCCCCTGGAGGAGCTC 2879
Db 759 TTBBSTSKBSTBTSTBKSTGTKTBTSBTTSCTSSSSSBBSTSYSYSTSCBSSSBSSTSYS 818
Qy 2880 CTGGTCTCCCCAGCCCTCGTTACGGCGACTGCCACGGGGTTGGTTGAGTGCTGTCTG 2933
Db 819 BCTSTSTSTSSBBSBSSSSSCGTSBTSSSSTSTTSCTSTTCKTSTGBSSYGTG 872

RESULT 8
CNS0073W
LOCUS CNS0073W 922 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR14D09 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
ACCESSION AL066784
VERSION AL066784.1 GI:4945247
KEYWORDS GSS.
SOURCE Drosophila melanogaster
 fruit fly.
ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

```
DEFINITION   AU101413 Rice panicle shorter than 3cm Oryza sativa cDNA clone
             E30779, mRNA sequence.
ACCESSION    AU101413
VERSION      AU101413.1  GI:9865663
KEYWORDS     EST.
SOURCE       Oryza sativa
  ORGANISM   Oryza sativa
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 452)
  AUTHORS    Sasaki,T. and Yamamoto,K.
  TITLE      Rice cDNA from panicle (2000)
  JOURNAL    Unpublished (2000)
COMMENT      Contact: Takuji Sasaki
             National Institute of Agrobiological Resources
             Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
             305-8602, Japan
             Tel: 81-298-38-7441
             Fax: 81-298-38-7468
             Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
             PROJECT ='RGP'.
FEATURES             Location/Qualifiers
     source          1..452
                     /organism="Oryza sativa"
                     /strain="Nipponbare"
                     /db_xref="taxon:4530"
                     /clone="E30779"
                     /clone_lib="Rice panicle shorter than 3cm"
                     /dev_stage="shorter than 3cm"
                     /note="Organ: panicle"
BASE COUNT      46 a     154 c     193 g      58 t
ORIGIN

Query Match             0.5%;  Score 47.4;  DB 9;  Length 452;
  Best Local Similarity 52.2%;  Pred. No. 2.5;
  Matches  105;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy    2461 GGAAGCTCGCTCGGGGAGCTTCCCGCTGCACTTTTGATGGGGATTTCGGCGACCCGCG 2520
           ||||||  ||  ||| || |||| ||| |  |||| || || |||| ||||||||||||
Db     252 GGAAGCCCGGGAGGTCCCCCATGCGCCACGCCCACGAAGAGGTTCTTCTTGTCCCTCCA 193

Qy    2521 GGCGCACCTCTGTCGCTCGGGGCCGAGTTCTGCTTCGATGCACATTCGAGGTGGACACTT 2580
           || ||||  ||  ||| || ||| | | |  |||| |   || ||||||||||| |||||
Db     192 CGCCCGCCGGTCCCGTGCCGTGCCGGGGCGCCGGGAGCGACGACGCCCGTCGTCGAGCCGT 133

Qy    2581 CGGTGTTGGGCTGGGTGGTGGCCAGCGTGGTGGCTTGGGCCATAGCGGCTCCTGAGCTCAA 2640
           || ||| ||||||| ||  ||||||  ||| ||||| |||||| |||| | |||||||||
Db     132 CGCCCGCGGGCACGGCCCTGCCCGGCCGTGCCGCGGCGTGCGCCATGGCCATGGCCAGAGCAGGA 73

Qy    2641 TGAGCGCAGGGGGGTGGAAGC 2661
           | || || ||| | |||||
Db      72 GGGACGACGCGACGCCGAAGC 52


RESULT 10
AU069689/c
LOCUS        AU069689                615 bp    mRNA    linear   EST 07-JUN-1999
DEFINITION   AU069689 Rice callus Oryza sativa cDNA clone C2047_1A, mRNA
             sequence.
ACCESSION    AU069689
VERSION      AU069689.1  GI:5005072
KEYWORDS     EST.
SOURCE       Oryza sativa
  ORGANISM   Oryza sativa
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 615)
  AUTHORS    Yamamoto,K. and Sasaki,T.
  TITLE      Rice cDNA from callus (1998)
  JOURNAL    Unpublished (1998)
```

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COMMENT      Contact: Takuji Sasaki
             National Institute of Agrobiological Resources
             Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
             305-8602, Japan
             Tel: 81-298-38-7441
             Fax: 81-298-38-7468
             Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
             PROJECT ='RGP'.
FEATURES             Location/Qualifiers
     source          1..615
                     /organism="Oryza sativa"
                     /strain="cultivar Nipponbare, sub_species Japonica"
                     /db_xref="taxon:4530"
                     /clone="C2047_1A"
                     /clone_lib="Rice callus"
                     /note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
                     NotI; cDNA prepared from rice callus mRNAs by using
                     oligo(dT) as a primer and ligating to the SalI-NotI site
                     of pBluescript II SK+ phagemid."
BASE COUNT      77 a     186 c     242 g     109 t       1 others
ORIGIN

Query Match             0.5%;  Score 47.4;  DB 9;  Length 615;
  Best Local Similarity 52.2%;  Pred. No. 2.9;
  Matches  105;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy    2461 GGAAGCTCGCTCGGGGAGCTTCCCGCTGCACTTTTGATGGGGATTTCGGCGACCCGCG 2520
           ||||||  ||  ||| || |||| ||| |  |||| || || |||| ||||||||||||
Db     254 GGAAGCCCGGGAGGTCCCCCATGCGCCACGCCCACGAAGAGGTTCTTCTTGTCCCTCCA 195

Qy    2521 GGCGCACCTCTGTCGCTCGGGGCCGAGTTCTGCTTCGATGCACATTCGAGGTGGACACTT 2580
           || ||||  ||  ||| || ||| | | |  |||| |   || ||||||||||| |||||
Db     194 CGCCCGCCGGTCCCGTGCCGTGCCGGGGCGCCGGGAGCGACGACGCCCGTCGTCGAGCCGT 135

Qy    2581 CGGTGTTGGGCTGGGTGGTGGCCAGCGTGGTGGCTTGGGCCATAGCGGCTCCTGAGCTCAA 2640
           || ||| ||||||| ||  ||||||  ||| ||||| |||||| |||| | |||||||||
Db     134 CGCCCGCGGGCACGGCCCTGCCCGGCCGTGCCGCGGCGTGCGCCATGGCCATGGCCAGAGCAGGA 75

Qy    2641 TGAGCGCAGGGGGGTGGAAGC 2661
           | || || ||| | |||||
Db      74 GGGACGACGCGACGCCGAAGC 54


RESULT 11
CNS0091P/c
LOCUS        CNS0091P                925 bp    DNA      linear   GSS 03-JUN-1999
DEFINITION   Drosophila melanogaster genome survey sequence TET3 end of BAC #
             BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
             fly), genomic survey sequence.
ACCESSION    AL053013
VERSION      AL053013.1  GI:4934461
KEYWORDS     GSS.
SOURCE       fruit fly.
  ORGANISM   Drosophila melanogaster
             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
             Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
             Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 925)
  AUTHORS    Genoscope.
  TITLE      Direct Submission
  JOURNAL    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
             BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
             - Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
             collaboration with the Berkeley Drosophila Genome Project (BDGP).
             The BDGP is constructing a physical map of the Drosophila
             melanogaster genome using these BACs. For further information
             please see http://www.fruitfly.org The BDGP Drosophila
             melanogaster BAC library was prepared by Kazutoyo Osoegawa and
             Aaron Mammoser in Pieter de Jong's laboratory in the Department of
             Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
             NY. The library is named RPCI-98 and was constructed by partial
             EcoRI digestion of Drosophila DNA provided by the BDGP from the
```

EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES   Location/Qualifiers
     source   1..1039
                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
                /clone_lib="RPCI-98"
                /clone="BACR39E22"
                /note="end : TET3"

BASE COUNT   461 a   213 c   119 g   58 t   188 others
ORIGIN

Query Match   0.5%;   Score 47;   DB 12;   Length 1039;
Best Local Similarity   36.8%;   Pred. No. 4.8;
Matches 127; Conservative 44; Mismatches 174; Indels 0; Gaps 0;

```
Qy  8863 CGGGTATCCTCCGGTCGCGGGTTGGGCGTAGGTTGGCGTGAGTTGGCTTGTGTGGCGTCCAG 8922
         |::||:||: |||: ::||||| ::  :: :| :| |: :|: :||:|:: :|||||
Db  1037 CKSYTTTTTTBTTCMGCGSTYGCGGCGCCGCGGSYTCSBGCCSCSCGSSGCCGGCCCCG 978

Qy  8923 GCCTGCGGCTTCCCCCTCCGGAGATTGCTGGTATCCCCGGGGGTTCCCCTTTCCCCC 8982
         :||| |||||||| :|||  :: :| :: |||| ::||:  :::|
Db  977 TKSTGCCGCTTCSCCGSCTCSCCCGGGSCGGGGYCGGGGGCCCKCGTSCCGCCGGSGG 918

Qy  8983 CCTATATGGGGTGGTTCATCAATTGGATTCACAAGCCAGAGAGTCGCTGGCGGGTGGT 9042
         : ||::| |:||||| |||:|| : || :||| ||::
Db  917 GCTTKCCGGSGGGTGGKTBTTGTCGGCGCGSCSKGGSCSTGCCCKCGSCGTCTTTGTG 858

Qy  9043 TGGGGTTCTTAGCCTGCTCATCGGTCGTGAACTAAAATTCATCGTGGG 9102
         |  :||||| ::|||||| :: || :|::| |: :|| ||| |:
Db  857 CGTGTBTGGTGCCTSGGCGYTCCGTKBCGCTTGCTKSTYCCCTTGCGTTTCTTTTCCC 798

Qy  9103 GCAAGGTCCGTGACTGATCATCACTGGAGGAGGTTCCCGCCCTCCCCGCCCCCAGGGGTC 9162
         |||     |  :: |||| ||||||::|:::::|
Db  797 KTCSTTCCCGCCCCGGSGCTGGGGCGGGGSSSTTTYCCTCGCCSTCCYKGSCGYTTGCGS 738

Qy  9163 TCCCCGCTGGGTAAAAACGGGCCCGGCCTTGGGAGGCATGGTGGTT 9207
         : |||||| ::|| |:  ||||| |||
Db  737 GGKGCGTGCGCGTSTTCGCGCGCGCCGCGTGGGGTGSSSGGCGTTGTT 693
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RESULT 13
BI329221/c
LOCUS   BI329221   755 bp   mRNA   linear   EST 30-JUL-2001
DEFINITION 602983911F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5136746 5',
            mRNA sequence.
ACCESSION   BI329221
VERSION   BI329221.1   GI:15013878
KEYWORDS   EST.
SOURCE   house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 755)
AUTHORS   NIH-MGC http://mgc.ncl.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1336 row: e column: 03
            High quality sequence start: 45
            High quality sequence stop: 639.

---

isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES   Location/Qualifiers
     source   1..925
                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
                /clone_lib="RPCI-98"
                /clone="BACR19D16"
                /note="end : TET3"

BASE COUNT   120 a   61 c   61 g   172 t   511 others
ORIGIN

Query Match   0.5%;   Score 47.2;   DB 12;   Length 925;
Best Local Similarity   13.1%;   Pred. No. 4;
Matches 43; Conservative 150; Mismatches 134; Indels 0; Gaps 0;

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Qy  2567 CGAGGTGGACACTTCGGTGTTGGGTGGGTGTGGCAGCGTGGTGCTTGGCCATAGC 2626
         ::: :: |  ||| :::||| ||::: || : |: || :|: :| : ::
Db  891 SSSBSSSTSMSSSSBSSSSGSSSSBSSSSGSSSGTSSACVKCNASSSCGCGMABCCMCSSSS 832

Qy  2627 GCTCCTGAGCTCAATGAGCCAGGGGGTGAAGCACAAGCCGTGATCTATAGGACGTG 2686
         :|: :|: | |||:|| : ||::||| ::| ::::  |::
Db  831 SCCGSASARGVKVRASGGAGKRGGGSGGASASHSSSSSACBSSSSSCSASCWSASSSSSAS 772

Qy  2687 GTGTAAAGGTGACCAGGCTGTGCGCCAGAGAGGTGGTGCGGAGCCCCTCGGGGAGGGGCG 2746
         ::: :: || || ::| :::::| :||| ::: || :| |: || ::::: ::
Db  771 SSRSRRGGGAGGSGASSRSSSSSSASAGSVVSSASSSSSSCSSSVSCSSVASSMSCSS 712

Qy  2747 TCCTACCAAGCTTCTGACGTTCGCCTGGTCCTTGGCCTCATACATCTGGCCGGATGCTGT 2806
         :|: :| ::| |||: || :: :|: || :::|:| :: :|
Db  711 BSSSSASASSSSSSSSACASCSCCCTSWSCSCSTSASMSAARSSSSSSCSSSSSMSAS 652

Qy  2807 GATGATGGTGTGGTGCCCTTGTGCCTTGGCCGGGTTCGACGGCACTGGGC 2866
         :|:: :: :| || | :|::: || :|:| ::|| :|
Db  651 SSASSSSASSSSSGGSSSSSGSACGBSMSSGGGSGVSASSGMSSVSSSGGRSSGGGG 592

Qy  2867 CCTGGAGGAGCTCCTGTCTCCCGGCC 2893
         || :: |:: :| :| :|: :: ::
Db  591 GGVGGSGSSSSGSGSGSGGSGGGSVCSCSS 565
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RESULT 12
CNS00JRF/c
LOCUS   CNS00JRF   1039 bp   DNA   linear   GSS 04-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR39E22 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL076642
VERSION   AL076642.1   GI:4956190
KEYWORDS   GSS.
SOURCE   fruit fly.
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1039)
AUTHORS   Genoscope.
TITLE   Direct Submission
JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial

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FEATURES             Location/Qualifiers
     source          1..755
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5136746"
                     /clone_lib="NCI_CGAP_Li9"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.9 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT   164 a   205 c   264 g   122 t
ORIGIN

Query Match          0.5%;   Score 46.2;   DB 10;   Length 755;
Best Local Similarity  49.0%;   Pred. No. 6.3;
Matches 123;   Conservative   0;   Mismatches 128;   Indels   0;   Gaps   0;

Qy  2749  CTACCAAGCTTCGACGTTCGCCTGGTGCTTGGCCTCATACATCTGGCCGGATGCTGTGA  2808
          | ||  ||| || | |   | | || || | |   |  ||   |    || |  |||| |
Db   544  CCATCAGTTCCTGGCTTCCCATGTTCTCCCCGGCATCCCTGTTCTCTCCCTTTTGGCA   485

Qy  2809  TGATGGTGGTGGTGGCCTTGGCTCCTCCTCTCTCGGCCTGTTCGACGCACTGGACTGGGCCC  2868
          |  ||    |||  |||||||   ||| ||  | || | | |  || |  |||||| |
Db   484  CCACGGAAGATCCAGCCGTGCACCTTCTTCTTCTCTGGGGACCAGGGAATGCCCTGGGCTC   425

Qy  2869  TGGAGGAGCTCCTGGTCTCCCGGCCCCTCGTTACGGCGACTGGCGACGGGTGGTTGAGTGCT  2928
          |   || |||      ||||   ||| |     ||||||   | |||||||   || || | |
Db   424  CATCGTCGTCCCAACTTCTCCCTTGGCTCCCAAGGTAGGCCTGGCACTCCAGGATCCCCCTT   365

Qy  2929  GTGTGATGGCGGGCGAGAAGGCCACCACCATCCGACTGGTCTCCAAGATGTCGCAAGAG  2988
          | ||||    |||    || | ||||| |||||   || |||||  | |    | | ||
Db   364  GAGTCCCCGGCGACCGCGGGAGAGGTCCCTGCAGCCCCATCCAGCAGAGCTTCGGCTGTG  305

Qy  2989  GGGCCTACCTG  2999
          ||| | |
Db   304  GGTATTCCAG   294
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RESULT 14
CNS006U0
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LOCUS       CNS006U0   884 bp   DNA   linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR14N21 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065923
VERSION     AL065923.1  GI:4944891
KEYWORDS    GSS.
SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 884)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
```

filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

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FEATURES             Location/Qualifiers
     source          1..884
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR14N21"
                     /note="end : T7"
BASE COUNT   230 a   62 c   139 g   124 t   329 others
ORIGIN

Query Match          0.5%;   Score 45.6;   DB 12;   Length 884;
Best Local Similarity  16.6%;   Pred. No. 9.5;
Matches 41;   Conservative 107;   Mismatches 99;   Indels   0;   Gaps   0;

Qy  2185  TGCTCTTGGATTTTGTATTTGTCCCTGCCTATCTGATGAGCTGGCTCGAGCCACGGTTGG  2244
          | :  :|:||| |||||  |:::|    ::|   :|| ::    |||  |  ||  |  | :|
Db   616  TKTKTKTTGKTGTTGTKKKGGGGGGKKKKSKGTGKGGGGGGKKKGGTKTKGGKDGTG   675

Qy  2245  TCCCGTTGATCTTGCTTCTGCTGCTGTCGTGGGTGAACCAGTTGGCGGTTCTAGGACTGC  2304
          |:|::| :::| :::|:::::|:::::|:||  :::| : :   :| ::| : : :
Db   676  GKKKTTKKKKKKKGTKGKGKGKTKKKSGTKKKKGGTGKGTGKGTGTKKKKKGGKGKGGK  735

Qy  2305  CGGCTGTGGCACGGCTGCCGTGGCGGGTGAAGTTTTGCGGGCCCTGCCTTGTCATGGTGTT  2364
          ::| ::|:| ::| :: :|:::|::|::::| :::|:||::|::::|::|::::||  :::::
Db   736  KKGGKGKGKKKKKKKKKGKKKKKKTGKKTKGKKGGKKTKKKGKKTKKKKKKKKK   795

Qy  2365  TGGGCTTCCCACTGTCAGTAGTGATGATACTAGGTCTTAGCAAACCTGGTGTTGTACTTTCGGT  2424
          | :::   :: :: ::: :::::::::::::::::::::K::::::::::::::K::::::::
Db   796  KKKKKKKKKKKKKKKKKKKKKKKKKKTKKKKKKKKKKKKCKKKKKKKKKKKKKKKKKK   855

Qy  2425  GGATGGG  2431
          :: :::::
Db   856  KKKKNKB   862
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RESULT 15
CNS00C2P
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LOCUS       CNS00C2P   914 bp   DNA   linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR26P05 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL059740
VERSION     AL059740.1  GI:4947405
KEYWORDS    GSS.
SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 914)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
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source          1..914
                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
                /clone_lib="RPCI-98"
                /clone="BACR26P05"
                /note="end : T7"
BASE COUNT    146 a    121 c    113 g    173 t    361 others
ORIGIN

Query Match        0.5%;  Score 45.6;  DB 12;  Length 914;
Best Local Similarity   19.0%;  Pred. No. 9.7;
Matches   48;  Conservative  111;  Mismatches  93;  Indels   0;  Gaps   0;

Qy  663 CCGGAAGACATCGGGTTCTGCCTGGAAGGCGATGCCTGGTGGCCCTGGGGTGCACGGTT 722
            | --::|·:|::|--||:||:|:|| :|::::|· ·|·|· |·|·|-|-|·|| ||
Db  603 CAGSSMGGAVSGSSGSGSGGCGSVASSCSAGGSCSCSCKCCGSCGTSGGGGSGGGGCG 662

Qy  723 TGCACCGACCGTTGCTGGCCACTGTATCAGGCGGGGTTTGGCGTGCGGCCCTGGCAAGTCC 782
            |:|·:: ·:|:::::| --| |||  :::::|  :::::|· : ::|: |
Db  663 MGSGCGCGSWGBGTSSSGBSWCGSSASCACVSSSBSKYSKSKGSTSWSGYSSGSGSGSGA 722

Qy  783 GCGGCCCAGCTCCTTGGGGAACTGGGGAGCCTCTACGGGCCCTTGTCCGTCTCGGCTTAC 842
            :|::·| ·|||·::||·:::||·::::|:::|::|:::::|::||:·:::||:: ||·:
Db  723 SGGKGSSGGGGKGGGGSGBTSTSKSTSSBSYBTBBBSSTSSYTSTSSBSTSBSBTTTTB 782

Qy  843 GTAGCCCGGATCCTGGGTCTGGCCAGGTTTACTCCCGGGTCCTGACAGTTGGTGTTGCG 902
            |··|·:::::|:|·|: ::  :::|:: :: :::|·::|· :|·:|:|:·:::
Db  783 TTTBTBSSBYSSBBBSTSTSTBSTSSSBSSSSTSBBTTBSSBTSTTTBTSBKTSTBBBB 842

Qy  903 TTGAGGCGCCGG 914
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Db  843 BTTSTSTSSSSS 854

Search completed: October  9, 2002, 05:09:02
Job time : 6430 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2002, 00:04:45 ; Search time 156 Seconds
(without alignments)
14793.120 Million cell updates/sec

Title: US-09-828-498-1
Perfect score: 9395
Sequence: 1 tgacgtggggggttgatcc.........cccaaaggccggttctact 9395

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7979	84.9	9392	1	US-08-466-033-14	Sequence 14, Appl
2	7979	84.9	9392	1	US-08-444-733-14	Sequence 14, Appl
3	7979	84.9	9392	2	US-08-464-134-14	Sequence 14, Appl
4	7979	84.9	9392	2	US-08-461-361-14	Sequence 14, Appl
5	7979	84.9	9391	1	US-08-485-910-14	Sequence 14, Appl
6	7971.8	84.9	9391	5	PCT-US95-06266-14	Sequence 1, Appli
7	7971.8	84.9	9391	1	US-08-638-911A-1	Sequence 14, Appl
8	7885.6	83.9	9327	1	US-08-466-033-234	Sequence 234, App
9	7885.6	83.9	9327	1	US-08-444-733-234	Sequence 234, App
10	7885.6	83.9	9327	2	US-08-464-134-234	Sequence 234, App
11	7885.6	83.9	9327	2	US-08-461-361-234	Sequence 234, App
12	7885.6	83.9	9327	2	US-08-485-910-234	Sequence 234, App
13	7760.6	82.6	9103	1	US-08-466-033-182	Sequence 182, App
14	7760.6	82.6	9103	1	US-08-444-733-182	Sequence 182, App
15	7760.6	82.6	9103	2	US-08-464-134-182	Sequence 182, App
16	7760.6	82.6	9103	2	US-08-461-361-182	Sequence 182, App
17	7760.6	82.6	9103	2	US-08-485-910-182	Sequence 182, App
18	7760.6	82.6	9103	5	PCT-US95-06266-156	Sequence 156, App
19	7141.2	76.0	9126	1	US-08-580-038-26	Sequence 26, Appli
20	7141.2	76.0	9122	2	US-08-639-857-3	Sequence 3, Appli
21	7106.6	75.6	9122	2	US-08-417-629B-1	Sequence 1, Appli
22	2143.4	22.8	2561	1	US-08-638-911A-24	Sequence 24, Appl
23	2141.8	22.8	2561	1	US-08-638-911A-26	Sequence 26, Appl
24	2141.8	22.8	2561	1	US-08-638-911A-30	Sequence 30, Appl
25	2140.2	22.8	2561	1	US-08-638-911A-28	Sequence 28, Appl
26	2084	22.2	2388	1	US-08-638-911A-56	Sequence 56, Appl
27	2005.2	21.3	2379	1	US-08-638-911A-52	Sequence 52, Appl
28	1883.8	20.1	2232	1	US-08-638-911A-53	Sequence 53, Appl
29	1674.2	17.8	1967	1	US-08-638-911A-51	Sequence 51, Appl
30	1568.6	16.7	1848	1	US-08-638-911A-34	Sequence 34, Appl
31	1351.2	14.4	1848	1	US-08-638-911A-40	Sequence 40, Appl
32	1315	14.0	9493	2	US-08-639-857-23	Sequence 23, Appl
33	1184	12.6	1377	1	US-08-638-911A-38	Sequence 38, Appl
34	1110.8	11.8	1290	1	US-08-638-911A-55	Sequence 55, Appl
35	1080	11.5	1288	1	US-08-466-033-39	Sequence 39, Appl
36	1080	11.5	1288	2	US-08-444-733-39	Sequence 39, Appl
37	1080	11.5	1288	2	US-08-464-134-39	Sequence 39, Appl
38	1080	11.5	1288	2	US-08-461-361-39	Sequence 39, Appl
39	1080	11.5	1288	2	US-08-485-910-39	Sequence 39, Appl
40	981	10.4	1181	1	US-08-466-033-98	Sequence 98, Appl
41	981	10.4	1181	2	US-08-444-733-98	Sequence 98, Appl
42	981	10.4	1181	2	US-08-464-134-98	Sequence 98, Appl
43	981	10.4	1181	2	US-08-461-361-98	Sequence 98, Appl
44	981	10.4	1181	2	US-08-485-910-98	Sequence 98, Appl
45	936.6	10.0	1302	3	US-08-932-823A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-466-033-14
; Sequence 14, Application US/08466033
; Patent No. 5766840
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, LaVonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,033
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Fabian, Gary R.
;      REGISTRATION NUMBER: 33,875
;      REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 324-0880
;      TELEFAX: (415) 324-0960
;    INFORMATION FOR SEQ ID NO: 14:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 9392 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: unknown
;      MOLECULE TYPE: cDNA
;      HYPOTHETICAL: NO
;      ANTI-SENSE: NO
;      ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE: HGV-PNF 2161 Variant
;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: 459..9077
US-08-466-033-14
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Query Match        84.9%;   Score 7979;  DB 1;   Length 9392;
Best Local Similarity  90.7%;  Pred. No. 0;
Matches 8515;  Conservative   1;  Mismatches  876;  Indels   1;  Gaps  1;

Qy      3 ACGTTGGGGGGGGTTGATCCCCCCCCCGGCACTGGGTGCAAGCCCATAAACCGACGCCT  62
            ||||||||||| |||||||||||||||||||||||||||| |||||||||||||||||||
Db      1 ACGTGGGGGAGTTGATCCCCCCCCGGCACTGGGTGCAAGCCCAGAAACCGACGCCT  60

Qy     63 ATCTAAGTAGACGCAATGACTCGGCGCGACCCGACGCCGCAAAAGGTGGTGGATGG  122
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     61 ATCTAAGTAGACGCAATGACTCGGCGCGACCCGACGCCGCAAAAGGTGGTGGATGG  120

Qy    123 GTGGTGACAGGGTTGGTAGTCGTAAATCCGGTCATCCTGGTAGCCACTATAGGTGGGT  182
            || ||||||||||||||||||||| |||||||||| - |||||||||||||||||||||
Db    121 GTGATGACAGGGTTGGTAGTCGTAAATCCGGTCACCTTGGTAGCCACTATAGGTGGGT  180

Qy    183 CTTAAGAGAAGGTCAAGACTCCTCTGTGCCTGCGCGGAGACCGCACGGTCCACAGGT  242
            |||||||||||| |||| ||||||||||||||||||||| ||||||||||||||||||
Db    181 CTTAAGAGAAGGTTAAGATTCCTCTTGTGCCTGCGCGGAGACCGCACGGTCCACAGT  240

Qy    243 GCTGGCCCTACCGGTGTGAATAAGGGCCCGACGTCAGGCTCGTCGTTAAACCGAGCCCGT  302
            |||||||||||||||||||||||||||||||| ||||||||| ||||||||||||||||
Db    241 GTTGGCCCTACCGGTGGGAATAAGGGCCCGACGTCGTCGTTAAACCGAGCCCGT  300

Qy    303 CACCCACCTGGGCAAAACGACGCCCACGTACGGCTCGCCCGCGCGCGCCCTTCAATGTCTCTCTTG  362
            ||||||||||||||||||||||||||||||| - |||||||||||||||||||||||||
Db    301 TACCCACCTGGGCAAAACGACGCCCACGTACGGCTCGCCCGCGCCCTTCAATGTCTCTCTTG  360

Qy    363 ACCAATAGGTTTATCCGGCAGTTGACAAGGACCAGTGGGGGCCCGGGGGTTATGGGGAAG  422
            |||||||| || | |||||||||||||||||||| ||||||||||||||| |||| ||
Db    361 ACCAATAGGCTAGCCGGCAGTTGACAAGGACCACCATGGGGGGCCCGGGGGCT-TGGAGAGG  419

Qy    423 GACCCCAAACCCTGCCCCTTCCCGGTGGGGCCGGGAAATGCATGGGGCCACCCAGCTCCGCG  482
            ||| |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GACTCCAAGTCCCGCCCCTTCCCGGTGGGGCCGGGAAATGCATGGGGCCACCCAGCTCCGCG  479

Qy    483 GCGGCCTGCAGCCCGGGGTAGCCGGGGTGGTCCCAAGAATCCTTCCGGGTGAGGGCCGGGT  542
            ||||||||||||||||||||||||||| ||||| |||||||||||||||||||||||||
Db    480 GCGGCCTGCAGCCCGGGGTAGCCGGGGTGGTCCCAAGAATCCTTCCGGGTGAGGGCCGGGT  539

Qy    543 TTCTATACCATCATGGCCAGTCCTTCTTCCTTCTGCGGTTGAGGCCGGCCATTCTG  602
            ||||||||||||||||||||| |||||||||||||||||||| |||||||||||||
Db    540 TTCTATACCATCATGGCCAGTCCTTCTTCCTTCTGCGGTTGAGGCCGGCCATTCTG  599

Qy    603 GCCCCGGCCACCCACACGCTTGTCGAGCGAATGGCAATATTCCTCACAAATTGCTGTGCC  662
            ||||||||||||||||||||||||| |||||| |||||| |||||||||||||||||||
Db    600 GCCCCGGCCACCCACGCCTTGTCGAGCGAATGGCAATATTCCTCACAAATTGTTGTGCC  659

Qy    663 CCGGAAGACATCGGTTCTGCCTGGAAGCGGATGGCCGTTGGGGTGCCACGGTT  722
            ||||| ||||||||| || ||||||||||||||||||||||| |||| ||||| ||
Db    663 ...
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Db     660 CCGGAGGACATCGGTTCTGCCTGGAGGGTGGATGCCTGGTGGCCTGGGGTGCCCTGGGTGGCCGGGTGGCCTGGGTGGCACGGATT  719
Qy     723 TGCACGACCGTTGCTGGCCACTGTATCAGCGGGTTTGGCTGTGTCGGCCTGGCAAGTCC  782
                  |||| ||||  |||||||||||||||||||||||||||||||||||||||||||||
Db     720 TGCACTGACCAATGCTGGCCACTGTATCAGCGGGTTTGGCTGTGTCGGCCTGGCAAGTCC  779

Qy     783 GCGGCCCCAGCTCGTTGGGAACTGGGAGCCTGTACGGGGCCCTGTCGGTCTCGGCTTAC  842
                  |||||| || ||||| |||||||||||||||||||||||||||||||||||
Db     780 GCGGCCAACTGGTGGGGAGCTGGGTAGCCTATACGGCGCCCTGTCGGCTCGGCCTAT  839

Qy     843 GTAGCCGGGATCCTGGGTCTGGGCGGAGGTTTACTCCCGGGTCCTGACAGTTGGTTGTTGCG  902
                  || ||||||||||| |||| |||  | |||| ||| |||||||||||||||||  ||
Db     840 GTGGCCTGGGATCCTGGGCTGGGTGTACTCGGGTGTCCTAACGGTGGGAGTGCGCG  899

Qy     903 TTGAGCGCCGGGTCTACCTGATGCCCAACCTGAAGTGTGCAGTAGAATGTACGTTAAG  962
                  |||| |||  ||||||||||||||||  |||| || |||||||||||||| ||||
Db     900 TTGACGCGCGGGTCTACCCGGTGCCTCAACCTGACGTCGCGTGTGAGCTAAAG  959

Qy     963 TGGGGAAGTGAGTTTGGAGATGACTGAGCAGTTGGCCTCCAATTACTGGATTTTGGAA  1022
                  ||| |||||||| |||||| || ||||||| ||||||| |||||||| ||||||||
Db     960 TGGGAAAGTGAGTTTTGGAGATGACTCGAACTACTGGATTCTGGAA  1019

Qy    1023 TACCTTTGGAAAGTCCCATTTGAATTTTGAATTTGATTTCTGGAGCACGGCAACGATTGTTCATCGTTTTCCTGCTGGTG  1082
                  ||| ||||||||| |||||||||||| |||||||||| |||||||||||||||||||||||||||| |||||||||
Db    1020 TACCTCTGGAAGGTCCCATTTGATTTCTGGAGCACGGCGGTGATAAGCCTGACCCCCTTGTTG  1079

Qy    1083 GTTTGGTGGCCGCATTGCTTTCTGCTGCAGCAACGATTGTCATGGTTTTCCTGCTGGTG  1142
                  ||| ||||||||||||||||| | |||||||||||||||||||| |||||||||||||
Db    1080 GTTTGCGTGCCGCATTGCTTTCTGCTGCAGCAACGATTGTCATGGTCTTCCTGTTGGTG  1139

Qy    1143 ACGATGGCGGGGATGTTGCAAAGGCGCCCCGCCTTTGGGGTCCCGCCCCTTTGAC  1202
                  |||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    1140 ACGATGGCGGGGATGTTGCAAGGCGCCCCGCCCTTGCCTCCGCTTTTGGGGTCACGCCCCTTTGAC  1199

Qy    1203 TACGGTTGAAGTGCCAGTCATGGTCCTGCAGGGTAACGGTCCGTATTCCCACTGGG  1262
                  ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    1200 TACGGTTGACTTGGCAGACCGTCTTGCAGGGCCAACGGTCCGTTTTTCGCGTTTTCGACTGGG  1259

Qy    1263 GAGAGGGTGTGGGATCGAGGGAATGTCACGGTCTCTTGTGTGACTGGCCCAACGGCCCCTGG  1322
                  ||||||||| |||| |||||||||||||||||||| ||| ||||||||| |||||||||
Db    1260 GAGAAGGTGTGGGACCGTGGGGACCGTGGGAACGTTACCGGTGTGACTGCCCTAACGGCCCCTGG  1319

Qy    1323 GTTTGGGTCCCGGCCTTTGCCCAGGCGGTTGGGGTGGGCGGACCCCCATTGGAGC  1382
                  || | ||||||| |||| ||||||||||||||||||| ||||||||| |||||||
Db    1320 GTGTGGGTGCCCGCAGCCTTTGCCAAGCAATGCGTCTGGGGTGACCCCATCACTTATTGGAGC  1379

Qy    1383 CACGGACAAAACCAGTGGCCCTATCATGCCCCAATATGTCTATGGGTGTGTCCGTA  1442
                  |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||
Db    1380 CACGGGCAAAATCAGTGGCGCCCCTTTCATGCCCGTCTATGGGTCTATGGGTCTACAGTC  1439

Qy    1443 ACGTGCGTGGGGTTCCGTTGCTTGTTTGCCTGCGGTCGTGATTCGAAGATC  1502
                  |  ||||||||||||||||  |||||||||||||||||||||||| ||||||||
Db    1440 ACTTGCGTGTGGGGTTTCCGCCTTCTGGTTTTGCCTCTCCACCAGTGGTCGCGGACTCGAAGATA  1499

Qy    1503 GATGTGTGGAGTTGGTGGTGCCGGTTGGTGGATCTGCCAGCTGCCAGCTGCCAGTCTCTAGGGTCA  1562
                  |||||||||||||| |||| | || |||||  |||||||||||||||||||||||| |||
Db    1500 GATGTGTGGAGTTTAGTGAGTTTAGTGCCTGCTCTGCCACCATAGCCCGACTTGGATCA  1559

Qy    1563 CTGGACCGTGGGCCTGCTTCATGTGAGTGCACCTGTGTGCGGCCCGAAACCGGG  1622
                  |||||||||||||| |||||||||| |||| |||||||||||||||| ||| |||
Db    1560 CTGGACCGTGGGCCTGCTTCATGTGAGTGCACCTGTGTGCGGCCCGAGAGCCGGG  1619

Qy    1623 TCGGTTAGATTCCTTTCCATCGTGCGCGACACCTCCTTCGGCTCGGCTGACAAAGGACTTGGAA  1682
                  ||||||| || | ||||| ||| |||||||||||||||||||||||||| ||||||||||||
Db    1620 TCGGATTCGGTTTAGGTTCCCATTCCACAGCAGGGCTGGCCTGGCTCGGCTGACAAAGGACTTGGAA  1679

Qy    1683 GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATAAGGGGCCCCTGGGCAACCAG  1742
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1680 GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATAGGGGGCCCCTGGGCAACCAG  1739

Qy    1743 GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGGCCCCTGGGCAACCAG  1802
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1740 GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGGCCCCTGGGCAACCAG  1799
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Qy  1803 GGGAGAGGCAACCGGTGCGGGTCGCGCCCCTGGGTTTTGGGTCCTACACCATGACCAAGATC 1862
         ||||||||||||||||||||||| ||||||||||||| |||||||| |||||||||| ||||
Db  1800 GGCCGAGGCAACCGGTGCGGGTCGCGCCCTTGGGTTTGGGTCCCATGACCATGACCAGGATC 1859

Qy  1863 CGGGATACCCTACATCTGGTGAAATGTCCCACCACCAGCCATAGAGAGCCTCGGACGAACG 1922
         ||| ||||  |||||||||||||||||| ||||||||| ||||||||||||||||||||||
Db  1860 CGAGATACCCTACATCTGGTGAGTGTCCCACCACCAGCCATTGAGCCTCCACCGGGACACG 1919

Qy  1923 TTCGGGTTCTTCCCCGGAGTCCCGCCCATTAACAACTGCATGCGCGTAGGCACGGAAGTG 1982
         || ||||||||||||||||| |||| |  |||||||||||||||||||||||||||||||
Db  1920 TTTGGGTTCTTCCCCGGAGCGCCGCCTTCTCAACAACTGCATGCTCTGGGCACGGAAGTG 1979

Qy  1983 TCTGAGGCATTGGCGGAGACTGGGCTTCTACGGCGGTTCTACGAGCCTCTGGTTCCGCAGG 2042
         ||| ||| |||||| |||||||||||||||||||||||||||||||||| |||| |||||
Db  1980 TCCGAGGCACTTGGGGCGGGCTGCCTCACGCGGGGGGGTTCTATGAACCCCTGGTGCGCAGG 2039

Qy  2043 TGTTCGGAGCTGAGCGACCGCGAAATCCGGTTGCCCGGGTACGCGTCGCTGTCCTCT 2102
         ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  2040 TGTTCGAAGCTGATGGAAGCCGAAATCCGGTTGTCCGGGTTTGCATGCGCTGTCCTCG 2099

Qy  2103 GGTAGACCTGACGGGTTCATACACGTCCAGGGGCACCTGCAGGAGGTGGATGCGGGCAAC 2162
         || ||||||||||| ||| |||| |||||||| |||| |||||||||||| ||||||||
Db  2100 GGCAGGCCTGATGGGTTTATACATGTCCAGGTCACTTGCAGGAGGTGGATGCAGGCAAC 2159

Qy  2163 TTCATCCCCTCCTTCCACGCTGGTTGCTCTTGATTTTGTATTTGTCCTGCTCTATCTGATG 2222
         ||| || |||||||||||||||||| ||||| |||| |||| ||| ||||| ||||||||
Db  2160 TTCATCCCCGCCGCCCCGCTGGTTGCTCTTGGACTTTGTATTTGTCCTGCTCTATACCTGATG 2219

Qy  2223 AAGCTGCTGAGGCACGTTGGTCCCGGCGTGTCGGACGCTGGGTGGCGTGGGGTGAAC 2282
         ||||||||||||||||||||| ||||||||||||||||||| || |||||||||||
Db  2220 AAGCTGGCTGAGGCACGGTTGGTCCCGGCGTGTCGGACGCTGGTGGTGTGGGGTGAAC 2279

Qy  2283 CAGTTGGCGGTTCATGGTGTTTCGGTGGATGCTGGACGCTGCGCGTGGCGGGGTGAAGTTTTTGCG 2342
         || |||||||||||||||| |||||||||||||||| |||| ||  ||||||||||||||| |||
Db  2280 CAGCTGGCAGTCCTAGGGCTCCTGGGGCCGGGCCGGCGTGGGAAGCCGCCGGTGCAGGTCTTCGCG 2339

Qy  2343 GGCCTTGCGGTTCATGGTGTTCCCACTGTTCAGTATGATGATACTAGGTCTAGCA 2402
         ||||| |||||||| || || ||||  ||||||||||||||||||||||| ||||
Db  2340 GGCCTCGCCGTGTCCTGGGTCCCGGTTCCCGTCGTCAGCTGATGATTGGGTTTGGCA 2399

Qy  2403 AACCTGGTGTGTACTTTCGGTGGATGGGCCCTCAGCCGCCTCATGTTCCTCGTTGTTGTGG 2462
         |||||||||||||||||| ||||| ||||||| |||||| |||||||||||||||||||||
Db  2400 AACCTGGTGCTGTACTTTAGATGGTTGGGACCCCAACGCCCTGTGTTCCTCGTTGTTGTGG 2459

Qy  2463 AAGCTCGCTCGGGGAGCTTTCCCGGCCGAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCG 2522
         ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  2460 AAGCTTGCTCGGGGAGCTTTCCCGGCCTGGGGGTTCGGCTTCGATGTCACATTCGAGGTGGACACTTCG 2519

Qy  2523 CCGCACCTTCGTCTGCGGGGCCAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCG 2582
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2520 CGCACCTTCGTCTGCGGGGCCAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCG 2579

Qy  2583 GTGTTGGGCTGGGTGGTGCCAGCGCTGCGGCCAGTGACTTGGCCTGGAGCTTGGGCCATATG 2642
         |||||||||||||||||||||||||||| |||||||||||| ||||||||||||||||
Db  2580 GTGTTGGGCTGGGTGGTGCCAGTGCTGTGTAGCTTGGCCTGGAGCTTGGGCCATCTCGATG 2639

Qy  2643 AGCGCAGGGGGGTGGAAGCACACAAGCCCTGATCTATAGGACGTGGTGTAAAGGGTACCAG 2702
         ||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||||||
Db  2640 AGCGCAGGGGGGTGGAGGCACACAAGCCCTGATCTATAGGACGTGGTGTAAGGGGTACCAG 2699

Qy  2703 GCTGTGCGCCAGAGGGTTGGTGCGGAGCCGTCGGGGGAGGGGCGTCTTACCAAGCTTCTG 2762
         |||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||||
Db  2700 GCAATCCGTCAAAAGGGTGCGGAGGAGCCCCGCGGGGAGGGGCGGCGCCAAAACCCCTG 2759

Qy  2763 ACGTTGGTCCTCCTTCGGCCTGTTCGCACGCACTGGACGTCTGATGATGGTGGTCGTG 2822
         || || |||||||||| |||||||||||||||||||  |||| |||||||||||||||
Db  2760 ACTTTGCCTGGTCCTCTTTGCCCTGTTCGCACGCACGTGGATTGGGTGGTGGTGGTGTT 2819

Qy  2823 GCCTTGGTCCTCCTTCGGCCCTGGGCGCCCTGGGGGAGCTCCTG 2882
         ||||||||||||||||||||| |||||||||||||||||||||
Db  2820 GCCTTGGTCCTCTTTGCCCTTTTTTTGGGCGTTGCGACGCCTTGGGGGAGGTCTTA 2879
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Qy  2883 GTCTCCGGCGCCCTCGTTACGGCGACTGGCACGGGCGGTGGTGAGTGCTGTGTGATGGCGGGC 2942
         |||||||||||||||||||  |||||     ||  ||   || ||||||||||| ||||||||
Db  2880 GTGTCCGGCGCCCTCGTTGCGGCGTTTGGCTGGGCCGGTTGGCTGTGAGTGCTGTGATGGCGGGT 2939

Qy  2943 GAGAAGGCACCACCATCGACTGGTCTCCAAGATGTCGGCAAGAGGGGCCTACCTGTTT 3002
         ||||||||||||||||||||||||||||||||||| || || |||||||||| | |||
Db  2940 GAGAAGGCCAACACCGTCAACCGGTCTCCAAGATGTCGCGAGAGGAGCTTATTTGTTC 2999

Qy  3003 GACCACATGGGCTCTTTCTCGCGCCGTGTCAAGGAGCGCGTTGTTGGAATGGACCGGCT 3062
         |||||||||||||||| | |||||||||| |||||||||||||||||||||||||||||
Db  3000 GATCATATGGGCTCTTTTTCGCGTGCTGTCAAGGAGCGCGTTGTTGGAATGGGACCAGCT 3059

Qy  3063 TTGGAGCCCTTGTCATTCACTAGGACGGACTGTCGCATCATCAGAGATGCCGAGGACC 3122
         || |     ||||||| |||||||||||||||| ||||||||||||| ||||||||||
Db  3060 CTTGAACCTCTGTCATTCACTAGGACGGACTGTCGCATCATACCGGATGCCGCGAGGACT 3119

Qy  3123 CTGTCCTGCGGACAGTGCGTCATGGGTTTCCCGGGTACGCACGGCGCGGTGATGAGGTT 3182
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  3120 TTGTCTCGGGGCAGTGCGTCATGGGTTTTACCCGGTTGCCGCCCGTGTCGTGATGAGGTT 3179

Qy  3183 CTCATCGGCTCTTTCAGGATGTGAATCATTTGCCTCCCGGGTTTGTCCCGACTGCACCA 3242
         |||||||||||||| || |||||||| ||||||||||||||||||||| ||||||||||
Db  3180 CTCATCGGCGTCTTCCAGGATGTGAATCATTTGCCTCCCGGGTTTGTTCCGACCGCGCCT 3239

Qy  3243 GTTGTCATCCGTGCGGCGGAAAGGCCTTCCTGGGGTCACGAAGGCAGCCTTGACAGGT 3302
         |||||||| ||||||||| ||||||||||| ||||||||||||||||||||||||||
Db  3240 GTTGTCATCCGACGGTGCGCGGAAAGGGCCTTCTTGGGGTCACAAAGGCGCCTTGACAGGT 3299

Qy  3303 AGGATCCTGACTTACATCCAGGAACGTCATGGGTTCATGGGGACGGCTACGTCACGAAGC 3362
         |||||| ||| |||| ||||||||||||||||||| |||||||||||| ||| ||||||
Db  3300 CGGGATCCTGACTTACATCCAGGAACGTCATGGGTTGGGGACGGCTACGTCGCGAAGC 3359

Qy  3363 ATGGCCACATGTCTGAATGGCCGCTTGGTGTTCACAACTTCCATGGGCTTCATCCCGAACC 3422
         ||| |||||||||||||||| ||| || |||||||||||||||||||| ||||||||||||
Db  3360 ATGGGAACATGCTTGAACCGCCCTATGGTGTTCACGACCTTCATCCCGAACC 3419

Qy  3423 ATCGCCACGCCGTGGGGCCCTAATCCCACTGGTGTGCTCAGCGTGATGACGTCACG 3482
         |||||||||||||||| |||||||||||||||||||||| ||||||||||||||||
Db  3420 ATCGCCACACCCGTGGGGGCCCTAATCCCACTGGTGTGCAGCGTGATGATGTCACG 3479

Qy  3483 GTGTACCCCGCTTCCAGATGGGCAACTTCGTTGCACCGCCCTGCACTTGCCAGGCGGAGTCC 3542
         |||||| ||| ||||||||||||||||| |  ||||||||||||||||||||||||||||||
Db  3480 GTGTATCCACTCCCCGATGGGCTACTTTCGTTAACACCTTGTACTTGCCAGGCTGAGTCG 3539

Qy  3543 TGTTGGGTTATTAGATCCGACGGGGCTTTGTGCCATGGCTTGAGCAAGGGGACAAGGTT 3602
         |||||||| ||||||| |||||||||||| |||||||||||||| |||||||||||||||
Db  3540 TGTTGGGTCATCAGATCCGACGGGGCCCTATGGCTTGAGCAAGGGGACAAGGTG 3599

Qy  3603 GAGCTGGATGTGGCCAGTGAGGTCTCTGACTTCCGTGGTTCGTCGGTCCTT 3662
         ||||||||||||||||||||||||||| ||||||||||||||| |||||||
Db  3600 GAGCTGGATGTGGCCAGTGAGGTCTCTGACTTCCGTCGGCTCCACCGGTCCTA 3659

Qy  3663 TGCGACAAAGGGCACGCAGTAAGAATGCTCGTGTCTGCTCCACTCTGCGGCCAGGGGTT 3722
         |||| |||||||||||||||||||| ||||| || |||| |||||||||||||||||||
Db  3660 TGTGACGAAGGGCACGCAGTAGGAATGGCTCGTGTGCTTCACTCCGGTGGTAGGGTC 3719

Qy  3723 ACTGCGGCCGGGATTCACTAGGCCCTGGACTACCAAGATGCCAAGACCGCCAGAACCACCACA 3782
         || |||||| |||||||||| |||||||||||| ||   |||| ||||||  |||||||||||
Db  3720 ACCCGCACGGTTCACTAGGCCCTGGACCCAGTGGACCCAAGTGCCAACAGATGCCAAAAACCACTACT 3779

Qy  3783 GAACCCCTTCCGGTGCCGGCAAAGGAGTTTCAAGGAGGCGCCCGTTGTTTATGCCTACG 3842
         ||||||||||||||||||||||||||||||| ||||||||||||| |||||||||||||
Db  3780 GAACCCCTTCCGGTGCCGGCAAAGGAGTTTCAAAGAGGCACCCGGTTGTTTATGCCTACG 3839

Qy  3843 GGGGCGGGAAAGAGAGCACCGCGTCCAACATGGGCAACATGGGTCACACGTCTTG 3902
         ||||||||| ||||| |||| |||| |||||||||||||||| |||| |||||||
Db  3840 GGAGCGGGAAAGAGCACTCGCTCCCGGTCCACATGGGCACAAGGCTTTA 3899

Qy  3903 ATCTTGAACCCTCGGTAGCTACCCTGAGGGCCCATACAATGGAGCGGCTGGCG 3962
         |||||||||  |||||||||| |||  || || |||||||||||||||||||||
Db  3900 ATCTTGAACCCCTCAGTGCCCACTGTGCGGGCCCGTACACTGGGCACGGCTGGCG 3959

Qy  3963 GGGAAACACCCCCAGTATTTACTGTGTGCCATGACACCACTGCTTTCACAAGGATCACTGAC 4022
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Db  3960 GGTAAACATCCAAGTATATACTGTGGGCATGGCAGACAACTGCTTTCACAAGGATCACTGAC 4019
         ||||||| || |||||| ||||| ||| || |||||||||||||||||||||||||||||||
Qy  4023 TCGCCCCTTACGTGATTCCACTTACGGAAGGTTTTGGCCAACCCTAGGCAGATGCTGAGG 4082
         || |||| |||||||| |||||| |  || ||||||||||||||||| ||  |||||||||
Db  4020 TCCCCCCTGACGTATTCAACCTATGGGAGGTTTTGGCCAACCCTAGGCAGATGCTACGG 4079

Qy  4083 GGTGTGCGGTGGTCATTTGACGAGTGCCACAGTCATGACTCAACTGTGTTGTTGGGC 4142
         || || |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  4080 GGCGTTTCGGTGGTCATTTGATGAGTGCCACAGTCATGACTCAACCGTGCTGTTAGGC 4139

Qy  4143 ATTGGGCGTGTCAGGGAGTGGCGCGAGGATGTGCAATTGCGAGTGCTTCTCACCGCCACT 4202
         ||||||||||| |||||| | |||| |  || ||||||||||||| |||||||||||||||
Db  4140 ATTGGGGAGTCCGGGAGCTGGCGCTGGCGTGGTGCGAGTGCTCAACTAGTGCTCTACCGCCACC 4199

Qy  4203 GCCACCCCTCCCGGATCCCCGATGACCCAGCACCCATCAATCATTGAGACAAAACTGGAC 4262
         |||||||||||||  ||||||||  | |||||||||||||||||| |||||||  ||||||
Db  4200 GCTACCCCTCCCGCAGTATGACGACAGCACCACCCTTCCATAATTGAGACAAAATTGGAC 4259

Qy  4263 GTGGGAGAGATCCCCTTTCTGAGCGGCATGGCGGATGCGGATGGGACCGGAAGG 4322
         ||||||||||||||||||| |||||||  ||| ||||||||||||||||||||||
Db  4260 GTGGGCGGAGATTCCCTTTTATGGGCATGGAATACCCCTCGAGCGGATGCGAACCCGAAAGG 4319

Qy  4323 CATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGGCGCGTTGGCCGGCCAGTTTTCGGCT 4382
         |||||||||||||||||||||||||| ||||| |||| |  ||||||||||||| | |||
Db  4320 CACCTCGTGTTCTGCCATTCTAAGGCTGAGTGCGAGCGCGTTGGCGAGCGCGTTGCTCGGCT 4379

Qy  4383 AGGGGGTAAATGCCATCGCCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATGGA 4442
         ||||||| ||||||||||| ||| |||||||| |||||  ||| |||||||||| ||||
Db  4380 AGGGGGTCAATGCCATTGCCTATTATAGGGGTAAAGACAGTTCTATCATCAAGGATGGG 4439

Qy  4443 GACCTGGTGGTTGTGTCTACAGAACCACTATCCACTGGGTACACTGGGAACTTCGATTCT 4502
         |||||||||||||||| |||||||||| |  ||||||||||||||||||||| ||||||||
Db  4440 GACCTGGTGGTCGTGTCTACAGACGCGCCGTTCCCACTGGGTACACTGGGAAATTTCGACTCC 4499

Qy  4503 GTCACCGATTGTGGGGTTAGTGGTGGAGGAGGTCGTCGAGGTGACCCTTGATCCCACCATT 4562
         ||||||||||||||||| ||||||||||||||||||||||||||||| |||| | ||||||
Db  4500 GTCACCGACTGTGGGATTAGTGGTGGTGGAGGTCGTTGAGGTGACCCTTGATCCCACCATT 4559

Qy  4563 ACCATCTCCCTGCCACGCGTGCCCGGCTCGGCTGAACTGTCAGCGGCGAGGACGC 4622
         ||||||||||| | || |  |||||||||  ||||||||| |||||||||| |||||
Db  4560 ACCATCTCCCTGACACGTGGCGACAGTGCCTCGGCTCGGCTGAACTGTCGATGCAAAGACGAGGACGC 4619

Qy  4623 ACGGTAGGGCAGTTCGGCGGGTCTGGGCTACTACGGCGGGTCGGCAAGGCCCCTGCTGGT 4682
         ||||| |||||||| ||| |||||||||||||||||||||| |||||||||||||||||||
Db  4620 ACGGTAGGGCAGTTCGGCGGGTCTGGGCTACTACGGCGGGTCGGCAAGGCCCCTGCTGGT 4679

Qy  4683 GTGGTCGCTCAGGTCGTCTGGTCGGCCGTGGAAGCCCGGTGACCGTGTACCGGTACCGGAATG 4742
         ||||||||||||||||| | |||| || |||||||||||||| ||||||||||||||||||
Db  4680 GTGGTCGCTCAGGTCGTCTGGTCGGCCGTGGAAGCCCGGTGACCGTGTACCGGTACCGGAATG 4739

Qy  4743 GAACCTGACCTGACAGCAAAACCTGCCCTTACGACAACCGCCAGCC 4802
         |||||||||| || || ||||| |  ||||||||||||||||||||
Db  4740 GAACCTGACCTGACAGCAAAACCTGCCCTTACGACAACCGCCAGCC 4799

Qy  4803 GTGCAGCTGACAGCATTGGGGAGCCCGGTGTGTTCTTTTCGCGGGGATGG 4862
         ||||| | ||||||||||||||||||||||||||| |||||| |||||||
Db  4800 GTGCAGCTGACAGCATTGGGGAAACTGGAGCCGGTTGCGCGGGTCTCGGGGATG 4859

Qy  4863 CATCCCGATGTTAGCTGGGCCAAAATCCGGTCTCAACTGGCCGTCTACCGGTGGTGTT 4922
         ||||| | ||||||||| |||||| |||||||||||||||||||||||||||||||||
Db  4860 CACCCTGATGTCTCAGTTGGGCCAAAATCCTGACCGTCAACTGGCCGTCTGGAGTGACCGGTGGTGTT 4919

Qy  4923 CAGCGGACCATGTGCCGGAAAACCGCCGGATGACCCCCAGTGGGCA 4982
         ||||| |||||||||||||| | ||||| |||||||||||||||||
Db  4920 CAGCGGACCATGTGTCGGGAAACAACACTGTCTGTTACCCCAAATGGGGCA 4979

Qy  4983 GGGTCTCGAAGGGCCCCAATCCTGTCTCCACTCCTGGTCGGTGGTGTT 5042
         ||||| ||| |||| |||| |||||||||| |||||||||||||||||
Db  4980 GGTCTCGAAGGGCCCAAATCCTGTCCCACTCCTGCTCGGTGGGGCAAC 5039

Qy  5043 AAAGTGGCCGCCCATCACATCGTGACGACCTGGTTCGGTGGCTCCGGAGGGT 5102
         |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  5040 AAAGTGGCCGCCCACCACATAGTGGACGACCTGGTTCGGTGGCTCCGGAGACTGCTCC 5099
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Db  5040 AAAGTGGCCGCCCACCACATAGTGGACGACCTGGTTCGGTGGCTCCGGAGACTGCTCC 5099
         |||||||||||| |||||||||||| |||||||||||||||||||||||||  |||
Qy  5103 TACGTCCGCTGCGACGTATACCCGGTCTCTCGTGGTTACAGACTGGAGTGAAGGGGGGT 5162
         |||||||||||||| |||||||||||| ||||||||||||||  ||||||||||||||
Db  5100 TACGTCCGCTGCGATCATCACACCGGACTTCGTGTGGTGTGACAGACTGGGAGGGGGGT 5159

Qy  5163 ATCTATGCGTCATACACCGGTGCTCTCGTGGTGGTTACAGACTGGGATGGAAGGGGGGGGT 5222
         |||| |||| |||||||||||| |||| |||||||||| ||| | |||||||||||| |||
Db  5160 ATCTACGCGTCATACACACCGGTGCTCTCGTGGTGGTGACAGACTGGGATGTGAAGGGGGGT 5219

Qy  5223 GGCAGCCCCTTTATCGGTCATGGAGACCAGGCCACCGCCCAGCCGGTTGTGCAGGTCCCC 5282
         ||| ||||||||||||| ||||||||||||||||||||||||||||| ||||| |||||||
Db  5220 GGCGCCCCCTTTATCGGTCAGTGGAGGCCAGGCCACCGCCGGTTGTGCAGGTTCCT 5279

Qy  5283 CCGGTAGACCATCGGCGGGGGGGTGGGGGTGGGGGTGGGGGTGACCCAGTGCCAACACAGTGACAGAT 5342
         |||||||||||||||||||||| |||||||||||||||| ||||||||| | ||||||||||||||||
Db  5280 CCGGTAGACCATCGGCGGGTGGTGAATCAGGCACCACCATCGGATGCCAAGACAGTGACAGAT 5339

Qy  5343 GCGGTGGCGGCCATCCAGTTGGTGCGGATTGCGATTGCCAGTCATGCATCGTGACCCTGTCGATCGGGGAA 5402
         |||||||||||||||||||| |||||| |||||||||||| ||||||| |||| ||| |||||||| |
Db  5340 GCGGTGGCAGCCAGTCCAGTTGGTGACTGGGACTGGGACTATGCATCATGCATCTGTGATCGTCGGAGAA 5399

Qy  5403 GTGCTGCTCCTTGCCCAGGCTAAGACGGCCGAGGCGCTACGGACGCTACCACCAAGTGCTT 5462
         |||||| ||||||||| ||||| ||| |||| | |||| |||| ||||||||||||||| |
Db  5400 GTGTTGTCCTTGCCTGCTCAGGCCTAAGACGGCCGAGGCGCTACAGACGCCCAAGTGCTC 5459

Qy  5463 GCTGGCTGCTACAGGGGACGGGCGGCCCGTCCCCACTCTTTCAATTGTTGACAAGCTCTTC 5522
         |||||||| |||||||||| ||||||||||||||||||||  ||||| |||||||| | |
Db  5460 GCTGGCTGCTATACGGGGACCGGGCGGCCCGTCCCCACTGTTATCATTGTTGACAAGCTCTTC 5519

Qy  5523 GCCGGGGCTGGGCGGTGGTGGTAGGCCATTCCCATTGGCGCCCCAGGCTCCGCCAGTGGCG 5582
         |||||| ||||||||||||||||||| ||| |||||||||||||||| ||||||||||||||
Db  5520 GCCGGAGGTGGGCCGGCGCTGGCGCGTGGCCATTGCCACAGCGTCGTGCGTGCCAGTGGCG 5579

Qy  5583 GCCTATGGGGCTTCTAGGAGCCCTCCATTGGCTGCTCCGCTTCCTACCTCATGGGGTTG 5642
         ||||| ||||||||||||||||| |||||||||||| |  ||||||||||||||||||||
Db  5580 GCCTACGGGGCTTCAAGGAGCCCGCCGCCCCGGCTTGGCAGCCCGTGCTTCCTACCTCGTGATGGGGTTG 5639

Qy  5643 GGGCTGGAGGCAACGGCAAACCCGCCAAACCCGGACGACGC 5702
         ||||| ||||||||| || | |||||| || ||  |||||||
Db  5640 GGCGGTGGAGGCAACGGCAACGCTCAGACGCGCCGTTCCCCCTCTATTGGGGCGTGCTGGA 5699

Qy  5703 ACGGCTCTGGGCCACGCCGTCGTGCGGGGTTAACCATGGCGGCCGGTTCATGGGAAGTGCT 5762
         ||||| |||||||| || ||||| ||||| | |||||||||| ||||||||||||||||
Db  5700 ACCGCCTGGGCCACTCCGTCGTGCGGGTCGGTTGACCAGGAGTGCGGCGTCATGGGGGGCGCCC 5759

Qy  5763 AGCCGTCTCCCCCTCCCTGGTCACATTTTACTGGGGGCTGTGACCGTGTACCGGTACGGAATG 5822
         |||||||||||||||| ||||||||| |||||||| ||||||||||||||||||||||||||
Db  5760 AGTGTCTCCCCCCTCCGTGGTCACCATTTTATTGGGGCCGGGCCGTGGGAGGGGGCCGTG 5819

Qy  5823 GTGAATGCGGCTAGCCTTGTCTGCTGGAAATATCATCAGAAGATCTG 5882
         ||| |||| ||||||||||| ||||||||| ||||||| ||||||||
Db  5820 GTCAACGCGGCAGCCTAGTCTTTGACTTTCATCGGGGAAACTTTCATCAGAAGATCTG 5879

Qy  5883 TGGTATGCCATCCCAGTGCTAACCCAGTTCCGGGGGCAGGACTTGCGGGGGATGCCCCTCGGG 5942
         ||||| ||||| ||||| || || ||  |||| |||||||||||  |||||||  ||||||||
Db  5880 TGGTATGCCATCCCGGTGCTAACCTACTCAGTTACTTTCAGCCACCGTGGTTGCCCTGGTCAAC 5939

Qy  5943 TTGGTGTTACTACTGGCCTCAGCTGACAACTCTGGCCACTCTTGCTTGGAACCTGCTGACT 6002
         ||||| |||| | |||| | |||||||| | ||| ||||| |  |||||||||| |||||||
Db  5940 TTGGTTTGTATTCAGCTGACAACTCTGGCACTCTTGGTTGAACCGTCTGACT 5999

Qy  6003 ACATTGCCAAGGTCCTTCATGCATCGCCTCGACAAGTTACTTTCAGCCGCCGATTACTGTGAC 6062
         || |||| ||||| ||||||||||||| || ||||||||||||||||||||||| ||||||||
Db  6000 ACGTTACCAAGGTCTTCATGTATCCGGACAGTTACTTTCAGCCACCGTGTACTGTGGAC 6059

Qy  6063 AAGGTCTCAGCTGCTTCCGGACCGCTTCACTCGCACCGTGCTTGCCCTGGTCAAC 6122
         ||||||||||||||||| ||||||||| ||||| ||||| ||||||||||||||||
Db  6060 AAGGTCTCAGCTGCTTCGCCGGCCTCTGAGCTTGTGGCTTGCCCCTGGTCAAC 6119

Qy  6123 AGGGAGGCCTAAGGTGCAGGTTCAGGTGGGGACTTGTGTGGGTACTTACCATCT 6182
         |||||||||||||||||||||||||||||||  ||||||||||| |||||||||||
Db  6120 AGGGAGGCCTAAGGTGGGGATGAGGTACAGGTGGGGTATTGTGTCTGGGGACTGGGAGTGGAGTCGATC 6179
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Qy  6183 ATGCGTCAAGTGCGCATGGTGATGGCCAGACTTCGGGCCCTCTGCCCCGTGGTGTCATTA 6242
         |||| |||||||||||| || ||||||||||||| |||||||||| ||||||||| | ||
Db  6180 ATGCGGCCAAGTGCGCGGTGGTCATGGCCAGACTCAGGGCCCTCGCCCCGTGGTGTCACTA 6239

Qy  6243 CCCTTATGGCACTGCCGCGGAGGGGTGGCTGTCCGGAGAATGGTTGTTGGACGGCCATGTTGAG 6302
         |||||| |||| ||||||||||||||||| |||| | |||||||||| | ||||||||||||||
Db  6240 CCCTTGTGGCATTGCCGTGTGGCTGGCTGGCTGGTGGTGACCCACGTGGTAATGCCATGTTGAG 6299

Qy  6303 AGTCGTGTCTTTGTGCTGCTGCCGATCACCGGTGATGTTTGAATGGGCAACTCAAAGAT 6362
         ||||||||||||||||||||||||||| || |||||||||||||||||||||||||||||
Db  6300 AGTCGCTGCCCTCGTCGCGCTGCCGTGATCAGTGACGTTCTGAATGGCAACTCAAAGAA 6359

Qy  6363 CCAGTTTACTTCACCAAGCTGTGCACGCATTATTGATGGGACAGTCCCTGTGAACATG 6422
         |||||||||||||||||||| || | ||||||||||||||||||||| || |||||||
Db  6360 CCAGTTTACTTCACCAAGCTGTGCCCGCACTATTGGATGGGACTTCTGAATGGCAACATG 6419

Qy  6423 CTGGGCTATGGCGAGACGTCGCCCTTGCTGCTCGCCCTCAGAGATCTGGGCCTGTACCATTC 6482
         |||||| |||| ||||| ||||||| ||||||| ||||||| ||| ||||||||||||||||
Db  6420 CTGGGCCTATGGTGAAACGTCGCCCTTGCTGCTCCGCCACCGAGAGGTGGGCCTGTACCATTC 6479

Qy  6483 GGGACTCTGGGTGGGCTGAGGTGGTGCGTGACCCTACCCACGTTGTGATCAGGCCGACA 6542
         ||||||||||||||| |||||| |||| ||||||||||||||| |||||||||||||||
Db  6480 GGGACGTCTGGCTGGCTGGTGGGTGGTGACCCTACCCACGTGGTAATCAGGAGGACC 6539

Qy  6543 TCCGGCCTACAAACTGCTGCGCCAGCAAATCTGTCGGCTGCTGTTGCTGAGCCCTATTAC 6602
         |||||||| | ||||||||||||||||||||| ||||||||||| |||| |||||||||||
Db  6540 TCCGGCCTATAAGCTGCTGCGCCAGCAAATCTCTGGGTGCTGTAGCCTGAGCCCTACTAC 6599

Qy  6603 GTCGACGGCCATACCGGTCTCATGGGACGCGGAGCGCCTGCCACCCTGCGTCTATGGC 6662
         |||| | | || |  |||||||||||||||||||||||||| | |||||||||||||||
Db  6600 GTCGACGACGCCATTCCGGTCTCATGGGACGCGGAGCGCCTCATGGCCCATGTCTATGGC 6659

Qy  6663 CCTGGGCAAAGTGTCACCATTCACGGGGAACCTACACCCTTCCGCATCAACTGCGGCTT 6722
         |||||| |||| |||||||||| || ||||||||| | ||||| ||| || ||||| |
Db  6660 CCTGGGCAAAGTGTTACCATTGACTGGGGAGCGCCTCACCCTCATCAACTGACACTGGC 6719

Qy  6723 AGGAATGTGGCCCCCTCGAGGTGTCATCGCCAGGTGTCCATTGACATTGGGACGGAGACT 6782
         ||||||||||| |||| ||||||||||||| ||||||||||| |||| |||||||||||||
Db  6720 AGGAATGTGGCACCCTCGAGGTTCATCGCCCAGGTGTCCATTGACATTGGGACGGAGACT 6779

Qy  6783 GAAGACTCAGAGACTGACTGAGGGCCCGACCTATCTCGCGCCGACCCTCAGGCGTATC 6842
         ||| ||||||||| ||||||||| || || |||||||||||||| | ||||||||||
Db  6780 GAAGACTCAGAGACTGACTGAGGGCCGATCTGCGCCGCTCTCCAAGCGATC 6839

Qy  6843 GAGAATCCTGCCAGAATTCTGAACCTCACATAGATCGATCATGGAAGATTGCAGTACA 6902
         |||||||| || |||| ||||||||| |||| || ||||| ||||||||| ||||||||
Db  6840 GAGAATCCTGCCAGGATTCTGAACCCGCACATTGATGTCATCATGGAAGACTGCAGTACA 6899

Qy  6903 CCCTCTCTTTGTGGGAGTAGCCGAGAGATGCCTGTGTGGGGAGAAGACCATACCCCCACCT 6962
         |||||||||||||||||||||||||||| |||||||||||||||| |||||||| |||||
Db  6900 CCCTCTCTTTGTGGTACTATGGAGGTCTAAGAGAGATGCCTGTATGGGGAGAAGACCATCCCCCGTACT 6959

Qy  6963 CCATCGCCAGCACTACTTATCTCGGTTACTGAGGAGGCCAGATGAGAAGACCCGTCGGTG 7022
         |||| ||||||||||||||| | |||| || ||||||||| ||||| | ||||||||||||
Db  6960 CCATCGCCAGCACTACTTATCTCGGTTACTGAGGAGGCCAGATGAGAAGACCCGTCGGTG 7019

Qy  7023 TCTTCCTCGCGGATACCCCTTCGACTCATTCGAGTCATCGTGTTGGAGAGTCCGAG 7082
         ||| ||||||||||| |||||||||||| |||||||||| | |||||||| | ||||
Db  7020 TCCTCCTCGCGGATACCCCTTCGACTCATTCGAGTCATCATCTCCAAGGTCCAAGAGTCCGAG 7079

Qy  7083 ACAGCCGAAGGGGGAGAAAGCGTCTTCAACGTGGCTCTTTTCCGTACTGTAAAGCCTTGTTT 7142
         |||||| ||||| |||||||||| |||||||| |||||||||||| | ||||||||||  |
Db  7080 ACAGCCGAAGGGGAGGAAAGTGTCTTCAACGTGGCTCTTTTTCCGTATTAAAAGCCTTTATTT 7139

Qy  7143 GTAACACGCTTCTTTTCATTGGATTGACGGCGTCGCTGCACGTGCGTGTGCTTGTCGTGATG 7202
         || |||||||  | | ||||| || | |||||||| ||| |||||||||||||||||||||
Db  7140 GTCACGCGCTTTTCTTCATTGGGTTGACGCGTGGCTGCTAGCCGCGATGACTCATGTGTGAGATG 7199

Qy  7203 GTAACCGCTTCTTTCATTGGGTTGACGGTTGACGGCCTGATGTTGCTAGCCTGTGTGAGATG 7262
         || ||||||||  ||||| ||| |||||||||| |||||||||||||||||||||||||||
Db  7200 GTCACGCGCTTTTTTCATTGGGTTCATTGCGGTTGACGGTGCTAGCCTGTGTGAGATG 7259
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Qy  7263 GAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCGCACTTGAATTGCAGGTT 7322
         ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  7260 GAAATCCAGAACCATACAGCCTATTGTGACCAGGTGCGCACTTGAATTGCAGGTT 7319

Qy  7323 GGGTGCTTGGTGGCAATGAACTTACCTTTGAATGCAAGTGTGAGGCTAGGCAAGAG 7382
         |||||| ||||||||||||| |||||||||||||||||||||||||||||||||||
Db  7320 GGGTGCTTGGTGGGCAATGAACTTACCTTTGAATGCAAGTGTGAGGCTAGGCAAGAA 7379

Qy  7383 ACCTTGGCTTCCTTCTCTTCTTTACATTTGGTCTCGGGTGCCACTGACGAGGGGCCACTCCGGCC 7442
         |||||||||||||||||||| || |||||||||||| |||||| ||||||||||||||| |||||
Db  7380 ACCTTGGCCTCCTTCTCTTTTTACATTTGGTCTGGGGTGCCACTGAGGAGGGGCCACGGCCGCC 7439

Qy  7443 AAGCCCCCTGGTGAGGCGGTTGGCTCCTTGCCGTGGTGCCGACCACCAAGGTGTAT 7502
         |||| |||| ||||||||||||||||||||| ||| ||| || |||||||||||||
Db  7440 AAGCCTCCCGGTGAGGCGGTTGGCCCGGTTGTTAGTGGCCGACTACTAAGGTGTAT 7499

Qy  7503 GTCACCAACCCGGACAAATGTTGGGAGAAGAGTTGACAAGGTTACCTTCTGGCGTGCCCCT 7562
         || |||| |||| |  |||||||||||||||||||||||||||||| |||||||||| ||
Db  7500 GTTACCAATCCAGACAATGTGGGACGGAGGTGACAAGGTGACCTTCTGGCGTGCTCCT 7559

Qy  7563 AGGGTTCATGACAAATTCCTCGTGGACTCCATAGAGCGGCCTAAGAGGCGCAGCTCAAGCC 7622
         ||||||||||||||| |||| |||||||| |||||| ||||||||||||||||||||||||
Db  7560 AGGGTTCATGATGATAGTACCTCGTGGACTCTATTGAGCGGCAATCTAAGAGGCGCCGCTCAAGCC 7619

Qy  7623 TGCCTAAGCACATGGTTACACTTATGGAGGCAATAAGGACCTGAAGGCTGAAGTCTGCC 7682
         |||||||||||| |||||| |||||||||||||||||||||||||||||||| |||||||
Db  7620 TGCCTAAGCACATGGGTTACACTTATGGAGGCAATAAGGACCACACATGGTAAGGCCACATGCTGCC 7679

Qy  7683 ATGGGCTGGGATCTAAGGTGTCGGTCAAGGACCTCGCGGGGGACATGGCT 7742
         ||||||||||||||||| |||| ||||||| |||||||||||||||||||
Db  7680 ATGGGCTGGGATCTAAGGTGTCGGTCAAGGACTTAGCCGGGGAAGATGGCC 7739

Qy  7743 GTCCATGACCGGCTCCAGGAGATGTCTGAAAGACTGAAGGACGCCAGTCCCCTTTACTGTG 7802
         |||||||||||||| ||||||||||| ||||||||||||||| || |||| |||||||||
Db  7740 GTCCATGACCGGCTTCAGGAGATCTGAAAGACTGAAGGACTCCGGTCCCCTTTACTGTG 7799

Qy  7803 AAAAGGAAGTGTTCTTCAAAGACCTGAAAAGCTTATTCTGGAGACCCTGGACGGGTAGCC 7862
         |||| ||||||||||||||||||||| ||||||||||||||||||||| ||||||||||
Db  7800 AAAAGGAGGTGTTCTTCAAAGACCTGAAAAGCTCATCTCTGGAGACCCTGGACGCCGGGTAGCC 7859

Qy  7863 CCCCCCTGGACTTCCGGATAGTAGCTGAAAAGCTTATTCTGGGGGGACCGTGGTAGCC 7922
         |||||| ||| | ||||||| |||| ||||||||| |||||| ||| |||||| ||||
Db  7860 CCCCCCTGGACTTCCGGATAGTAGCTGAAAAGCTCATCTGGAGGGGACCGCGGGTAGCC 7919

Qy  7923 AAGGCGGTGTGTGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGGAATTAGGAG 7982
         |||||||||| ||||||||||||||||| ||||| ||||||||||||| |||||||||||
Db  7920 AAGGCGGTGTTGTGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAGTTAAGGAG 7979

Qy  7983 ATGTCAAACTGTGGAATCAAAGAGACACCATGCGTGTGGACGCGCCACATGC 8042
         ||||| || |||| |||||||||||| ||| ||| || ||||| ||||||||
Db  7980 ATGTCAAGCTATGGGAGTCAAGGAGTCTAAGAGAGCCCCTGCGCGCCGACCTGC 8039

Qy  8043 TTCGACAGTAGCATAACTGAAGAGGACGTGGCGCTGGACAGAGCTTTATGCCCCTGGCT 8102
         ||||||| |||||| ||||||||||||||||| || |||| ||||| ||||||||||||
Db  8040 TTCGACAGTAGCATAACTGAAGAGGACGTGGCGCTTTGGACAGAGCTATACGCTCTCGGCC 8099

Qy  8103 TCAGACCATCCAGAATGGGCTGCGTGCGCTTGGGAAAATATCTTCTGGCGCACAATGGTA 8162
         |||||||||||| ||| |||| ||||||||| ||||| |||||| ||||||||||||| |
Db  8100 TCTGACCATTCCAGAATGGGCGGGCACTTGGGAAATACTCTCAGGCCACCATGGTC 8159

Qy  8163 ACCCCCGAGGGGGTGCCAGTGGGTGAGGTGTATTGTGAATCCTGACCACC 8222
         |||||||| || ||||| || ||||||||||||| |||||| |||||||||
Db  8160 ACCCCGGAGGGGTGCCAGTGGGTGAGGTGTATTCAGATTCCTGCCCACCTGC 8219

Qy  8223 AGTGCGAGCAACTGCTTGACTTGGTCATTAAGTGAAAGCCGAAAGGCGTGGGG 8282
         ||||| ||||||||| ||||| |||||||| |||||||||||||| ||||||
Db  8220 AGCGCGAGCAACTGCTTGACCTGCTCTACATCAAGGTGAAGCTGCCGTGTGGGG 8279

Qy  8283 CTGAAAAATGTCTTTTGATCATATGGCAACGGCCT 8342
         |||||||||||| ||||||| |||| ||| |||||
Db  8280 CTGAAAAATGTCTTCTCTCATAGCCGCGATGACTGCTTGATCATATGTGAGCGGCCA 8339

Qy  8343 GTGTGCGGATCCTAGCGACGCTTTGGGCAGCCCTGGCGAGCTACGCGGGTACGCATGCGAG 8402
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Db   8340 GTGTGCGACCCAAGCGACGCTTGGCAGAGCCCTAGCGAGCTATGGTACGCGTGCGAG 8399
          ||||||||  || |||||||||||||||||||||||||||  |||||||||  ||||||
Qy   8403 CCTTCGTATCATGCATCACTGGACACGCCCCTTCTGCTTCCCACTTGGCTAGCTGAGTGC 8462
          || || |||||||||| || |||||||||||||||||||||| |||||||||||||||||
Db   8400 CCCTCCATATCATGCATCATTGGACACGGCCCCCTTGCTTCCCACTTGGCTCTGAGTGC 8459

Qy   8463 AATGCAGATGGGAAACGCCATTTCTTCCTGACCACGGACTTTCGGAGGCCCCTGCTCGC 8522
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   8460 AATGCAGATGGGAAGCGCCATTTCTTCCTGACCACGGACTTCCGGAGGCCGCTCGCTCGC 8519

Qy   8523 ATGTGGAGCGAGTACAGTGACCCAATGGCTTCGGCCTGCGTTACATCCGGTTACTCCTATACCCT 8582
          ||||||| |||||  ||||| |||||||||||||||||||||| ||| ||| || ||
Db   8520 ATGTCGAGTGAGTATAGTGACCCGGATGGCTTCGGCCGATCGGTTACATCCTCCTTTATCCT 8579

Qy   8583 TGGCATCCTATCACACGGTGGGTCATCATCCTCACGTGCTCACCTGCCGCGTTTAGGGGT 8642
          ||||| || |||| |||||||||||| |||| ||  ||||| ||||||||||| ||||||
Db   8580 TGGCACCCCATCACACGGTGGGTCATCATCCTCATGTGCTAAGTGCCCATTCAGGGGGT 8639

Qy   8643 GGTGGCACACCGTCTGATCCTGTGTGGTGGTCCAGGTACATGGTAATTACTACAAGTTTCCA 8702
          || ||||||||||| |||| ||||||  |  || ||||||||||| |||| ||||||||| ||
Db   8640 GGAGGCACACCGTCTGATCCTGGTTTGGTGGCCAGGTGCATGGTAACTACTACAAGTTTCCA 8699

Qy   8703 CTGGACAAACTGCCTAACATCATCGTGGCCCTCCACGGACCAGCAGGCGGTTGAGGGTTACC 8762
          |||||||||||||||||||||||||  || |||||| ||| ||||||| |||||||||||
Db   8700 CTGGACAAACTGCCTAACATCATCGTGGCCCTCCACGGACCAGCGTTGAGGGTTACC 8759

Qy   8763 GCAGACACAACTAAGACAAGAAATGGAGGCTGGCAAGGTGCTGAGCGACCTCAAGCTCCCT 8822
          ||||||||||||| ||| ||||||||||| |||||||||||||||||||||||||||||||
Db   8760 GCAGACAACTAAAAACAAGATGGAGGCTGGTAAGGTTCTGAGCGACCTCAAGCTCCCT 8819

Qy   8823 GGCCTTAGCAGTCCACCGGAGAAGGCCGGGCATTGCAACGCGTATGCTCCGGTCCGCGC 8882
          || ||||||||||||||||||| |||||||||| |||||||||||||||||||||||||||
Db   8820 GGCTTAGCAGTCCACCGGAGAAGAGCCGGGCGTTGCAACGCCATGCTCCGGTCCGCGC 8879

Qy   8883 GGTTGGGCTGAGTTGGCTAGGGGCTGTTGTGGCGTCCAGGCCTGCCCCTCCGTTCCCCTCCG 8942
          |||||||||||||||||||||||| |||||| |||| ||||| |||||||| || |||||||
Db   8880 GGTTGGGCTGAGTTGGCTAGGGGCTTGTTGTGGCATCCAGGCCTACGGCTTCCTCCCCCT 8939

Qy   8943 GAGATTGCTGTGTATCCCGGGGGGTTCCCCCTTTCCCCCTATATGGGGGTGGTTCAT 9002
          ||||||||||||||||||||||| ||||||||||  || |||||||| ||| ||  ||
Db   8940 GAGATTGCTGTGTATCCCGGGGGTTCCCCTTCCCTCTCCCCCTATATGGGGGTGTGTACAT 8999

Qy   9003 CAATTGGATTTCACAAGCCAGGAGAGTCGCTGGCGTGGTTCTTAGCCCTGCTC 9062
          ||||||||||||||||||||||||||||||| ||||| |||||||||||||||
Db   9000 CAATTGGATTTCACAAGCCAGGAGAGTCGCTGGCGTGGTTCTTAGCCCTGCTC 9059

Qy   9063 ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGCAAGGTCCGGTGACTGATC 9122
          ||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||||
Db   9060 ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGCAAGGTCCGGTGACTGATC 9119

Qy   9123 ATCACTGGAGGAGGTTCCCGGCCGTCCCCCAGGGGGTCTCCCCGCTGGGTAAAAAGGG 9182
          ||||||| ||||||| |||||||||||||||||| |||||||||||| |||||| ||||
Db   9120 ATCACCGGAGGAGGTTCCCGCCCCTCCCCCCAGGGGGTCTCCCCGCTGGGTGGGTAAAAAGGG 9179

Qy   9183 CCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCTGGCAGGGTCAAAGCCTGATGGTGC 9242
          |||||||||||||||| |||||||| ||||||||||||||||| |||||||||||||||
Db   9180 CCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCTGGCAGGGTCAAAGCCTGATGGTGC 9239

Qy   9243 TAATGCACTGCCACTTCGGTGGCGGGTCGCTAACGTTATATGCGTAATCCGTGACTACGGGC 9302
          ||||||||| |||||||||||||||||||||| ||| |||||||| ||||||||||||||
Db   9240 TAATGCACTGCCACTTCGGTGGCGGGTCGCTAACGTTATATAGCCGTAATCCGTGACTACGGGC 9299

Qy   9303 TGCTCGCAGAGCCCTCCCCGATGGGGCACAGTGCCACTGTGATCTGAAGGGGTGCACCCC 9362
          |||| ||||||||||||||||||||||||||||  ||| ||||||||||||||||||||||
Db   9300 TGCTCGCAGAGCCCTCCCCCGATGGGCACAGTGCCACTGTGATCTGAAGGGGTGCACCCC 9359

Qy   9363 GGTAAGAGCTCGGCCGCCAAAGGCCCGGGTTCTACT 9395
          || |||||||||||||||| |||||||||||||||||
Db   9360 GGGAAGAGCTCGGCCGCCCGAAGGCCCGGSTTCTACT 9392
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Query Match   84.9%;   Score 7979;   DB 1;   Length 9392;

RESULT 2

Best Local Similarity 90.7%; Pred. No. 0;
Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;

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Qy      3 ACGTGGGGGGTTGATCCCCCCCGGCACTGGGTCGCAGCCCCATAAACCGACGCCT 62
          ||||||||| ||||||||| ||||||||||||||||||||||| ||||||||||||
Db      1 ACCTGGGGAGTTGATCCCCCCCGGCACTGGGTCAAGCCCCAGAAAACCGACGCCT 60

Qy     63 ATCTAAGTAGACGCAATGACTCGGCCGCCGACTCGGCCGCCGACTCGTGGATGG 122
          |||||||||| |||||||||||||||||||||| ||||||||||||||||||||
Db     61 ATCTAAGTAGACGCAATGACTCGGCCGCCGACTCGGCCGCCGACTCGTGGATGG 120

Qy    123 GTGGTGACAGGGTTGGTAGGTCGTAAATCCCGTCATCCTGGTAGCCACTATAGGTGGGT 182
          ||||||||||||||||||||||||||||  |||| ||| ||||||||||||||||||||
Db    121 GTGATGACAGGGTTGGTAGGTCGTAAATCCCGTCACCTTGGTAGCCACTATAGGTGGGT 180

Qy    183 CTTAAGAGAAGGTCAAGACTCCTCTTGTCGCTCGCGGCACCGCACGGTCCACAGGT 242
          ||||||||| ||| |||||  |  |||||||||||||||||||||||||||||||||
Db    181 CTTAAGAGAAGGTTAAGATTCCTCTTGTCGCCTGCGGCACCGCACCGGTCCACAGGT 240

Qy    243 GCTGGCCCTACCGGTGTGAATAAGGGCCCGACGTCAGCCTCGTCGTTAAACCGAGCCCGT 302
          |  |||||||||| |  ||| |   |||| ||||||||||||||||| ||||||||||||
Db    241 GTTGGGCCCTACCGGTGGAATAAGGGCCCGACGTCTCGTCGTTAAACCGAGCCCGT 300

Qy    303 CACCCACCTGGGCAAACGACAGCCCACGTACGGTCCACGTCGCCCTTCAATGTCTCTCTG 362
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TACCCACCTGGGCAAACGACGACGCCCACGTACGGTCCACGTCGCCCTTCAATGTCTCTCTTG 360

Qy    363 ACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAGTGGGGGCCGGGGTTATGGGAAG 422
          |||||||||||||| |  |||||||||||||||||||| ||| |   ||  ||
Db    361 ACCAATAGGCGTAGCCCGGCGAGTTGACAAGGACCAGTGGGGGGCCGGGGGCT -TGGAGAGG 419

Qy    423 GACCCCAAAACCCTGCCCTTCCCGGTGGGCCGGGAAATGCATGGGCCACCCAGCTCCCG 482
          ||||||| || | ||||| | ||||||||| ||||||||||||||||||||||||||||
Db    420 GACTCCAAGTCCCGCCCTTCCCGTGGGCCGGGAAATGCATGGGCCACCCAGCTCCCG 479

Qy    483 GCGGCCTGCAGCCCGGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGGCATTTCTCTT 542
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    480 GCGGCCTGCAGCCCGGGGGTAGCCCAAGAATCCTTCGGGTGAGGGGGAATCCCGTGCGTGTT 539

Qy    543 TTCTATACCATGCAGTCCTTCGCTCCTCTTCGGTTGAGGCCGGGCCATTCTG 602
          |||| ||||||||| |||| ||  ||||| ||||| ||||||||||||||||
Db    540 TTCTATACCATGGCAGTCCTTCGCTCCTCTTCGGTTGAGGGCACTGTGTGAGGACCGGG 599

Qy    603 GCCCCGGCCACCCACGTTGTCGAGCGAATGGCAATATTCCTCACAAATTGCTGTGCC 662
          ||||||||||||||||  |  |||||||||||||||||||||| ||||||||||||
Db    600 GCCCCGGCCACCCACGTTGTCGAGCGAATGGCAATATTCCTCACAAATTGTTGTGCC 659

Qy    663 CCGGAAGACATGGGTTCTGCCTGGAAGGCGGATGGCCTGGTGCCTGGGGTCACGGTT 722
          ||||| || |||||||||||||||||||||| || ||||||| |||||||||||||
Db    660 CCGAGGAGGACATCGGGTTCTGCCTGGAGGTCCTGGGGTGCCCTTAGGGGCACCAG 719

Qy    723 TGCACCGACCGGTTGCTGCCACTGTATCAGGCCGGTTTGGCGTGTCGGCCTGGCAAGTCC 782
          |||| ||||||||||||||||||||||  |||||||| | ||||||||||||||||||||
Db    720 TGCACTGGCCAATGCTGCCACTGTATCAGGCCGGGTTTGGCGTGTCGGCCTGGCAAGTCC 779

Qy    783 GCGGCCCCAGCTCGTTGGGGAACTGGGAGCCCTGTGTACGGGAGCCCTCGGTCTTCGGCTTAC 842
          |||||||||||||||||||||||||||| |||||||||||| |||||| ||||||||||
Db    780 GCGGCCCCAACTGGTCGGGGGAGCTGGGTAGCCTATACGGGCCCCGTCCTGGGGTGTCTCGGCCCTAT 839

Qy    843 GTAGCCGGGATCCTGGGGTCTGGGCGGAGGTTACTCCCGGTCCAGTTGGTTGTTGCG 902
          || |||||||||||||||||||||||||||| |  ||||||||||||||||||| |||
Db    840 GTGGCTGGGATCCTGGGGTCTGGGCGGAGGGTGTACTCCGGTCCTAACGGTGGAGTCGCG 899

Qy    903 TTGAGGCCGCCGGGTCTACCTGGGTGTCCCAACCTGAAGTGCAGTAGAATGTGACGTTAAG 962
          ||| ||||||||||||||||| | |||| |||| || |||||||||| ||
Db    900 TTGACGGCCGCCGGGTCTACCTGGGTGTGTCCCAACCTGACGTGCAGTGCGCCTGTGAGCTAAAG 959

Qy    963 TGGGAAGTGAGTTTGGAAGTCGAGCAGATGGGACGCCGAAATCACTGACTTTGGAA 1022
          ||||| | | |||||||  | |||||||||| |||||| |||||||||||| |||
Db    960 TGGGAAAGTGAGTTTGGAGAGTCGAGCTGTGTGTGCCTTCCAACTACTGGATTCTGAA 1019

Qy   1023 TACCTTTGGAAAGTCCCATTGAATTTGAATTTCTGGGATGATGAGCCCTGACCCCTCTGTTG 1082
          ||||| |||||||| ||||||||||||| | |||||||||||||||||||||||||
Db   1023 ...

Qy   1079 TACCTCTGGAAGGTCCCATTTGATTTCTGGAGAGGCGGTGATAAGCCTGACCCCCTTGTTG 1079
          ||||  |||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db   1083 GTTTGGGTGCCGCCATTGCTTTTCTGCTGGAGCAACGATTGTCATGGTTTCTCGCTGGTG 1142

Qy   1080 GTTTGCGTGCCGCCATTGCTTGCTCTGCTGGAGCAACGATTGTCATGGTCTTCGCTGTTGGTG 1139
          ||||||||||||||||| |||||||||||| ||||||||||||| |||||| |||||||| 
Db   1140 ACGATGGCGGGATCTTGCAAGGCGCCCCGCCTTCGGGGTCCCGCGCCCCCTTTGAC 1199

Qy   1143 ACGATGGCGGGGATCTTGCAAGGCGCCCCGCCTTCGGGTCCCGTTTGGGGTCCCGCCCCTTTGAC 1202
          |||||||||||||||| |||||||||||||| ||||||||||||| |||||||||| 
Db   1200 TACGGGTGACTTGGCAGACCTGCGTTTTCGCAGGGGCCAACGGGCGCCCCCTGG 1259

Qy   1203 TACGGGTTGAAGTGGCAGTCATCGTCCTGCGAGGTCTAACGTCGCGTATTCCCACTGGG 1262
          ||||||| |||| || ||||||||||| | |||||||||| |||| ||  |||||||||
Db   1263 GAGAGGTGGATCGGAGGGAATGTCAGGTTACGCTTCAGTGTGACTGCGCCCCAGGCCCCCTGG 1322

Qy   1263 GAGAGGTTGGGATCGAGGGAATGTCAGGTCTTGTGTGACTGCGTCCTGTCTGCGCCCCCTGG 1322
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1320 GTGTGGTTGCCAGCCTTTGCCAAGCAATCGGCTCGTGGTGTCCACCATCACCTATTGGAGC 1379

Qy   1323 GTTTGGGTCCCGGCCTTTTGCCAGGCGGTTGGTGGGGGCGACCCCATCACACCCATTGGAGC 1382
          || |||| ||| ||||| |||| ||| |  ||||||||||||  |||||||| |||||||
Db   1383 CACCGACAAAACCAGTGGCCCCTATCATGCCCCAAATATGTCTATGGGTCTGTGTTCCGTA 1442

Qy   1383 CACCACCTGGGCAAACGACAGTGGCCCCTATCATGCCCCAATATGTCTATGGGTCTGTTCCGTA 1442
          ||||||  ||||||||| | |||||| |||||  |||||| |||| |||| | ||||||||||
Db   1443 ACGTGCGTGTGGGGTTCCGTGTCCTGTGGTTGCCTGCGTCGTGATTCGGATTCGGAGATC 1502

Qy   1443 ACGTGCGTGTGGGGTTCCGGTCGGTTGGTGTCCTTGGTTGCCTCCAGCTGCACCGCTCTAGGGTCA 1502
          | |||||||||||||| | ||  |||| |||| || |||||||| ||||||||||||||
Db   1500 GATGTGTGGAGTTTAGTGCCTCGTTGCTCTGCAACTGCCTGGGTCGCACTGGGTGACTGGAATCA 1559

Qy   1503 GATGTGTGGAGTTTGGTGCCGGTTGATCGTGCAACTGCCTGGGTGCACTGGGTGACTTGGGATCA 1562
          |||||||||||||||| ||  | |||||||||||| |||| |||||||||||||||||||||
Db   1563 TCGGATCGGCACGGTGTTGACCTCTCCGAGTGGGAGTCCCGTGCTTGCTTGCTAAGTGTATT 1622

Qy   1563 TCGGATCGGCACGGTGTTGAGCTCTCCGAGTGGGAGTCCCGTGCTTGCTAAGTGTGTGTT 1622
          ||||||||||||||||||||| |||||||||| |||||||  | |||||||| |||||||
Db   1623 CTGGACCGTCGCCGCTGCTTCATGTGGCGGACTGCTGCCCGGAGGACCGGG 1682

Qy   1623 CTGGACCGTCGGCCCTGCTTCATGGCGGGCCTGGGCCCGAAACCGGG 1682
          ||||||||||||| | |||| |||| ||||||| |||||||||| ||
Db   1680 CTGGACCGTCGGCCCTGCTTGAGGGACTGCTGCCCCGAGACCGGG 1739

Qy   1683 TCGGTTAGATTCCCTTCCATCGGTGTGCACGGCCTCGGCCTGACAAAGGACTTGGAA 1742
          ||||| ||| ||||| |||||  |  ||||||||||||||||||||||||||||||
Db   1743 TCGGTTAGGTCCCATTCCATTCATCGGTGTGCGGCCTCGGCCTGACAAAGGACTTGGAA 1802

Qy   1743 GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCGTCAACAGGACAACTCCCTGGGCAACCAG 1802
          ||||| |||| |||||||||||||||||||||||||||||| ||||||| |||||||||||
Db   1740 GCTGTCCCTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGCGCCCCTGGGCAACCAG 1799

Qy   1803 GGGAGAGGCAACCCGGTGTGTCGTCATTGACCAAGATC 1862
          ||  |||||||||||||||| |||| |||| |||||||
Db   1862 GGGAGAGGCAACCGGTGGGGCTTACGCGGGGTTCACGCAGG 1922

Qy   1863 CGGGATTCCCTGCATTGGTGAAATGTCCACACAGAGCCTCCGACTGAACG 1922
          || ||  ||| | ||||| |||||||||||||||||||||| |||||||
Db   1860 CGAGATACCCTACATCGTGGAGTGTCCACACAGCCCATTGAGCCTCCACCGGACG 1919

Qy   1923 TTCGGGTTCTCCCCGAGTCCCGCCATTAACAACTGCATGCCGCTGGAAGTG 1982
          |||| |||||||  ||| |||| ||||||||||||||||||||| ||||
Db   1980 TTTGGTTCTCTTCCCGGACGCCGCCTCTCAACAACTGCATGCATGCTTGGCACGGAAGTG 1979

Qy   1983 TCTGAGGCATTGGGCGGAGCTGGTTCAGTAGAATGTGACGTTAAG 2042
          | ||| ||| |||||||  ||||||||||||||||||||||||
Db   1980 TCCGAGGCACTTGGGGGTGCCTGCGTTCATGAACCCCTGTGCGCAGG 2039

Qy   2043 TGTTCGAGCTGATGGGACGCCGAAATCCGTTTGCCCGGGGTACGCAGTGTCCTCT 2102
          |||||||||||| ||| |||||||| ||  |  |||||||||| |||| ||
Db   2099 TGTTCAAGCTGATGGGAAGCCGAAATCCGTTTGTCCGGGGTTTGCCGGATGGCATGGCCTCTTCG 2099

Qy   2103 GGTAGACCTGACGGGTTCATCACGTGTTATACATGTCCAGGGCAGGGCAAC 2162
          |||||||||||||||||| |||| ||  |||| ||||||||||||||||||
Db   2100 GGCAGGCCTGACGGGTTTATACATGGTTCCAGGGCACTTGCGAGGTGGATGCAGCGCAAC 2159
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Qy   2163 TTCATCCCTCCTCACGCGTTGGTTGCTCTCTTGGATTTTGTGTATTTGTTCCTGCTCTATCTGATG 2222
          ||||||||| ||   || ||||| ||||||||||| ||| ||| ||||||||||||||||  ||||
Db   2160 TTCATCCCGCCCCCGCCGCTCGGTTGCTCTTGACTTTGTATTTGTTGTCCTGCTCTATACCTGATG 2219

Qy   2223 AAGCTTGGCTGAGGCACGGTTGGTCCGTTGGTCATCCTTGCTTCTCTGCTGTGTTGGTGGGTGAAC 2282
          |||||||||||||||||||   |||||| ||| |||| ||||  ||| |||||  |||||| |||||
Db   2220 AAGCTTGGCTGAGGCACGGTCCCGGGCTGGTCCGGGCCTGTGTCCGGCCGTGTGGGGCGGGTGAAC 2279

Qy   2283 CAGTTGCGGGTTCGACTGTCGCCGGCTGTGACGCGTCGCCGTGGCGGTGAAGTTTTGCGG 2342
          ||| ||||| ||| || ||| || ||||| ||||||| ||||||||||||||||| |||||
Db   2280 CAGCTGGCAGTCCTAGGGCTGCGGAAGCCGCCCGTGTGGCCGGTGAAGGTCTTCGCG 2339

Qy   2343 GGCCCTGCCTTGTCATGGTGTTTCGGTGGATGGTTCCCACTGTCAGTATGATACTAGGTCTAGCA 2402
          |||||||||||   |   |  |  ||||||||||||||||||||||||||    ||||||||||||
Db   2340 GGCCCTGCCGCCCCGTGGGTGTGTCGGGGGCGTGTTGGAAGCCGCCCGTGTGGCCGGTGAAGG 2399

Qy   2403 AACCTGTGTGTTGTACTTTCGGTGATGGGCCTCAGCGCCTCATGTTCCTCGTTGTTGTGG 2462
          |||||||| ||||| ||| |  |||| ||||||||||||||||||||  ||  |||| |||
Db   2400 AACCTGGTGCTGTGCTGTTAGATGGTTGGGACCCCAAACGCCTGATGTTCGTCGTTGTGG 2459

Qy   2463 AAGCTCGGCTTCGGGGAGCTTTCCCGCTGGCACTTTGATGGGGATTTCGGCGACCCGGGG 2522
          ||||| |||||||||||||||||||||| |||||   || |   ||||||| |||||||||
Db   2460 AAGCTGGTGCTGTCTCGGGGAGCTTTCTTGATGGGGATTTCGGACCCCTGGGTACCGGGG 2519

Qy   2523 CGCACCTCTGCTCGGGGCCGAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCG 2582
          |||||||||||||||||  | ||||| |||| ||| | |  |||||||| |||||||||
Db   2520 CGCACCTCAGTGCTGCTCGGGGCCGAGTTCTGCTTCGATGCTACATTCGAGGTGGACACTTCG 2579

Qy   2583 GTGTTGGGCTGGTGGTGCCAGCCTGGTGGCCTGGCCATAGCCGCTTCCTGAGCTCAATG 2642
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 GTGTTGGGCTGGTGGTGGCCAGCCATGTGGTAGCTTGGGCCATTGCGGCTTCCTGAGCTCGATG 2639

Qy   2643 AGGCAGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGTACCAG 2702
          |||||||||||||||| |||||||||||||||||||| ||||||||| |||||||||
Db   2640 AGGCAGGGGGTGGAGCTGGAGCAAAGCCGTGATCTATAGGACGTGTGTAAGGGGTACCAG 2699

Qy   2703 GCTGTCGCGCCAGAGAGGTGGTGCGGAGCCCCTCGTTCCTACCAAGCTTCTG 2762
          ||||||||||||||||||||||||||| |  |  |||||||| |||||  |||
Db   2700 GCAATCCGTCAAAGGGTGTGAGGAGCTGGACTGGCACTGGAGGGCGCCTGCCAAACCCCTG 2759

Qy   2763 ACGTTCGCCTGTGTCGTTGGCCTCATACATCTGGCCAGATGCTGTCGTGATGGTGGTG 2822
          ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 ACCTTTGCCCTGTGTCGTTGGCCTCTGTACATCTGGCCAGATGCTGTCGTGATGGTGGTT 2819

Qy   2823 GCCTTGGTCTCCTCCTCTTCGACGCACTGGACTGGCCCTGGACTGAGGAGCTCCTG 2882
          |||||| |||||||||||||||||||||||| ||||||||||||||| |||||||  ||
Db   2820 GCCTTGTCGTCCTCCTCTTTCGACGCGTTGGACTGGCCCTGGAATGGGGAGATCTTG 2879

Qy   2883 GTCTCCCGGCCCTCGTTACCGGACTGGCACGGGTGGTGTGATGGCGGGC 2942
          || |  |||||| ||||| || |||||||||||||||| ||| ||||||
Db   2880 GTGTCCCGGCCCTCGTTGCCGGACTGGCACGGGTGGTGTGATGGCGGGGT 2939

Qy   2943 GAGAAGGCCACCACCATCCCCGGACTGTCTCCAAGATGTGCCAAGAGGGGCCTACCTGTTT 3002
          ||||||||||||| |||  |||||||||||  |||||||||||  ||||||  ||||||
Db   2940 GAGAAGGCCACAACCGTCCCGGCTGTCTCTCCAAGATGTGCCGAGAGGAGCTTATTTGTTC 2999

Qy   3003 GACCACATGGGCGCTTGTCTCCGGACTGGCCATGGGTAGCACGGCGCTTGTTGGAATGGCGGCT 3062
          |||||  |||||| ||| |||||||||||| || |  |||   ||  || || |||||||||||
Db   3000 GATCATATGGGCGCTTCTCTGTTGGCGTCATGGGTTGGAATGGCGGACCAGCT 3059

Qy   3063 TTGGAGCCCTTGTCATTCACTAGGACGACGGATCGCATCATCAGAGATGCCGCGAGGACC 3122
          || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3060 CTTGAACCTCTGTCGCGGCGGATGTGCCATCATCAGAGATGCCGCGAGGACT 3119

Qy   3123 CGTGTCCTGCGGACAGTGCGTCATGGGTTACCCGTGGTAGCACGGCGCTTGATGAGGTT 3182
          ||||||||||||||||||||||||||||| ||||||||||||||  || ||||||||||
Db   3120 TTGTCCTGCGGGGTCAGTGGTCATGGGTTTACCCGTGGTTGCCGCCGTGTGGTAGTGGTT 3179

Qy   3183 CTCATCGGGCTCTTTGCGGATGTGAATCATTTGCCTCCCGGGTTTGTCCGACTCACCA 3242
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   3180 CTTCATCGGGCTCTTTCCAGGATGTGAATCATTTTATGGGCATGGAATACCCCTGTGTTCTTCCGACCGCCT 3239
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Qy   3243 GTTGTCATCCGTGCGGTGCGGAAAGGCTTCCTGGGGTCACGAAGGCAGCCTTGACAGGT 3302
          |||||||||||| |||| ||||||||||||||||||||||||||||| |||||||||||
Db   3240 GTTGTCATCCGACGACGGTGCGGAAAGGCTTGGGGGTCACGAAGGCTCGCCTTGACAGGT 3299

Qy   3303 AGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTTGGGGACGGCTACGCTCACGAAGC 3362
          |||| |||||||||||||||||||||||||||| ||| |||||||||||||||||||||||
Db   3300 CGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTTGGGGACGGCTACGCTCGCGGAAGC 3359

Qy   3363 ATGGCGACACATGCTGAATGTCGTGTTCACAACTTCCATGGGCTTCATCCCGAACC 3422
          ||||  |||||||||||  ||| || |  ||||||||||||||||||||||||| ||
Db   3360 ATGGGAACATGCTTGAACGCCTGCTGTTCACGACCTTCATGGGCTTCATCCCGAACC 3419

Qy   3423 ATCGCCACGCCCGTGGGGGCCCTTAATCCCAGGTGGTCAGCCAGTGGTCAGCGATGACGTCACG 3482
          ||||||||||||| |||||||||||||  |||||||| ||||||||||| |||||||||||||||
Db   3420 ATCGCCACACCCGTGGGGGCCCTTAATCCCAGATGGTCAGCCAGTGGTCAGCGATGATGTCACG 3479

Qy   3483 GTGTACCCGCTTCCAGATGGGCAACTTCGTTGACGGGCGTTGTGACCCTGCACTTGCCAGGCGGAGTCC 3542
          ||| |||||||| || ||||| |||  |||| |||||||    ||||||||||||||||||  ||||||
Db   3480 GTGTATCCACTCCCGGATGGGCTACTTCGTTGACACCTTAACACCTTGTTAACACCGTTGCCAGGGGACAAGGTT 3539

Qy   3543 TGTTGGTTATTAGATCGACGGGCGTTGTGCCATGGCTTGAGCAGGGGACAAGGTT 3602
          |  |||| |||  ||||  ||||  |   |||||||||||||||||||||||||||
Db   3540 TGTTGGGTCATCAGATCCGCAGATCCGACGGGCGCCCTATGCCATGGCTTGAGCAGGGGACAAGGTG 3599

Qy   3603 GAGCTCGATGTGGCCATGGAGTCTCGACTTCGTCGTCTGGTTCGTCGTGCTCGTCTGGTTCAGTGCTCTT 3662
          |||||||| ||||| ||| |||| || |||||| |   |||| |   || ||||||||||||||||||| |
Db   3600 GAGCTGGATGTGGCCATGGAGTCTCGACTTCGTCACTGGTTCGTCTCGCTCGTCACCGGCGGCAGGGTT 3659

Qy   3663 TGCGACAAAGGCACGCAGTAAGAATGCTCGTGTCAGTGCTCCACTCTGGCGCGCAGGGTT 3722
          ||  ||||| ||||||||| || || ||||||||||| | |||| | |||  |  ||||||
Db   3660 TGTGACGAAGGCACGCAGTAGGAATGCTCGTGTCTCGTCTCCGGTGCCGGTGTAGGGTC 3719

Qy   3723 ACTGGCGGCGATTCACTAGGCCGTGACTGCCAAGTACCAACAGATGCCAAGATACCACCA 3782
          ||  |||||||  | ||| ||||||||||    ||||||||  |||| ||||| |||||||
Db   3720 ACCGGCGGCACGGTTCACTAGGCCGTGACCCAAGTGCCAACAGATGCCAAAACCACTACT 3779

Qy   3783 GAACCCCTCGGTGCCGGCAAAAGAGTTTTCAAGGAGGCCCGTTGTTTATGCCTACG 3842
          |||||| ||||| |||||||| |||||||||||||||| ||||||||| ||||||||
Db   3780 GAACCCCTCGGTGCCGGCAAAAGAGTTTTCAAAGAGGCCCGTTGTTTATGCCTACG 3839

Qy   3843 GGGGCGGGGAAAAGAGCACCCGGTACCCGTGGCAACAGAGCAACATGGCCAAGGCTCTTG 3902
          ||| |||||||| ||| ||||||||||| || |||| |||||||||  ||||| ||||| 
Db   3840 GGAGCGGGGAAAAGAGCACTCGCCGTGGGCCACAGATAACATGGGGCACAAGGCTCTTA 3899

Qy   3903 ATCTTGAACCCGTCGGTAGCTACCGTGAGGGCCATCATGGAGCGGCGGCTGGCG 3962
          |||||||| || |||||||||||| ||||||||| | | |||||| |||| |||
Db   3900 ATCTTGAACCCCTCAGTGGCCACTGTGTGCGGGCCATGGCCCGTACATGGACGGCGGCG 3959

Qy   3963 GGGAAACACCCCAGTATTACTGTGCCCATGACACACTGCTTCCACAAGGATCACTGAC 4022
          |||||  ||||||||| |||| |||||||||||||||||| ||| |||| |||||||||
Db   3960 GGTAAACATCCAAGTACTATATACTGTGGCCATGCATCAGCTGTCTTCAACAAGGATCACTGAC 4019

Qy   4023 TCGCCCCTTACGTATTCCACTTACGGAGAGGTTTTGGCCAACCCTAGGCAGATGCTGAGG 4082
          ||  || |||||  || |||| ||| |||||||||||||||||||||||||||||||||||
Db   4020 TCCCCCCTGACGTATTCAACCTCAACCCTAGGCAGATGTCTTTGGCCAACCCTAGGCAGAGTGTACGG 4079

Qy   4083 GGTGTCTCGGTGGTCATTTGTGACGAGTGCCACAGTCATGACTCAACTGTGTTGTTGGGC 4142
          ||||| |||| |  ||||  ||| || ||||||||||||| |||||  ||||  |||| |
Db   4080 GGCGGTTTCGGTTCATTTGTGATGAGTGCCACAGTGCCACACTCATGACTCACGTGCTGTCGTTAGGC 4139

Qy   4143 ATTGGCGTGTCAGGGAGCTGCGCCGATGCGGGGGCGTCAATTGGTGCTCTACGCCACT 4202
          ||| ||||||||| |||| ||||| ||||||||| ||  || |||| || |||||||||
Db   4140 ATTGGGAGAGTCCCAAGTACATACTGTGGCATACTGTCTTCACAACTAGTGCTCTACGCCACC 4199

Qy   4203 GCCACCCCCTGGGATCCCCGATGCGCCACCAGCACCCATCAATCATTGAGACAAAACTGGAC 4262
          |||||||||  |  |||| ||| | | |||| |||| ||||  ||| ||| ||||| |||||
Db   4200 GCTACACCGTGGGATCCCCGATCCGCCACCATGACCAGCACCCCTTCCATAATTGAGACAAAATTGGAC 4259

Qy   4263 GTGGGAGAGATCCCCTTTGTCCGGGTTTGTCCCGACTCACCA 4322
          ||| |||||  || | |||| |||||||||| ||||| |||||
Db   4260 GTGGGCGAGATTCCCTTTTATGGGCATGGAATACCCCTCGAGCGGATGCCGAACCGGAAGG 4319

Qy   4323 CATCTCGTATTCTGCCACTCCAAGGCTGAGCGCCTCGGCGGCCCAGTTTTCGGCT 4382
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Db  4320 || ||||| |||||||| || |||||||||||||||  ||||||||||| |||||||| |||
         CACCTCGTTCTTGCCATTCTAAGGCTGAGTGCGAGCCGCCCTTGCTGCTGGCTCTCCGCT 4379
Qy  4383 AGGGGGTAAATGCCATCCATTATTACAGGGGAAAGACAGTTCTATCATCAAAGATGA 4442
         ||||||| ||||||||||| |||||||||| ||||||| |||||| ||||||| ||||
Db  4380 AGGGGGTCAATGCCATCCATTATTATAGGGGTAAAGACAGTTCTATCATCAAGGATGGG 4439

Qy  4443 GACCTGGTGGTGTGTCTACAGACGCACTATCCACTGGGTACACCTGTCGATTCT 4502
         |||||||||||||||||||| ||||||||| |||||||||| ||| ||||||| |
Db  4440 GACCTGGTGGTCGTGTCTACAGACGCGCTTCCACTGGGTACACCTGGAAATTTCGACTCC 4499

Qy  4503 GTCACCGATTGTGTGGTTAGTGTGGTGGAGGAGGTCGTCGAGGTGACCCTTGATCCCACCATT 4562
         |||||||||||||||| ||||||||||||||| |||||||||||||| ||||||||||||||
Db  4500 GTCACCGACTGTGATTAGTGTGGTGGAGGAGGTCGTTGAGGTGACCCTTGATCCCACCATT 4559

Qy  4563 ACCATCTCCCTGCCACCGTGCCCGTCGGCTGAACTGTCGATGCAGCGGCCAGGACGC 4622
         |||||||||||||||||||||||||||||||||||||| ||| |||||||||||||||
Db  4560 ACCATCTCCCTGCCACCGTGCCCGTCGGCTGAACTGTCGATGCAAAGACGAGGACGC 4619

Qy  4623 ACGGGTAGGGGCCAGGTCTGGGCGTCAGCTACTACGCCGCGGGTCGGCAAGGCCCCTGCTGGT 4682
         ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  4620 ACGGGTAGGGGCCAGGTCTGGACCGTCTGGGCGTCAGCTACTACGCCGCGGGTGGGCAAAGCCCCTGCGGGT 4679

Qy  4683 GTGGTGGCCTCAGGTCTCTGTCGGCGTGGAAGCCGGTGTGACCGGTGTACGGAATG 4742
         ||||||||||||||||| |||||||||||||||||||||||||||| |||||||||
Db  4680 GTGGTGGCCTCAGGTCCTGTCGGCGTGGAAGCCGGTGTGACCGGTGTACGGAATG 4739

Qy  4743 GAACCTGACCTGACAGCAGAAAACTACTGAGACTTTACGACAACTGCCCTACACCGCCAGCC 4802
         ||||||||||||||||||||| |||||||||  ||||||| ||||||||||||||||||||
Db  4740 GAACCTGACTTGACAGCTGAACCTACTGAGACTTTACGACAACTGCCCTACACCGCCAGCC 4799

Qy  4803 GTCCAGCTGACATTGGGGAAGCCGCGGTGTCTTTTCGGGGCTTGCCCCGTTGAGGATG 4862
         |||||||||||||| ||||||||||||||||||||||||||||| |||||||||||||
Db  4800 GTCGCGGCTGATATCCGGGAAATCCTGTCCCACTCCTGCGGGGCAATGATTTACCATCT 4859

Qy  4863 CATCCCGATGTTAGCTGGCAAAAGTTCGCGGCGTCAACTGGCCCCTTCCTGGTGGGTGTT 4922
         | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4860 CACCCTGATGTGCAGCTGGCAAAAGTTCGCGGCGTCAACTGGCCCCTTCCTGGTGGGTGTT 4919

Qy  4923 CAGCGGACCATGTGCCGGGAAAACTGTCTCCCGGCCCATCGGATGACCCCAGTGGGCA 4982
         |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  4920 CAGCGGACCATGTGCCGGGAAAACACTGTCTCCCGGCCCATCGGATGACCCCAATGGGCA 4979

Qy  4983 GGTCTGAAGGGCCGAATCCTGTCCCACTCCTGCTGCTGAGGTGGGCAATGATTTACCATCT 5042
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Db  4980 GGTCTGAAGGGCCCAAATCCTGTCCCACTCCTGCTGCTGAGGTGGGCAATGATTTACCATCT 5039

Qy  5043 AAAGTGGCCGGCCATCACATCGTGGACGACTGGTCCTGAGCCTCGGGTGCGGAGGGT 5102
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Db  5040 AAAGTGGCCGGCCACCACATAGTGGACGACTGGTCCTGAGCCTCGGGTGTGGGAGGGT 5099

Qy  5103 TACGTCCCGCTGCCATGCGGGAGACCCATCTTGATGTGGGCCTTCGCCTATTGCGGGGCATG 5162
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Db  5100 TACGTCCCGCTGCCATGCGGGAGACCCATCTTGATGTGGGCCGATCGTCTAGCTATGCGGGGAATG 5159

Qy  5163 ATCTATGCGTCATACACCGGGTCTCTGTCCACTCGTCAGTGTGATGGTACAGACCGGGGGT 5222
         ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db  5160 ATCTACGCGTCATACACCGGGTCTCTGTCCACTCGTCAGTGTGATGGTACAGACGGGGGT 5219

Qy  5223 GGCAGCCCCCTTTATCGGACGAGACCCAGCCACGCCCGTTGTGCAGGTCCCC 5282
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Db  5220 GGCGCCCCCTTTATCGGACGAGACCCAGCCACGCCCGTGTGCAGGTGCCAGGTTCCT 5279

Qy  5283 CCGGTAGACCATCGGCCGGGGGAGTCTGCGCATCGGATGCGGGGGCATG 5342
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Db  5280 CCGGTAGACCATCGGCCGGGGGTGAATCAGCAGCCAAGAACACAGTGACAGAT 5339

Qy  5343 GCGGTGGCCATCAGTTGCGATTGTGCAGTTCGTCGATCGGGGAA 5402
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Db  5340 GCGGTGGCAGCCATCAGTTGCGATTGCGATTGGCAACTGCGATCATCATGACTCTCGATCGGAGAA 5399

Qy  5403 GTGCTGTCCTTGGCCCCAGGCTAAGACGCGCTAAGACGCGTACCCAGCTACCACCAAGTGCTT 5462
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Db  5400 GTGTTGTCCTTGGCTCAGGCTAAGACGGCGGCCGTCCCACTGTTCAATTGTTGACAAGCTCTC 5459
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Qy  5463 GCTGCTGCTACAGGGGACCGGGACCGCTGGGCGCCGGCGTTCCCACTGTTCAAAGCTCTTC 5522
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Db  5460 GCTGCTGCTGTATACGGGGACGCGGCGGCCGGCGTATCCCACTGTTGTTGACAAGCTCTTC 5519

Qy  5523 GCCGGGGCTGGGCGCCGGCGTGGTAGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGGGCG 5582
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Db  5520 GCCGGAGGGTGGGGCGGGTGGCCATTGCCACAGTGTCGGCGGGTGCTGCGGCGGTGGGCG 5579

Qy  5583 GCCTATGGGGCTTCTTAGGAGCCCTTCCATTGGCTGCTGCTGCGGCCTTCTACTTCATGGGGTTG 5642
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Db  5580 GCCTACGGGGCTTCAAGGAGCCCGTCGGCGGGGCCTTCGTCCTACTAGGGGCTTG 5639

Qy  5643 GGCTCGGAGGCAACGCGCCAAACCCGTCTAGCCTTCAGCGGCGCCAGGACGC 5702
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Qy  5703 ACCGGCTCTGGGCAACCCGTGTCGGGGGTTAACCATGCGGCGGCGCGTTAATCGCCAGTGCT 5762
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Db  5700 ACCGGCTTGGGCCACTCCGTGTCGGGGGTTGACCATGCGGCGGCGCGTTCATGGGGGGGCC 5759

Qy  5763 AGCGTCTCCCCTCCTTGGTCACCATTTTACTGGGGCCGTGGGGGGCGTGGGGAGGGCGTG 5822
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Db  5760 AGTGTCTCCCCTCCTTGGTCACCATTTTATTGGGGCCGGGGTTGGGAGGGTTGGGAGGGTGTT 5819

Qy  5823 GTGAATGCGGCTAGCCTTGTCGTTGTCGACTTTATGGCGGGGAAACTATCATCAGAGATCTG 5882
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Db  5820 GTCAACGCGGCGAGCCTAGTCTTTTGACTTCATGATCCCGGACAGTTTCATCAGAGATCTG 5879

Qy  5883 TGGTATGCCATCCCAGTGCTCAACCAGTGCGACTTGAGCCTCACGCGTGCCCGGTGGTCAAC 5942
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Db  5880 TGGTATGCCATCCCAGTGCTCAACCAGTGCGACTTGAGCCTCACGCCGCCACAGTCGTTGCCCTGGTCAAC 5939

Qy  5943 TTGGTGTGTTACTCAGCTAACAACTCTGGTTGAGCCGTCAACTGGTTGGGAGTTGGGGATC 6002
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Db  5940 TTGGTTTGTTATTCAGCTAACAACTCTGGTTGAGCCGTGCTGCTGACTGGTTGGGAGTTGGGGATC 5999

Qy  6003 ACATTGCCAAGGTCCTCATGCATCCGACAGTTACTTCAGCAGGCCGATTACTGTGAC 6062
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Db  6000 ACGTTACCAAGGTTTTCATCCCGGACGTTACTTGGATGCAGTTGACTATTTGCGAC 6059

Qy  6063 AAGGTCACGCTGTGCTCCCGACGCTTGAGCCTCACCGCCCGACAGTCGTTGCCCTGGTCAAC 6122
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Db  6060 AAGGTCACGCTGTGCTCCCGACGCTTGAGCCTCACCGCCCGACAGTCGTTGCCCTGGTCAAC 6119

Qy  6123 AGGAGCCTAAGGTGGATGAGGTTCAGGTTGGGACTTGTGGGGACTTGTGGGGGATC 6182
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Db  6120 AGGAGCCTAAGGTGGATGAGGTGGTATGTCTGGGACCTGGGTGGGAGTGGGATC 6179

Qy  6183 ATGCGTCAAGTGCGCGCATGCGATGGCCAGACTTCGGGCCCTCTGCCCCGGTGTGTCATTA 6242
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Db  6180 ATGGCGCCAAGTGCCGGCGTGGTCATGGCCAGACTCAGGGCGCTCATGGGGTGTCCCTGTGTACTA 6239

Qy  6243 CCCTTATGGCACTGCGGGGAGGGGGGTTGTCGGGATGGTGTTGGACGGGCCATGTTGAG 6302
         ||||||||||||||||||||||||||| |||| ||||||||||||||| |||||||||||
Db  6240 CCCTTGTGGCATTGCGGGGAGGGGGGTTGTCGGGATGGTGCTTGACGGGTCATCGTGAG 6299

Qy  6303 AGTCGTTGTCTTTGTGTTGCGTGATCACCGGTGATGTTTTGAAGTGGGCAACTCAAAGAT 6362
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Db  6300 AGTCCCTGCCGCCTGTCGTGATCACTGTGATCACTGGTGACGTTCGAATGGGCAACTCAAAGAA 6359

Qy  6363 CCAGTTACTTCTACCAAGCTGTGCACAGTGTCGGAGGGCATTATTGGATGGGACAGTCCTGTGAACATG 6422
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Db  6360 CCAGTTACTTCTACCAAGTTGGATGGGACTATTGGATGGGACACTGTTCCCTGTGAACATG 6419

Qy  6423 CTGGGCTATGGCGAGACGTCGCCTTTGCTCGCGGCCATTCGGAGCGCCGAAGGTGGTACCATTC 6482
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Db  6480 GGGACGTCTGGGTGGCTGGCTGAGGTGGTGGTGACCCACCGTTACCACCACGTGTAATCAGGAGGACC 6539
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Qy  6543  TCCGCCTACAAACTGCTGCCCAGCAAATCCTGTCGCGCTGCTGTTGCTGAGCCCTATTAC  6602      Qy  7623  TGCCTAAGCAGTGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCC  7682
          |||||||| ||  |||||||||||||||||||| ||||||||  || |||||| ||||                   |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  6540  TCCGCCTATAAGCTGCTGCCCAGCAAATCCTATCGGCTGCTGTAGCTGCCCTACTAC    6599      Db  7620  TGCCTAAGCAGTGGGTTACACTTATGAGGAGGAAGCAATAAGGACTGTAAGGCCACATGCTGCC  7679

Qy  6603  GTCGACGGCATACCGGTCTCATGGGACGCGCGACGCGCGAGCGCCTTGCGCTTGGTCTATGGC  6662      Qy  7683  ATGGGCTGGGATCTAAGGTGTCGGTCAAGGACCTCGCCCACCCTGCGGGGAAGATGGCT  7742
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Db  6600  GTCGACGGCATTCCGGTCTCATGGGACGCGGACGCGCGACCGTGCGCCCCAGTGTCTATGGC   6659      Db  7680  ATGGGCTGGGATCTAAGGTGTCGGTTAAGGACTTAGCCCACCCTGCGGGGAAGATGGCC  7739

Qy  6663  CCTGGGCAAAGTGTCACCATTGACGGGAACGCTACACCCTTCCGCATCCGGGCTT   6722      Qy  7743  GTCCATGACCGGCTCCAGGAGATACTGAAGGGACCCAGTCCCGTTCCCTTTACTCTTACTGTG  7802
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Db  6660  CCTGGGCAAAGTGTTACCATTGACGGGAGCGCTACACCTTGCCTCATCAACTGAGGCTC  6719      Db  7740  GTCCATGACCGGCTTCAGGAGATACTTGAAGGGACTTCCGGTCCCTTTACTCTTACTGTG  7799

Qy  6723  AGGAATGTGGCGCCCTCTGAGGTGTCATTCCGAGGTGTCCATTGACCGGACCGGAGACT  6782      Qy  7803  AAAAAGGAAGTGTCTTCAAAGACCGAAAGGAAGAGGAGAAGAGGCCCCCGCCTCATTGTTC  7862
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Db  6720  AGGAATGTGGCACCCTCTGAGGTTTCATCCGAGGTGTCCATTGACCGGACCGGAGACT  6779      Db  7800  AAAAAGGAGGTGTCTTCAAAGACCGAAAGAAGAAGAGGAAGAGGCCCCCGCCTCATTGTTC  7859

Qy  6783  GAAGACTCAGAACTGACTGAGGCCGCGACCTGCCGGCCTGCCGAGCCCTTCAGGCTATC  6842      Qy  7863  CCCCCCTGGACTTCCGGATAGCTGAAAAGCTTATTCTGGGACACCCAAATCAGCGACGGGGTAGCC  7922
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Db  6780  GAAGACTCAGAACTGACTGAGGCCGCGACCTGCTGCCCGGCTGCCGATC   6839      Db  7860  CCCCCCTGGACTTCCGGATAGCTGAAAAGCTCATCTGGGACACCCAAATCAGCGAGTTAAGGAGCC  7919

Qy  6843  GAGAATGCTGCGAGAATTCTTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTAGA  6902      Qy  7923  AAGGGCGGTGTTGGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGACCGGCCACATGC  7982
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Db  6840  GAGAATGCTGCGAGATTCTTGTAGTAGCCGAGAAGTCATCATGGGAGAAGAGTCGCAGTACA  6899      Db  7920  AAGGGCGTGTTGGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAGTTAAGGAG  7979

Qy  6903  CCCTCTCTTGTGGAGTAGCCGAGATGCCTGTGTGGGAGAAGACATACCCCGCACT  6962      Qy  7983  ATGCTCAAACTGTGGAATCAAAGAAGACACCATGCGCCATCTGTGTGGACGCCACATGC  8042
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Qy  6963  CCATCGCCAGCACTTATCTGGTTACTGGTTCCGTACTAAAAGCTTTGTTG  7022      Qy  8043  TTCGACAGTAGCATAACTGAAGAGGACGTGGCGCTGGACAGAGCTTTATGCCCCTGGCT  8102
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Db  6960  CCATCGCCAGCACTTATCTGGTTACTGAGAGCAGCTCAGATGAGAAGACCCCCGTCGGTG  7019      Db  8040  TTCGACAGTAGCATAACTGAAGAGGACGTGGCGCTTGGGTGTCTGTGTCTAACAACT  8099

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          |||||||||||||||| |||| || |||||||||||||||||||||                              |||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
Db  7020  TCTTCCTCGCAGGAGGATACCCCGTCTTCTGAGAGTCCAAGAGTCCGAG  7079      Db  8100  TCTGACCATCCAGAATGGGTGCGGCACTTGGGGAAATACTATGCCTCAGGCACCACATGGTC  8159

Qy  7083  ACAGCCGAAGGGGGAGGAGGAGAAAGCTCTTCAACGTGCTCTTTCCGTACTACAAAAGCTTTGTTT  7142      Qy  8163  ACCCCCGAGGGGGTGCCAGTGGGTGAGAGGTATTGTGAGATCCTCAGGGGTCTTGACCACC  8222
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Db  7080  ACAGCCGAAGGGGGAGGAGGAGAAAGTGTCTTCAACGTGCTCTTTCCGTATTAAAAGCCTTATTT  7139      Db  8160  ACCCCCGAGGGGGTGCCAGTGGGTGAGAGGTGTCGGTGTGTCCTAACAACT  8219

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Qy  7203  GTAACACGCTTCTTTTTCATTGGGATTGACGGGTTGACGCGCTGGCCAAGCCTGTGTGAGATG  7262      Qy  8283  CTGAAAAATGTCTCCGCTCCTCATCGTGTTGATCATATGCGAACGGCCT  8342
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Db  7200  GTCACGCGCTTTTTCATTGGGGTTGACGGTTGACGCCTGCTGTGTAGCGTTGTGTGAGATG  7259      Db  8280  CTGAAAAATGTCTCCGATCCTCTTCCATAGCCGGATGAGCTTGATCTGTGAGCGGCCA  8339

Qy  7263  GAAATCCAGAACCATACAGCCTATTGTGACAAGTGCGCACTCCGCTTCCGCTTCCCTTGCAGGTT  7322      Qy  8343  GTGTCGGATCCTAGCCGACGCGCTTGGGCGACGCCTTGCGAGCTACGCATCGAG  8402
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Db  7260  GAAATCCAGAACCATACAGCCTATTGTGACCAGGTGCGCACTCCGCTTCCGCTTCCCTTGCAGGTT  7319      Db  8340  GTGTCGGACCCCAAGGCAGCGCTTGGGCGAGCAGTGGGTACGCGTGCGAG  8399

Qy  7323  GGGTGCTTGGTGGTGGAATGAGAAGTGAGGCAGTGTGACAAGTGTGAGGCTAGGCAAGAG  7382      Qy  8403  CCTTCGTATCATGCATCACTGACACGGCCCCCTTCTGCTCCACTTGGCTGCTCCAGTGC  8462
          ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||                       ||||||| |||| |||||| || ||||||||||||||| ||||||||||||||||||||
Db  7320  GGGTGCTTGGTGGTGGAATGAGAAGTGAGGCAGTGTGACAAGTGTGAGGCTAGGCAAGAA  7379      Db  8400  CCCTCATATCATGCATCACTGACACGGCCCCCTTCTGCTCCACTTGGCTGCTCCAGTGC  8459

Qy  7383  ACCTTGGCTTCCTTCTCTTTACATTTGGTCTGGGGTCCACTGACGAGGGCCACTCCGGCC  7442      Qy  8463  AATGCAGATGGGAAACGCCCATTCTTCCTGACCACCGGACTTTCGGAGGCCCCCTCCGCGC  8522
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Db  7380  ACCTTGGCTTCCTTCTCTTACATTTGGTCTCTGGAGTCTGGAGTGCCACTAGGGCCACCGGCC  7439      Db  8460  AATGCAGATGGGAAGCGCCCATTCTTCCTGACCACCGGACTTCCCGGAGGCCCCGCTCCGC  8519

Qy  7443  AAGCCCTGTGGTAGGCCGGTTGGCTCCTTGGCTGGTGGCGCCGACACCACCAAGGTGTAT  7502      Qy  8523  ATGTCCGAGCGACTACAGTGACGTGACCCAATGCCTTCGGCCATCGGTTACATCCTCCTATACCCT  8582
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Db  7440  AAGCCCTCCCGTGGTGAGCTTGGCTGGTTGGCTGGCGCCGACAACTACTAAGGTGTAT  7499      Db  8520  ATGTCGAGTGAGTAGTGACGTGACCCGATGGCTTCGCGGCTTGATCGGATCCTTCTTATCCT  8579

Qy  7503  GTCACCAACCCGGTCACCGGACAATGTGGGGAGAAGAGTTGACAAGGTTACCTTCTGCGGTTCGTGCCCCT  7562      Qy  8583  TGGCATCCTATCACACGGTGGCTCATCCCTCACGTGCTCACCTGCGCGTTTAGGGGT  8642
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Db  7500  GTCACCCCCATCACACGGTCACCGGACAATGTGGGGAGCAGTTGACAAGGTGACCTTCTGGCGTCCT  7559      Db  8580  ATGTCAGTGAGTAGTGACCCCGATGGCTCATCATCCCTGCGCCCTGGCCATTCAGGGGT  8639

Qy  7563  AGGGTTCATGACAAATTCCTCGTGGACTCCATGAGCCGTTGGGACTCATTGGATGTGACTG  7622      Qy  8643  GGTGGCACACCGCTGTCATCCTGTGTGTGGCAGTTACATGGTAATTACTACAAGTTTCCA  8702
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Db  7560  AGGGTTCATGATAAGTTCACCGTGGACTGTGAGGTAACTAACTACTACAAGTTTCCA  7619      Db  8640  GGAGGCACACCGCTCATGTGATCCGGTTTGGTGTGCCAGTTAACTACTACAAGTTTCCA  8699

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Db  8700 CTGGACAAACTGCCTAACATCATCGTGCCCTCCCACGGACCAGCAGCGTTGAGGGTTACC 8759
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Db  8760 GCAGCACAACTAAAACAAAGATGGAGGCTGGCGAAGGTTCTGAGCGACCTCAAGCTCCCT 8819
Qy  8823 GGCCTAGCAGTCCACCGGAAGAAGGCCCGGGCATTGCGAACGCGTATGCTCCGGTCGCGC 8882
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Db  8820 GGCTAGCAGTCCACCGGAAAGAGAGGCCGGGGCGTTGCGAACACGCCATGCTCCCGCGCGC 8879
Qy  8883 GGTTGGGCTGAGTTGGCTAGGGGGCTGTGTGTGGCGTTCCCAGGCGTTCCCCCTCCG 8942
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Db  8880 GGTTGGGCTGAGTTGGCTAGGGGGCTTAGGGCTGCGATCCAGGCCTACGGCTTCCTCCCCCT 8939
Qy  8943 GAGATTGCTGGTATCCCGGGGGTTCCCCTTATATGGGGGTGGTTCAT 9002
         ||||||||||||||||||| || ||||| || |||||||||||||
Db  8940 GAGATTGCTGGTATCCCGGGGGTTCCCTCTCCCCCCCTATATGGGGTGGTACAT 8999
Qy  9003 CAATTGGATTTCACAAGCCAGCAGAGAGTCGCTGCCGGTGGTTGGGGTTCTTAGCCCTGCTC 9062
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Db  9000 CAATTGGATTTCACAAGCCAGCAGAGAGTCGCTGCCGGTGGTTTGGGGTTCTTAGCCCTGCTC 9059
Qy  9063 ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGGCAAGGTCCGGTGACTGATC 9122
         |||||||||||||||||||||||||||||||||||| |||| |||||||||||||||
Db  9060 ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGGCAAGGTCTGGTGACTGATC 9119
Qy  9123 ATCACTGGAGGAGTTCCCGCCCCTCCCCCCAGGGGTCTCCCGCTTGGGTAAAAAGGG 9182
         |||| ||||||||||||||||||||||||||||||||||||||||||||
Db  9120 ATCACCGGAGGAGTTCCCGCCCCTCCCCCCAGGGGTCTCCCGCTTGGGTAAAAAGGG 9179
Qy  9183 CCCGGGCCTTGGGAGGCATGGTGGTTACTAACCCCTGCCAGGGTCAAAGCCTGATGGTGC 9242
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Db  9180 CCCGGGCCTTGGGAGGCATGGTGGTTACTAACCCCTGCCAGGGTCAAAGCCTGATGGTGC 9239
Qy  9243 TAATGCACTGCCACTTCGTGGCGGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC 9302
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Db  9240 TAATGCACTGCCACTTCGTGGCGGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC 9299
Qy  9303 TGCTCGCAGAGCCCTCCCCGATGGGGCACAGTGCACTGATCTGAAGGGGTGCACCCC 9362
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Db  9360 GGGAAGAGCTCGGCCCGAAGGCCCGGGSTTCTACT 9392
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RESULT 3
US-08-464-134-14
; Sequence 14, Application US/08464134
; Patent No. 5849532
; GENERAL INFORMATION:
;   APPLICANT: Kim, Jungsuh P.
;   APPLICANT: Wages, John
;   APPLICANT: Young, LaVonne M.
;   APPLICANT: Fry, Kirk E.
;   APPLICANT: Linnen, Jeffrey M.
;   TITLE OF INVENTION: Hepatitis G Virus and Molecular
;   TITLE OF INVENTION: Cloning Thereof
;   NUMBER OF SEQUENCES: 277
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dehlinger & Associates
;   STREET: 350 Cambridge Ave., Suite 250
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/464,134
;   FILING DATE:
;   CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/389,886
;   FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/357,509
;   FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/329,729
;   FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/344,271
;   FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,558
;   FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,543
;   FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/246,985
;   FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Fabian, Gary R.
;   REGISTRATION NUMBER: 33,875
;   REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
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; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 9392 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: unknown
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   INDIVIDUAL ISOLATE: HGV-PNF 2161 Variant
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 459..9077
US-08-464-134-14

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Query Match             84.9%;  Score 7979;  DB 2;  Length 9392;
Best Local Similarity   90.7%;  Pred. No. 0;
  Matches 8515;  Conservative 1;  Mismatches 876;  Indels 1;  Gaps 1;

Qy    3 ACGTGGGGGGTTGATCCCCCCCCCCCGCACTGGGTGCAAGCCCCATAAACCGACGGCCT   62
        ||||||||| ||||||||||||||||||| |||||||||||||||||  |||||||||||||
Db    1 ACGTGGGGGAGTTGATCCCCCCCCCCCGGCACTGGGTGCAAGCCCCCAGAAACCGACGGCCT   60

Qy   63 ATCTAAGTAGACGCAATGACTCGGCGCCCATCGGCGCCCGGCACTCGGCCGGCGGTCGGATGG  122
        |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   61 ATCTAAGTAGACGCAATGACTCGGCGTAGTCGGCGCCCGGCACTCGGCCGGCGGTCGGATGG  120

Qy  123 GTGGTGACAGGGTTGGTAGTCGTAAATCCCGGTAAATCCCGGTGTAGCCACTATAGGTGGGT  182
        || |||||||||||||||||||| |||||||||  |  |||||||||||||||||||||||||
Db  121 GTGATGACAGGGTTGGTAGTCGTAAATCCCGGTAAATCCCGGTGTAGCCACTATAGGTGGGT  180

Qy  183 CTTAAGAGAAGGTCAAGACTCCTCTTTGTGCCGTGCGCGGGAGACCCGCGCACGGTCACAGT  242
        |||||||||||||||||||||| |||||||||||| |||||||||||||||||||||||||||
Db  181 CTTAAGAGAAGGTTAAGATTCCTCTTTGTGCCGTGCGCGGGGAATAAGGGCCCGAGCAGGTCCACAGT  240

Qy  243 GCTGGCCCTACCGGTGTGGTGAATAAGGGCCCGTCCGGTGGAATAAGGGCCCGT  302
        |||||||||||||||| ||||| |||||||||||||||||||||||||||||||||||
Db  241 GTTGGCCCTACCGGTGGGAATAAGGGCCCGAGCAGGTCCAGGTCCTCGTCGTTAAACCGAGCCCGT  300

Qy  303 CACCCACCTGGCAAACGACGCCCACGTACGGTCCACGTGCCCCTTCAATGTCTCTCTTG  362
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Db  1380 CACGGGCAAAATCAGTGGCCCCTTCATGCCCCAGTAGTGTCTATGGGTCTGCTACAGTC 1439
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Qy  1443 ACGTGCGTGGGGTTCCGTGTCTGGGTTGCCTCGACCGGCGGTCGTGATTCGAAGATC 1502
         || |||||| ||||||||  ||||| ||| ||||||||||  | ||||||| |
Db  1440 ACTTGCGTGCGTGGGGTTCCGTCTTGGTTGCCTCCACCAGTGGTCGCGAAGATCGAAGATA 1499

Qy  1503 GATGTGTGGAGTTTGGTGCCGGTTGGATCTGCACCATAGCCGTCTCAGGGTCA 1562
         ||||||| |||| |||||||| ||||| ||  |||||| ||||||||||  | |||
Db  1500 GATGTGTGGAGTTTAGTGCCAGTTGGCTCTGCACCATAGCCGCACTTGGATCA 1559

Qy  1553 TCGGATCGCGACACGGTTGGTTGAGCTCTCCGAGTGGGGAGTCCCGTGCGTAACGTGTATT 1622
         ||||||||||||||||  |||| | |||||| |||||||||| |||||||||| ||||| ||
Db  1560 TCGGATCGCACACGGTTGCGTGCCTCGGCTCTCCGACTGGGGAATCCGTGCGTGACGTGTGTT 1619

Qy  1623 CTTGACCGTCGGCCTGCTTCATGTGCCACCGTGTGCGACGGGACTGCTGGCCCGAAACCGGG 1682
         ||||||||||||| |||||||||||| |  ||||| ||||| |||||| |||||||  | |||
Db  1620 CTTGGACCGTCGGCCTGCCTGCGGCACCTGTGTGAGGACGGGACTGCTGGCCCGAGACCGGG 1679

Qy  1683 TCGGTTAGATTCCCTTCCATCGGTGCGCGACGGGCTCGGCTGACAAAGGACTTGAA 1742
         |||||| ||||| |||||  ||||||||||||||| |  ||||| |||| ||||||||
Db  1680 TCGGTTAGGTTCCCATTCCATCGGTGCGCGTGGGGCTCGGCTGACAAAGGACTTGAA 1739

Qy  1743 GTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATAAGGGGCCCCTGGGCAACCAG 1802
         |||||||||||| ||||||||||||||||| |||||||||||||||  |||||| |||||
Db  1740 GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGCCCCTGGGCAACCAG 1799

Qy  1803 GGGAGAGGCAACCCGGTCGGTCGCGGCTGGGGTTCACCATGACCAAGATC 1862
         ||  |||||||||||||||||||||  ||||| |||| |||| || |||||||
Db  1800 GGCCGAGGCAACCCGGTCGGTCGCGGCTGGGGTTCTATGAACCCTGGGTGCGCAGG 1859

Qy  1863 CGGGATTCCCTGCATTGTGAAATGTCCACACCAGCCATAGAGCCTCGACTGGAACG 1922
         ||||||||||||| ||  |||||  || |  |||||||||||| ||| |||| |  |||
Db  1860 CGAGATACCCTACATCTGGTGAGTGTCCCACACCAGCCATTGAGCCTCCCACCGGGACG 1919

Qy  1923 TTCGGGTCTTCCCCGAGTCCCGGGTTACTCCTCGGTGGCATGGGGTTCGCAGGAAGTG 1982
         |||||||| |||||| | |||||||||||| |||||  ||||| | |||| ||| |||||||
Db  1920 TTTGGGTTCTTCCCCGGGACGTGGGCTGGCTTTTATACAGTGTCTCAGGGTCGCGATGTG 1979

Qy  1983 TCTGAGGCATTGGGCGGAGCCCAACCTGGGGTTCTACGGAGCCTCTGGTTCGCAGG 2042
         ||||||||||||||||||||||| ||  |  ||||  ||| |||||||||||||||||||
Db  1980 TCCGAGGCACTTGGGGCGGGGGGTTCTATGAACCCTGGTCGGTGCGCAGG 2039

Qy  2043 TGTTCGGAGCTGATGGAGCGCCCAAATCCGGTTTGCCCGGGTACGCATGGCGTGCTCCTCT 2102
         ||||||| |||| |||| |||||| |||||||||| || | || ||| ||||||| ||| ||
Db  2040 TGTTCGAAGCTGATGGAGCGCCGAAATCCGGTTTGTCTCCGGTTTGCATGGTTTCATGGGC 2099

Qy  2103 GGTAGACCTGACGGGTTCATACACGTGCAGGGGTTCATGGATGCGGAGGTGGATGCGGGCAAC 2162
         ||||||| ||| ||||||   |||||||||  | |||||||| |||| |||| ||||||| |||
Db  2100 GGCAGGCCGTGATGGGTTTATACATGTCCAGGGTCCTTGGATTGTGTCCTGCTCATATCGATG 2159

Qy  2163 TTCATCCCTCCTCCACGCGGTTGCTGATTTGTATTGTCCTGCTCATCTGATG 2222
         |||||| |  | ||||||||| ||||||| |||  |||||||||||||||| |||||
Db  2160 TTCATCCCGCCCCCGTCCTGGTTGTCTTGTGGACTTTGTATTGTCCTGTTATACCTGATG 2219

Qy  2223 AAGCTGGCTGAGGCACGGTTGGTCCCGATGGGCCTCAGCCCCTTCATGTTCCTCGTGGTGAAC 2282
         |||||||||||||| |||||||||||||| ||||||| ||||||  ||||| || || ||||||
Db  2220 AAGCTGGCTGAGGCACGGTTGGTCCCGATGGTTGGGACCCCAACGCCTTGGCTCCTATGTGGTGGAAC 2279

Qy  2283 CAGTTGGCGGTTCTAGGACTGCCGGCTTGTGCAGCGCTGCCGGGTGAAGTTTTTGCG 2342
         || | ||| |||| |||| ||  ||||| ||||||||||| |||||||| |||| |||
Db  2280 CACTGGCAGTTGGCTCTAGGGCTGCCGGCTGTGCAGCGCTGCCGGGTGAGGTCTTCCCG 2339

Qy  2343 GGCCCTGCCTTGTCATGGTGTTTGGGCCTTCCCACTGTCAGTATGATACTAGCTCTAGCA 2402
         |||| ||||| | | |||||||| ||| |  |   |||| ||||  | |||| ||| |  |
Db  2340 GGCCCTGCCGTCCGGTGTCCTGGTGGGACTCCCGGTCGTCAGTATGATATTGGGTTTGCA 2399

Qy  2403 AACCTGGTGTTGTACTTTCGGTGATGGGCCCTCAGCCGCCTCATGTTCCTCGTGTGG 2462
         ||||||||||| || |||||||||  |  || ||||| |||||||| |||||||||||
Db  2400 AACCTGGTGCTGCTACTTTAGATGGTTGGGACCCCCAACGCCTCGATGTTCCTCGTGTTGG 2459

Qy  2463 AAGCTTGCTCTGCGGGAGCTTTCCCGCTGGGATTTTGATGGGGATTTCGGCGACCCGCGGG 2522
         |||||||||||| ||||||||| ||||||||| ||||||||| || |||||||||||||||
Db  2460 AAGCTGGCTGTGCTGGGAGCTTTCCCGCTGGGATTTTGATGGGGATTTCGGCGACCCGCGGG 2519
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Db   301 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 360
         TACCCACCTGGGCAAACGACGCCCACGTACGGTCCCACGTCTGGGGCCCGGCTTCAAGTGTCTCTTG

Qy   363 ACCAATAGGTTATCCGCGAGTTGACAAGGACCAGTGGGGCCGGGGGGTTATGGGGAAG 422
         |||||||  || |  || |||||| |||||||||| ||||| | || | |
Db   361 ACCAATAGGGCGTAGCCGGCGAGTTGACAAGGACCAGTGGGGCCGGGGGGGCT-TGGAGAGG 419

Qy   423 GACCCCAAACCTGCCCTTCCCGGTGGGCCGGGAAATGCATGGGGCCACCCAGCTCCGCG 482
         |||| ||  || |||||||  | |||||||| |||| ||||| |||||||||||||||||
Db   420 GACTCCAAGTCCCGCCCCTTCCCGGTGGGCCGGGAAATGCATGGGGCCACCCAGCTCCGCG 479

Qy   483 GCGGCCGTCCAGCCGGGGTAGCCAAGAATCCTTCGGGTGAGGGGCGGGTGGCATTTCTCTT 542
         ||||||||||||| | |||||||||||||| |||||||||| |||||||||||| ||| |||
Db   480 GCGGCCGTCCAGCCGGGGTAGCCAAGAATCCTTCGGGTGAGGGGCGGGTGGCATTTCCTTT 539

Qy   543 TTCTATACCATCATGGCAGTCCTTCTGCCTCCTTCTCGGTGGCCGGGCCATTCTG 602
         |||||||||||| || ||||||||| |||||||| |||||||||| |||||||||||
Db   540 TTCTATACCATCATGGCAGTCCTTCTGCCTCCTTCTCGGTGGCCGGGCCATTCTT 599

Qy   603 GCCCGGCCACCCACGCTTGTCGAGCAATGGCAATATTTCCTCACAAATTGCTGTGCC 662
         ||||||||||||||||||||||||||||| |||||||| |||||||||| ||||||||
Db   600 GCCCGGCCACCCACGCTTGTCGAGCAATGGCAATATTTCCTCACAAATTGTTGTGCC 659

Qy   663 CGGGAAGACATCGGGTTCTGCCTGGAAGGCCGGATGCCCGGTGGTGGCCCTGGGGGTGCACGGTT 722
         ||||  | ||||| |||||||||||  |  |||||| | || |||||||||| |||||| ||||||
Db   660 CCGGAGGACACTCGGGTTCTGCCTGAGGGTGAGGGTGATGGCCTGGTGCCCTGGGGTGCACGATT 719

Qy   723 TGCACCGACGGTTGCTGCCACTGTATCAGGCGGTTTGGCTGTGGCCTGGCAAGTCC 782
         ||||  ||||||| ||||||||||  |||||||| ||||||| | |||||||||||||
Db   720 TGCACTGACCAATGCTGCCACTGTATCAGGCGGTTTGGCTGTGTGGCTGGCAAGTCC 779

Qy   783 GCGGCCCAGCTCGTTGGGGAACTGGGAGCCTGTACGGGCCCTTGTCGGTCTCGGCTTAC 842
         ||||||||||||||||||| ||||||| ||||  || |||||||||||||||||||| |
Db   780 GCGGCCCAACTCGTTGGGGAGCTGGGAGCTGGTAGCCTATACGGGCCCTGTCGGTCTCGGCCTAT 839

Qy   843 GTAGCCGGGATCCTGGGTCTGGGCGAGGTTTACTCCGGGGTTGCTGGTGTTGTGCG 902
         || ||  ||||||| |||| | |  |||| |||| || |||| ||||||||| |||
Db   840 GTGGCTGGGATCCTGGGTGTGGGCTGAGGTGTCCTAACGGTGGGAGTGCGTCGCG 899

Qy   903 TTCAGGGCCCGGGTCTACCTGGTCCAACTGGAAGTGTGCAGTAGAATGTGACGTTAAG 962
         |||| ||||||||| |||||||  ||||||||  ||  |  |  ||||| |  ||| |||
Db   900 TTGACGCGCCGGGGTTACCCGGTGACGTCGAGCAGTGTCGTGTGAGCTAAAG 959

Qy   963 TGGGGAAGTGAGTTTTGGAGATGGACTGAGCCAGTTGGCCTCCAATTACTGGATTTTGGAA 1022
         ||| |||||||||||| ||||| || ||| |||||| ||||| |||| |||| |||||||
Db   960 TGGGAAAGTGAGTTTTGGAGATGGACTGGGACTGGCCTCCAACTACTGGATTCTGGAA 1019

Qy  1023 TACCTTTTGGAAAGTGGCAGTCCCATTTGAATTTGGAGGAGGGTGATGAGCCTGACCCCTGTGTTG 1082
         || ||| |||| ||||| ||||||||| |||||  ||||| | |  |  |||| |||| | |||||
Db  1020 TACGGGTTGACTTGGCAGTGCCATTTGATTTCTGGAGGACGGGCTGATAAGGCCTGACCCCCTGTTG 1079

Qy  1083 GTTTGGGTGGCCGGATCCGCATTGCTTTTGCTGGAGCCAACGGATTGTCATGGGTTTTCCTGCTGGTG 1142
         |||| ||| ||||||  ||||||  || | |||||| | ||| |||| |||||  | ||| |||| ||
Db  1080 GTTTGGGTGGCCGGGCCGCATTGCTTTTGGACGTGTGAGCAACGGATTGTCATGGTTTCCTGCTGGTG 1139

Qy  1143 ACGATGCGGGGAGTGTTGCAGGCGCGCCCCCGTCCTCCGGCCCCTTGAC 1202
         |||||||||| |||| | | |||| || ||| || | | ||||||||  |||
Db  1140 ACGATGCGGGGATGTGTTGCAAGCGCGCCCCCTGCCTCCCCGGGGTCACGCCCCTTGAC 1199

Qy  1203 TACGGGGTTGAAGTGGCAGTCATGGCTCGCAGGGCTATCCCCACTGGG 1262
         ||||||||||||| | || | | |||||| | |||||  | ||||||  |
Db  1200 TACGGGGTTGACTTGGCAGACCTGCTCTTCGCCGTTTTTTCGCGACTGGG 1259

Qy  1263 GAGAGGTGTGGAATGTCAGCGAGGAATGTCACGGCTCTCTGTCCCAACGGCCCCTGG 1322
         |||| ||| |||| | | ||| | ||||||| ||   ||  ||||||||||||||||||
Db  1260 GAGAAGGTGTGGGACGTGGGAACGTTACGCGTTCAGTGTGACGCCCTAACGGCCCCCTGG 1319

Qy  1323 GTTTGGGTTCCCGGCCTTTTGCCAGGGCGGTTGGGTGGGGCGACACCCATCACCCATTGGAGC 1382
         || |||| | | | ||| | | |||| | |||  |  ||| ||| |||| ||| |||| |||
Db  1320 GTGTGGGTTGCCAGCCTTTTGCCAAGCAATCGCTGGGGTGACCCCCATCACTTATTGGAGC 1379

Qy  1383 CACGGGACAAAACCAGTGGCCCCTATCATGCCCCAATATGTCTATGGGTCTCGTGTGTCCGTA 1442
         |||||  ||||  |||| |||||||| |||| |||||| |||||||||||| | ||
Db  1380 CACGGGCAAAATCAGTGGCCCCTTCATGCCCCAGTATGTCTATGGGTCTGCTACGCGGG
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Qy  2523  CGCACCTCTGTCGCTTCGCTTCGATGTCACATTCGAGGTGGACACTTCG  2582
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Db  2520  CGCACCTCAGTGCTCGGGGCCGAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCG  2579

Qy  2583  GTGTTGGGGTGGTGGGTGGCCAGCGTGGCTGGCCATAGCCTCCTGAGCTCAATG  2642
          |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  2580  GTGTTGGGGTGGTGGGTGGGTAGCTTGGGCCATTGCCCTCTGAGCTTCGATG  2639

Qy  2643  AGGCAGGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGTACCAG  2702
          |||||||||| ||||||||||||||||||||||||||||||||||| ||||||||
Db  2640  AGGCGGGCGGGGTGGACCAAAGCCGTGATCTATAGGACGTGGTGTAAGGGGTACCAG  2699

Qy  2703  GCTGTCGCGCCAGAGGTGGTGCGGAGCCCCTCGGGAGGGGCGTCCTACCAAGCTTCTG  2762
          |||| || ||||||||| |||||||||||||||||||||||||||||||||||||||
Db  2700  GCAATCCGTCAAAGGGTGGAGGAGCCCCTCGGGAGGGGCGTGCCAAACCCCTG  2759

Qy  2763  ACGTTCGCCTGCTGGCTCATACATCTGGCCCGATGCTGTGATGATGGTGGTGGTG  2822
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  2760  ACCTTTGCCTGTGTCTGGCTTGGCCCGTACATCTGGCCCAGATGCTGTGATGATGGTGGTT  2819

Qy  2823  GCCTTGGTCTCCTCTTCGGACCTGTTCGCACTGGACTGGGCCCTGGAGGAGCTCCTG  2882
          |||| ||||| |||||||||||||||||||||||||||||| ||||||||||||||
Db  2820  GCCTTGGTCTCCTCTTTCGGACCTGTTCGACGCGGTTGGCCGTGTCGGGGAGGAGATCTTG  2879

Qy  2883  GTCTCCCCGGCCCCGTTACGGGCCAGTGGCACGGTGGTTGAGTGCTTGTGTGATGGCGGGC  2942
          || ||||||||||||||||||||||||||||| |||| ||||||||||||||||
Db  2880  GTGTCCCCGGCCCCGTTCGACGGCGTTGGGCGTTGGGCTGTCGGGTGCTTGTGTGATGGCGGGT  2939

Qy  2943  GAGAAGGCCACCACCATCCGACTGGTCTCCAAGATGTGCGCAAGAGGGGCCTACCTGTTT  3002
          ||||||| || ||||||||||||||||||||||||||||||| ||||||||||||
Db  2940  GAGAAGGCCACAACCGTCGGCTGGTCTCCAAGATGTGCGCAGAGGGAGCGTTATTTGTTC  2999

Qy  3003  GACCACATGGGCTCTTTCTCGCGGCCGTGTTCGAAGGAGCGCTTGGAATGGGACGCGCGCT  3062
          |||||| |||||||||||||||||||| ||| |||||||||||||||||||||| |||
Db  3000  GATCCATATGGGCTCTTTTTTCGCGGCCGTGTTCGAAGGAGCGCCGTGGACCGCAGCT  3059

Qy  3063  TTTGGAGCCCTTGTCATTCACTAGGACGGACTGTCGCATCATCAGAGATGCCGCGAGGACC  3122
          || |||||||| |||| ||||||||||||||||||| |||||||||||||||||||
Db  3060  CTTGAACCTCTGTCATTCACTAGGACGGACTGTCGCATCATCACGGGACTGGGACT  3119

Qy  3123  CTGTCCTGCGCAGCAGTGCGTCATGGGTTACCCGGGTTGCCCTCCCGGGTTGTCCCGGGGAC  3182
          ||||||||||||||||||||| ||||||||||||||||||| |||||||||||||||
Db  3120  TTGTCCCTGCGCAGCAGTGCGTCATGGGTTACCCGGGTTGCCGCCCGTGGTGATGAGGTT  3179

Qy  3183  CTCATCCGGCTGCTTTCAGGATGTGAATCATTGCCCCGGGTTGTCCCGGGACTGCCACCA  3242
          ||||||||||||||| |||||||||||||||||| |||| |||||||||||||||||
Db  3180  CTCATCCGGCTGCTTTTCCAGGATGTGAATCATTGCCCCGGGTTGTTCCGACCGCCGCCT  3239

Qy  3243  GTTGTCATCCGTCGCGGTGCGAAAGGGCCTTCTGGGGTCACGAAGGCAGCTTGACAGGT  3302
          ||||||||| ||||||||||||||||||||||| |||||||||||||||||| |||||
Db  3240  GTTGTCATCCGTCGACGGTGCGAAAGGGCGCGGAAAGGCGCCTTGACAGGT  3299

Qy  3303  AGGGATCCTGACTTACATCCAGGGGACGCTGTTGGGGGACGTCATGGCTACGTCACGAAGC  3362
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db  3300  CGGGATCCTGACTTACATCCAGGAACGGGTCATGGTTGGGGGACGTCGGCTACGTCGCGAAGC  3359

Qy  3363  ATGGGCACATGTCGAATGGGGCCTTCACAACTTCATCCCGGGTTCATCCGAACC  3422
          ||||| || |||||||||||||||||||||||||| |||| |||||||||||||
Db  3360  ATGGGAAACATGTCGAACGGGGCCTTCACAACTTCACGCGTTTCATCCCGAACC  3419

Qy  3423  ATCGACCACGCCCGTGGGGCCCTAATCCAGGTGGTGGTCAGCCAGTGATGACGTCACG  3482
          ||||||||||||||||||||||| |||||||| |||||||||||||||||||||||
Db  3420  ATCGACCACGCCCGTGGGGCCCTTAATCCAGGTGGTGGTCAGCCAGTGATGTGTCACG  3479

Qy  3483  GTGTACCCGGCTTTCCACTCCCGATGGGGCTACTTCGTTAACACCTTGTACTTGGCCAGGT  3542
          ||||||||| ||| ||||||||| ||| || |||| |||||||||||||||||||||
Db  3480  GTGTATCCACTTCCCGATGGGGCTACTTCGTTAACACCTTGTACTTGGCCAGGTG  3539

Qy  3543  TGTTGGGTTATTAGATCCGACGGGCTTTGTGCCATGGCTTGAGCAAGGGGACAAGGTT  3602
          ||| ||||||||||||||||||||||| || ||||||||||||||||||||||||||
Db  3540  TGTTGGGTCATCAGATCCGACGGGCCCATGGCTTGAGCAAGGGGACAAGGTG  3599
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Qy  3603  GAGCTGGATGTGGCCATGGAGGTCTCTGACTTCCGTGGTCGTCTGGTTCACCGGTCCTT  3662
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Db  3600  GAGCTGGATGTGGCCATGGAGGTCTCTGACTTCCGTCGTCTGGTGGCTCGTCACCGGTCCTA  3659

Qy  3663  TCCGACAAAGGCACGCAGTAAGAATGCTCGTCGTCAGTGCTCCACTCTGGCGCGCCAGGGTT  3722
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3660  TGTGACGAAGGGCACGCAGTAGGAATGCTCGTCGTCTGCTTCGCTCTGGGCGTGGTAGGGTC  3719

Qy  3723  ACTGCGGCCGGATTCACTGACCTGGACTCAGGTCAAGTACCAACAGATGCCAAGAGACTACCACA  3782
          ||  ||||||| ||||||||||||||||||| ||||| ||| ||||| ||| ||||
Db  3720  ACCGCGGCACGGTTCACTGACCGTGACCCAGGTGTTCAACAGTGCCAACAGATGCCAAACCACTACT  3779

Qy  3783  GAACCCCTCCGGTGCCCGCCGGCAAAAGGAGTTTCAAGGAGTTTCAAAGAGGCCACG  3842
          ||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||
Db  3780  GAACCCCTCCGGTGCCCGCCGGCAAAAGGAGTTTCAAAGAGGCCACG  3839

Qy  3843  GGGGCGGGAAAGAGCACCCGCGTTGGACTACGGCACGCCAACATGGGCACAAGGTCTTG  3902
          || |||| ||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  3840  GGAGCGGGAAAGAGCACTCGCGTCCGTTGGAGTACGGCACGCCAACATGGGCACAAGGTCTTA  3899

Qy  3903  ATCTTGAACCCGTCGGTAGCTACCGTGAGGGGCCCATACATGGCCGGCCGGCTGCGCG  3962
          ||  |||||||| ||||||| |||||||||| ||||||||||| ||||||||||||
Db  3900  ATCTTGAACCCCTCAGTGCCACTGTGCGGGGCCCATACATGGCCGGCCGGCTGCGCG  3959

Qy  3963  GGGAAACACCCCAGTATTTTACTGTGGGCCATGACAGCCCACCACTGCTTTCACAAGGATCACTGAC  4022
          || ||||| ||||||||| |||||||||| |||||||||| ||||||||||||||||||||||
Db  3960  GGTAAAACATCCAAGTATATACTGTGGGCCATGATGTGGGCATGATTCAGGTTTCACAAGGATCACTGAC  4019

Qy  4023  TCGCCCCTTACGTATTCCACTTACGGAGAGTTTTTGGCCAACCCTAGGCAGATGCTGAGG  4082
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  4020  TCCCCCCTGACGTATTCAACCTATGGGGAGGTTTTTGGCCAACCCTAGGCAGATCTACGG  4079

Qy  4083  GGTGTGTCGGTGTCATTGTGACAGTGCCACAGTCAACTGTGTTGTTGGGC  4142
          ||||||| |||||| |||||||||| ||||| |||||||| |||||||||
Db  4080  GGCGTTTCGGTGTCATTTGTGATGAGTGCCACAGTCAATGACTGTGTTAGC  4139

Qy  4143  ATTGGGCGTGTCAGGGAGCTGGCCGCGAGGATGTGAGTGCAATTGGTGTCTCTACGCCACT  4202
          |||||||||| |||||||| |||||||||||||||||||||||||| ||||||||||||||
Db  4140  ATTGGGAGAGTCCCGGGAGCTGGCCGCGAGGGTGCAACTAGTGCTCTACGCCACC  4199

Qy  4203  GCCACCCCTCCCGGATCCCCAGCACCCAGACCCTGCCGGTAATCATTGAGACAAAACTGAC  4262
          || |||| |||||||| ||  |||| || ||||| |||||||||| |||||||||||||
Db  4200  GCTACACCTCCCGGATCCCCCATGACCAGCAGCACCACCCTTCCATAATTGAGACAAAATTGGAC  4259

Qy  4263  GTTGGGAGAATCCCCTTCTATGGGCAT  ||||| ||||||||||||||||||||GACCGGAGG  4322
          ||||| ||||| |||| ||||||| ||
Db  4260  GTTGGGCGAGATTCCCTTTTTATGGGCAT CGAGGCGGATCGGAACGGGATCGGAACCGGAGG  4319

Qy  4323  CATCTCGTATTCTGCCACTCCAAGGCTGAGTCGCGCCTGCGCGGCCAGTTTTCGGCT  4382
          ||| ||| |||| |||||||||| ||||||||||||||||||||| ||||||||||
Db  4320  CACCTCGTGTTCTGCCATTCTAAGGCTCTAAGGCTGCCTGGCCCAGTTCTCCGCT  4379

Qy  4383  AGGGGGTAAATGCCATGCGCCTATTACAGGACAGTTCTATCATCAAAGATGA  4442
          |||||||  || |||||| |||||||||||| ||||||||||||||||||||
Db  4380  AGGGGGGTCAATGCAGTCATTGCCTATTATAGGGGTAAAGACAGTTCTATCATCAAGGATGGG  4439

Qy  4443  GACCTGGTGGTGTGTGCTACAGACGCACTATCCACTGGGTACACTGGAACTTCGATTCT  4502
          |||||||||||| ||||||||||| |||||||||||||||||||||||||||||||||
Db  4440  GACCTGGTGGTGTGTGCTACAGACGCGCTTTCCACTGGGTACACTGGAAATTTCGACTCC  4499

Qy  4503  GTCACCGATTGTGGGTTAGTGGTCGGGGGTCTCGAGGTGGAGGCCCTTGATCCCACCATT  4562
          |||||||||| |||||||||||||  ||||||||||||| |||||||||||||||||||
Db  4500  GTCACCGACTGTGGATTAGTGGTCGGGGTCTCGATGGTCGGGGCCCTTGATCCCACCATT  4559

Qy  4563  ACCAATCTCCCTGCGCCACCGTGGGCGTGAACTGTGCAGCGGCTGGAGGACGCGC  4622
          ||||||||||||||||||||||| | ||||||| |||||||||| |||||||||
Db  4560  ACCATCTCCCTGCGACCACCGTGTCGCGGCGTGAACTGTGCGATGCTCGAAAGAGGAGGACGCC  4619

Qy  4623  ACGGGTAGGGGCCAGGTCTCGGGGCCTACTACGGCCGGGTCGGCCAAGGCCCCCTGCTCGT  4682
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  4620  ACGGGTAGGGGCCAGGTCTCGGACGCCTACTACTACGGCCCGGGGTGGGCAAAGCCCCTGCGGGT  4679

Qy  4683  GTGGTGCGCTCAGGTCCTGTCTCGGCCGGCGTGAAGCCGGTGTGACCTGGTACGGAATG  4742
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Left column:

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Db 4680 ||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||| 4739
        GTGGTGCGCTCAGGTCCGTCTGCTGGCGGTGAAGCTGGAGTGACCTGGTACACCGGAATG

Qy 4743 GAACCTGACCTGACAGCAAACTACTGAGACTTTACGACAACTGCCCTTACACCGCAGCC   4802
        |||||||||| |||||| |||||||||||||||||||||||| |||||||||||||||||
Db 4740 GAACCTGACTTGACAGCTAGACTGAGACTTTACGACGACTGCCCTTACACCGCAGCC     4799

Qy 4803 GTCCGCAGCTTGACATTGGGAAGCCGCGGTTGTTCTTTCGGGCTTGCCCCGTTGAGGATG 4862
        |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db 4800 GTCCGCGGCTGTATCGGAGAGAGCCGCGGTTGTTCTCTCGGGCTCGCCCCATTGAGGATG 4859

Qy 4863 CATCCCGATGTTAGCTGGGCAAAAGTTCCGGCCTCAACTGGTCCCTTCCTTGGTGGTGTT 4922
        || || |||||||||||||||||||||||||||||||||||| | ||||||||||||||||
Db 4860 CACCCTGATGTCAGCTGGGCAAAAGTTCCGGCCTCAACTGGGCCCCTTCCTTGGTGGTGTT 4919

Qy 4923 CAGCCGACCATGTGCCGGGAAACTGTCTCCCCAGTGACCCCAGTGGGCA           4982
        |||||||||||| ||||||||| ||||| ||||||||||||||| ||||||
Db 4920 CAGCCGACCATGTGCCGGGAAACACTGTCTCCCCAGTGACCCCATGGGCA         4979

Qy 4983 GGTCTGAAGGGCCCGAATCCTGTCCCACTTCCTGCTGAGGTGGGCAATGATTTACCATCT 5042
        ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db 4980 GGTCTGAAGGGCCCAAATCCTGTCCCACTTCCTGCTGAGGTGGGCAATGATTTACCATCT 5039

Qy 5043 AAAGTGCCGGCCATCACATCGTGGACGACCTGGTCCGTGGGGTCGGGGTGGCCGAGGGT   5102
        |||||||||||||||||||||| |||||||||| ||||||||||||| ||||||||||||
Db 5040 AAAGTGCCGGCCACCACAGTGGACGACCTGGTCCGGAGACTCGGTTGCGGGGTGGCGAGGGT 5099

Qy 5103 TACGTCCGCTGCGATCGGCGGACCCATCTTGATGTGGGGCCTCGCTATTGCGGGGGCATG 5162
        |||||||||||||||||||||||||||||| ||||| ||||| || ||||||||||| |||
Db 5100 TACGTCCGCTGCGATCTTGATGATCGGCGATCTTGATGATCGGCGAATG           5159

Qy 5163 ATCTATGCGTCATCACACCGGTCTCTCGTGGTGGTTACAGACTGGGATGGAAGGGGGT   5222
        |||||||||||||||||||||||||| |||||||| ||||||| |||||||||||||||
Db 5160 ATCTACGCGTCATCACACCGGTCTCTCGTAGTGTGTGCAGACTGGGATGGAAGGGGGT   5219

Qy 5223 GGCAGCCCCCTTTATCGGCCCAGGCCACGCCCCAGCCGTTGTCGCAGTCCCC         5282
        || |||||||||| |||||||||||||||||||||||| || |||||||||||||
Db 5220 GGCGCCCCCCTTTATCGGCTCAGGCCACGCCCCAGCCGTTGTCGCAGTTCCT       5279

Qy 5283 CCGGTAGACCATCGGCCGGCGGGGGAGAGTCTGCCGATGCCAAACAGTGACAGAT       5342
        ||| ||||||||||||||||||||| || | |||||||||||||||||||||||||
Db 5280 CCGGTAGACCATCGGCCGGCGGGGGTGAATCAGCACACCGATGCCAAGCAGTGACAGAT 5339

Qy 5343 GCGGTGGCGGCCATCCAGTTGGATTGCGATTGGTTCAGTGTAATAGCTCGGGATGACCCT 5402
        |||||||||||||||||||||||| ||||| ||||||||||||||||| |||||||||||
Db 5340 GCGGTGGCGGCCAGCAGTCCAGGTGTCGACTGGCTATCATGACTCTGTCTCGATCGGGAGA 5399

Qy 5403 GTCCGTGCTTCCTTGGGCCCAGCTGTCTTAGGAGCGGCCTAAGACGGGCCGAGGCTA     5462
        || | ||||||||||||||||||| |||| |||||||||||||| ||||||||||||||
Db 5400 GTCGTGCTTCCTTGGGCTCAGGCTCGTCAGCTCAGGAGCGGCCTAAGACAACCGCCAAGTGGCTC 5459

Qy 5463 GCTGGCTGCTGCTACAGGGGCACGCGGCACCCGCAAAGCCTTCCGCTCTCCACTAGGGGC 5522
        |||||||||||||||||||||||||||| | |||||||| ||||||||||||| |||||||
Db 5460 GCTACGGGGTGGAGGCAACGTCAGACGCGCGGCGCCGCCTCCCACTTCCCACTTCCTTC 5519

Qy 5523 GCGGTGGCCAGCCATCCAGTGGTGGGCGCCATTGGTAATAGCTGCCACAGTGTAATAGCT 5582
        |||||||||||||||||||||||||||| ||||||||||||||||||||||||| ||||||
Db 5520 GCGGTGGCCAGCCATCCAGTGGTGGGCGCCATTGGTAGTGTAATGGCCACAGTGTAATAGCT 5579

Qy 5583 GCCTATGGGCTTCTTAGGAGCCCTTCCATGGGGTTG                         5642
        |||||||||||||||||||||||||| | |||||||||
Db 5580 GCCTACGGGGTCCTTCAAGGAGCCCTTCACCGATGGGGTTG                   5639

Qy 5643 GGCGTCGGAGGCAACGGCCGCAAAACCCGGCCTTCCGCTCTCCGCTCTCCTGGG       5702
        |||||||||||||| ||||||||||||| | |||||||||||||||||||||||||
Db 5640 GGCGTCGGGGAGGCAACGTCGAGCCGGCCGCCTTCCGCTCTCCTATTGGGGGGCTGCTGGA 5699

Qy 5703 ACGGTCTGCTGTGGGCACGCCGGCCTCTGCTGTGGGCGTTAACCATGGGAAGTGCT     5762
        |||| ||||||||||||||||||| | |||||||||||||||||||||||||||||||
Db 5700 ACGGTCTGCTATAGGGCAACGTCGCTCCTGCTGTGGCCTTCATGGCAGTGCTGCTTC   5759

Qy 5763 AGCGTCTCCCCTCCTTGGTCACCATTTTACTGGGGGCCGTTGGGGGGGTGGAGGGGCGTG 5822
        || ||||||||||||||||||||||||||||||||||||| ||  ||||||||||||||||
Db 5760 AGTGTCTCCCCTCCTTGGTCACCATTTATTGGGGCCGTCGCGGAGGTTGGGAGGGTGTT  5819
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Right column:

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Db 5760 AGTGTCTCCCCTCCTTGGTCACCATTTATTGGGGCCGTCGCGGAGGTTGGGAGGGTGTT  5819
        (continued)

Qy 5823 GTGAATGCGCTAGCCTGTTCTCGAGGTGAAGCTGGGGAAAACATCATCAGAAGATCTG   5882
        || || ||||||||||||||| |||||||||||||||||||||| ||||||||||||||
Db 5820 GTCAACGCGGCGAGCCTAGTTCTTTGACTTCATGGCGGGGAAAACTTTCATCAGAAGATCTG 5879

Qy 5883 TGGTATGCCATCCACGTGCTAACCAGTCCGGGGACTCCGGGGATCGCGGGGATCGCCCGGG 5942
        ||||||||||||||||| ||||| |||||||||| || ||||||||||||||||| ||||||
Db 5880 TGGTATGCCATCCACCGTGCTGACCAGTACCGGGCCTCGGGGGATCGCTCGGGGATCGTCAAC 5939

Qy 5943 TTGGTTGTTGTTACTCAGCTAACAACTCTGGCACTAACAACTGGCACTAACAACTGGGAGC 6002
        |||||| | |||||| |||||||||||||| |||||||||||||||||||||||||||||||
Db 5940 TTGGTTTGTTTATTCAGCTAACAACTCTGGCACTAACAACTGGTGTCTGCTGTGCTGAC  5999

Qy 6003 ACATTGCCAAGGTCCTCATCGCCATCCCTGACGATTACTTTCGACACCGTGGTCCTGTCAAC 6062
        || || |||||||||||||||||||||||||| ||||||| ||||||| ||||||||||||||
Db 6000 ACGTTACCAAGGTCTTCATGTATCCCGACAGTTACTTTCAGCAAGTTGACAGTTGCCGAC  6059

Qy 6063 AAGGTCTCAGCTGCTGTCCTCGACGCTTGAGCCTCACTCGCCTGGTTGCCCTCGGGTCAAC 6122
        ||||||||||||||||| |||||| ||||| | |||||||||||||||||||||||||||||
Db 6060 AAGGTCTCAGCCGTCGCCGTCTCCGGGGTGAGCCTCAGCTGGTTGCCCTCGGGTCAAC   6119

Qy 6123 AGGGAGCCTAAGGTGGATGAGGTTCAGGTGGGTACGTCTGGGACTTGTGTGGGAGTGGATC 6182
        |||||||||||||||||||||||||| |||||| |||||||||||||||||||||||||||
Db 6120 AGGGAGCCTAAGGTGGATGAGGTGGGTATGCTCGGGACCTGTGGGGAGTGGATC       6179

Qy 6183 ATGGCTCAAGTGCGCATGGTGCTGATGTGCCAGACTTCGGGCCCTTCTGCCCGTTGGTGTCATTA 6242
        |||||||||||||||| |||||| ||| ||||||||||||||| ||||| ||||||| ||||||
Db 6180 ATGGCCCAAGTGCGCGTGGTGGTCATGTGGCCAGACTCAGGGCCGTCCGTGGTGTGTCACTA 6239

Qy 6243 CCCTTATGGCACTGCGGGAGGGGTTGTCCGGAGGGTTGTTCCGGGAATGGTTGCTTGAGGATGTTGAG 6302
        ||| || |||||||||||||||||| |||||||||||| | |||||||||||||||| ||||||||||
Db 6240 CCCTTGTGGCCATTGCGGGGAGGGGGTGGTGTCCGGGGAATGGTGGTTGCTTGACGGTCATGTTGAG 6299

Qy 6303 AGTCGTTGTCTTTGTTGGCTGTCGTGTGATCACCGGTGATGTTTGTTGAATGGCAACTCAAAGAT 6362
        |||||||||||||| |||| |||||||| ||||||||| |||||| |||||||||||||||||||
Db 6300 AGTCGCTGCCTCTGGCTGGCTGCTGGCTGATCACTGGTGACGTTCTGAATGGCAACTCAAAGAA 6359

Qy 6363 CCAGTTACTTCTACCAAGCTGTGCGAGCGTGTGCAGGCATTATTGGATGGGACAGTCCCTGTGAACATG 6422
        ||||||||||||||||||||| ||||| |||||| |||||||| ||| |||||||||||| |||||||
Db 6360 CCAGTTACTTCTACCAAGCTGTGCGGCTGGCCACTGTGTCCCCGGGCACTGTCTCCCGTGTGAACATG 6419

Qy 6423 CTGGACCTATGGCGAGACGTCGCCTTTGCTCGCCTCCTGCCCCTCAGACACCCGAAGTGGTACCATTC 6482
        ||||| |||||||||| |||| |||||||||| ||||| |||||||||||| || ||| ||||| |||
Db 6420 CTGGGTTACGGTGAAAACGTCGCCCTCTCCTGCCCCCGAGAGTTGTGCCTTC                 6479

Qy 6483 GGGACCTCTGGTGGCTGGCTCGAGGTGGTTGGACCCGTGTGTCGATCAGGCCGCAACA         6542
        ||||||||||||||||||||||||||||||| ||||||| || |||||||||| |||||||
Db 6480 GGGACCTCTGGCGGCTGGGCTGGAGGTGGTGGACCACTACCACCACGCGGGTAATCAGGAGACC 6539

Qy 6543 TCCGGCTACAAATCTGCGCCGCCGCCAAAATCCTGTCGCCTGTTGTTGCTTATTAC         6602
        ||||||| |||||| || |||||||| ||||| ||| ||||| | ||||||||| ||||
Db 6540 TCCGGCTATAAGCTGTGCGCGCCGCCGCCAAATCCTATCCGGCTGCTGTAGCTGTACTAC   6599

Qy 6603 GTCGACGGCGATACCGGTCTCATGGGACGCGCGAGCGCTGCCGAGCGCCGGCTGCCATGGC 6662
        |||||||||| ||||||||| |||||||||| ||||| || |||||||||||||||||||||
Db 6600 GTCGACGGCATTCCGGTCTCATGGGAAACGTCGTCGCCGGCCCATCGCCCATGTCTATGGCC 6659

Qy 6663 CCTGGGCAAAGTGTCACCATTGACGGGACGGAACGTCGCCCTTCGGCATCAACTGCGGCTT 6722
        |||||||||||| |||||| ||||||||||||||| || ||||||| |||| ||||||||||
Db 6660 CCTGGGCAAAGTGTTACCATTGACGGGAGGGCGCTAGCGTCGCCATCAACTGCCATCAACTGAGGCTC 6719

Qy 6723 AGGAATGTGCGCCCTCTGAGGTGTCATCCGAGGTGTCCAGAGTGTCCATTGACATTGGACGGGAGACT 6782
        ||||||||||| ||||||| ||||| |||||||| ||| |||||||||||||||||| ||||||||||
Db 6720 AGGAATGTGGCCACCCTCGAGGTGTTCATCCGAGGTGTCCAGAGTGTCCATTGACATTGGACGGGAGACT 6779

Qy 6783 GTGACGGCAGAACTCAGACTCGACTAGGCCGATCTGCCGCCGCCGGCCCTTCAGCTATC     6842
        ||||| |||||||||||||||||||| | ||||| |||||||||||||||| ||||||||
Db 6780 GTCGACGGCATTCCGGTCTCATGGGAAACGTCGTCGCCGGCCCATCGTCTCCAAGCGATC   6839

Qy 6843 GAAGACTCAGAATTCTTGAACCTTGAAGTCATCATGAGTCATCACAGTGCCACAGTACA   6902
        ||||||||||||||| |||||||| ||||||||||||||||||||||||||| |||||||
Db 6840 GAGAATGCTGCGAGGATTCTTGAACCGACCACATTGATGTCATGATGTCATCATGGAGGACGTCAGTACA 6899
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Qy  6903 CCCTCTCTTGTGTGGGAGTAGCCAGAGAGATGCCTGTGTGGGGAGAAAGACATACCCCGCACT 6962
         |||||||| |||||||| ||||||||  ||||||||  || ||  ||| |||||||||| |||
Db  6900 CCCTCTCTTTGTGTGGTAGTAGCCGAGAGAGATGCCCGAGAGAGATGGGGAGAAAGACATCCCCCGTACT 6959

Qy  6963 CCATCGCCAGCACTTATCTCGGTTACTGAGAGCCCAGATGAGAGACCCCGTCGGTG 7022
         ||||||| ||||||||||| ||| |||||||||||| ||||||||  ||||| |||
Db  6960 CCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCTCAGATGAGAGACCCCGTCGGTG 7019

Qy  7023 TCTTCCTCGCAGGAGGATACCCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCGAG 7082
         | |||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db  7020 TCCTCCTCGCAGGAGGATACCCCGTCCTGCTGACTCATTCGAGGTCATCCAAGAGTCCGAG 7079

Qy  7083 ACAGAGAGCGATGCCAAGAGGAAAGCGTCTTCAACGTGCTCTTTCCGTACTAAAGCCTTGTTT 7142
         |||||| ||  |||||| ||  |||||||||||||||||||| || ||||  |||||||| ||
Db  7080 ACAGCGCAGCGACCGCGACCAGGAGAAAGTGTCTTCAACGTGCTCTTTCCGTATTAAAGCCTTATTT 7139

Qy  7143 CCACAGAGCGATGGCCACAAGAAAGCTTACCGTTAAGAGTCATCGTGTGTTGAGAAGAGC 7202
         |||||||| |||| || |||||||||||||||||| ||||  |||| ||||||||||||
Db  7140 CCACAGAGCGACGCGACCAGGAGAAGCTTACCGTTAAGATGTCGTTGCTGCGGTTGAAAAAGC 7199

Qy  7203 GTAACACGCTTCTTTTCATTGGATTGACGGTCCCTGACGTGCCAAGCCTGTGTGAGATG 7262
         ||   |||||||  ||||||||||||| || |||||||| |||||||||||||||||||
Db  7200 GTCACGCGCCTTTTTTCTCATTGGGTTGACGGTGGCTAGCCGTGTGTTGCTAGCGTGTGAGATG 7259

Qy  7263 GAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCCGCACTCGCCGCTTGAATTGCAGGTT 7322
         |||||||||||||||||  |||||| |||||| ||||||||||||||||||||||||||||||
Db  7260 GAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCCGCACTCGCCGCTTGAATTGCAGGTT 7319

Qy  7323 GGGTGGCTTGGTGGGCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAGAG 7382
         ||| ||||||||||| |||||||||||| ||||||||||||||||| || |||||||||||
Db  7320 GGGTGGCTTGGTGGGCAATGAACTTACCTTTGTTGAATGTGAGGGCTAGGCAAGAA 7379

Qy  7383 ACCTTGGCTTCCTTCTCTTACATTGGTCTGGGGTGCCACTGACGAGGGCCACTCCGGCC 7442
         |||||||| || || |||| || ||||||||||||||||||||||| || || |||||
Db  7380 ACCTTGGCTTCCTTCTCTTACATTTGGTCTGGAGTGCCGCTGACGTGCCACTCCGGCC 7439

Qy  7443 AAGCCCCTGTGTGGGAGGCCGGTTGGCTCCTTTGCTGGTGGCCGACACCACCAAGGTGTAT 7502
         |||||||||||||||||||| ||||| ||| ||||| |||||| ||| |||||||||||||
Db  7440 AAGCCCCTGTGTGGGAGGCCTGGTGGCTCTTTGTTGGTGGCCGACACTACTAAGGTGTAT 7499

Qy  7503 GTCACCAACCCGGACAATGTTCGGTGAGAGAGTTGACAAGGTTACCTTCTGGCGGTGCCCCT 7562
         ||| || || |||||| ||||||| ||||||||||||||||| ||||| |||||| |||||
Db  7500 GTTACCAATCCAGACAATGTGGGGACGAGGTGACAAGGTGACCTTCTGGCGGTGCTCCT 7559

Qy  7563 AGGGTTCATGACAAATTCCTCGTGGACTCCATAGAGCGCGCAGCTCAAGGC 7622
         |||||||| ||  |||||||| ||||||||| ||||||||||||| ||||||
Db  7560 AGGGTTCATGATGAATGTACTCCGTGGACTCCTATTGAGCGGCGTCAAGGC 7619

Qy  7623 TGCCTAAGCATGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCC 7682
         |||||||||||||||||||||||||||||||||||| |||| ||||| |||||||||
Db  7620 TGCCTAAGCATGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCC 7679

Qy  7683 ATGGGCTGGGGATCTAAGGTGTCGGTCAAGACTCCGCCCACCCGGGGAGATGGCT 7742
         |||||||||||||| |||||||||| ||| ||||||||||||| |||||||||||
Db  7680 ATGGGCTGGGGATCTAAGGTGTCGGTTAAGGACTTAGCCACCCGGGGAGATGGCC 7739

Qy  7743 GTCCATGACGGCTCCAGGAGATACTTCGGAAGGACGCCAGTCCCTTTACTCTTACTGTG 7802
         || |||||||| |||||||||||||||  ||||||| |||| |||||||||||||||||
Db  7740 GTTACCATGACCGCGGCTCCAGGAGATACTTCGGAAGGACTCTTGGGACCCCGGTCCCCTTACTCTTACTGTG 7799

Qy  7803 AAAAGGAAGTGTTCTTCAAAGACCGAAAGGAAGGAAGAGGCCCCCCCGCCCTCATTGTGTTC 7862
         |||||||| || ||||||||||||||||||||||||||||  |||||||||||||||||||
Db  7800 AAAAGGAAGTGTTCTTCAAAGACCGAAAGGAAGGAAGAGGCCCCCCCGCCCTCATTGTGTTC 7859

Qy  7863 CCCCCCCTGGACTTCCGGATAAGCTGAAAAGCTTATTCTGGACCCTGGACGCGGGTAGCC 7922
         ||||||| |||| |||||||| |||||| |||| |||| |||||| || ||||||||
Db  7860 CCCCCCCTTGGACTTCCGGATAAGCTGAAAAGCTCATCTTGGGACGCGGGGTAGCC 7919

Qy  7923 AAGCGGGTGTTGGGGGGCCTACGCGGGTAGCCCCAAATCAGCGAATTAGGGAG 7982
         |||||||||||||||| |||||||||||||| ||||||||||||||||||||
Db  7920 AAGCGGGTGTTGGGGGGCCTACGCGGGTAGCCCCAAATCAGCGAGTTAAGGAG 7979
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Qy  7983 ATGCTCAAACTGTGGGAATCAAAGAGACACCATGCGCCATCTGTCTGGGACGCCACATGC 8042
         ||||||| || |||||| || |||||||| |||||||||||||||||||||||||||||
Db  7980 ATGCTCAAGCTATGGGAGTCTAAGAGAGACCCCTTGCGCCATCTGTGTGGGACGCCACCTGC 8039

Qy  8043 TTCGACAGTAGCATAACTGAAGAGACGTGCGCGTGGAGACAGAGCTTTATGCCCTGGCT 8102
         |||||||||||||||||| ||||| | |||| || ||||||||| ||||| || |||||
Db  8040 TTCGACAGTAGCATAACTGAAGAGACGTGCGCGTGGAGACAGAGCTATACGCTCTCGGCC 8099

Qy  8103 TCAGACCATCCAGATGGGTGCGTGCCCTGGGAAATACTATGCCTCTGCGCACAATGGTA 8162
         | || ||||||||||||  | |  | ||||||  ||| || || || || |||||||
Db  8100 TCTGACCATCCAGATGGGTGCGGCACTTGGGAAATACTATGCCTCAGGCACCACCATGGTC 8159

Qy  8163 ACCCCGAGGGGTGCCAGTGGGTGAGAGGTATTGTAGATCGGAGTCCTCAGGGG 8222
         |||||||| | ||||||||||||||||| |||| |||| || || |  ||
Db  8160 ACCCCGAGGGGTGCCCCGTCGGTGAGAGGTATTGCAGATCCTCCGGTGTCTAACAACT 8219

Qy  8223 AGTGCGAGCAACTGCTTGACTGCTTATATCAAGGTGAAAGCCGCCTGTGAGAGGGTGGGG 8282
         || ||| |||||||| |||||| | ||||||| |||||||| | ||||||||| |||||
Db  8220 AGCGCGGAGCAACTGCTTGACCTGCTACATCAAGGTGAAAGCCGCCTGTGAGAGAGTGGGGG 8279

Qy  8283 CTGAAAAATGTCTCGCCTCCATCGCTCGGCGATGACTGTTGATCATATGCGAACGGCCT 8342
         ||||||||||| | |||| ||| |||| ||||||||||||||| |||||||| |||||
Db  8280 CTGAAAAATGTCTCTTCTTCTCATAGCCGGCCATGACTGCTTGATCATATGGAGCGGCCA 8339

Qy  8343 GTGTGCGATCCTAGCGACGCGTTTGGGCAGAGCCCTGGGCGAGCTACGGCATGCGAG 8402
         |||||||||| |||||||||||||||||| |||||||||||| | ||||||||||||
Db  8340 GTGTGCGACCCCAAGCGACGCGTTTGGGCAGAGCCCTAGGCAGAGCTATGGGTACGCGTGCCGAG 8399

Qy  8403 CCTTCGTATCATGGATCACTGGACACGGCCCCCCTTCTGCGTCCACTTGGCTAGCTGAGTGC 8462
         ||| |||| ||||| || |||||||  ||||||| || |||| ||||| ||||||||||||
Db  8400 CCCTATATCATGGATCATCATGGACACGGCCCCCTTCTGCGTCCTCCACTTCGGCTGCTGAGTGC 8459

Qy  8463 AATGCAGATGGAAACGCCATTTCTTTCCTGACCACCAGACTTCGGAGGCCCCTCGCTCGC 8522
         |||||||||||||||| |||| |||||| ||||||||||||||||||||| || |||||
Db  8460 AATGCAGATGGGAGAACGCCCATTTTCATCCTGACCACCAGACTTCGGAGGCCCTCGCTCGC 8519

Qy  8523 ATGTCGAGCGAGTACAGTGACCAATGGCTTCGGCGACCATCGGTTACATCCTCTATACCCT 8582
         ||||| || ||||| ||| ||||| || | ||||||| |||||||  |||  ||| ||| |
Db  8520 ATGTCGAGTGAGTACAGTACGTGACCCGATGGCTTCGGCGATCGGTTACATCCTCTTTATCCT 8579

Qy  8583 TGGCATCCTATCACACGGTGGGTCATCATCCCTACGTGCTCACCTGCGCGTTTAGGGGT 8642
         |||||||| |||||| |||| || |||||| || |||||||||||| || ||||||||
Db  8580 TGGCACCCCATCACACGGTGGTCATCATCCCTCATGTGCTCAACGTGCATCAGGGGT 8639

Qy  8643 GGTGCCACACCGTCTGATCCTGTGGTGCCAGTGGCTACATGGTAATTACTACAAGTTCCA 8702
         || |||||||| |||||| | || ||| ||||||| ||| ||||| |||||||||||||
Db  8640 GGAGGCCACACCGTCTGATCCGTGGTGCCAGTGGTCATGGTAACTACTACAAGTTCCA 8699

Qy  8703 CTGGACAAACTGCCTAACATCGTGGCCCTCAACATCGTGAGGCCGTTGAGGGTTACC 8762
         |||||||||||||||||||| |||| ||||||||| |||||||||||||||||||||
Db  8700 CTGGACAAACTGCCTAACATCGTGGCCCTCAACATCGTGAGGCCGTTGAGGGTTACC 8759

Qy  8763 GCAGACACAACTAAGACAAAAATGCAGAAGAAGTGCTGAGGCGACTTCAAGCTCCCT 8822
         |||| ||||||| |  ||| ||||| ||||||||||| || |||||||||||| ||
Db  8760 GCAGACACAACTAAAACAAAGATGGGAGAAGAAGTGCTGGGCGGGACCTCAAGCTCCCT 8819

Qy  8823 GGCCTAGCAGTCCACCCGGAAGAAGCCGGGGCATTGCAACCGGGGCGTATGCCCGCGGC 8882
         ||||||||||| ||||||||||||||||||||||||||||||| ||| ||||| |||||
Db  8820 GGCCTTAGCAGTCCCACCCGGAAGAAGCCGGGGCGTTGTGCAACACGCCGTTCCGCGGC 8879

Qy  8883 GGTTGGCTGAGTTGGCCTGAGGGGCGTGTTGTGGGGCCTTCCCCCTCCG 8942
         ||||||||||||||||  ||| |||||| |||| |||||||| | |||
Db  8880 GGTTGGCTGAGTTGGCCTGAGGGGCGTGTTGTGGGGCCTTCCCTTCCCCCT 8939

Qy  8943 GAGATTGCTGGTATCCCGGGGTTTCCCCCCTTTCCCCTTCGTTCAT 9002
         ||||||||||||| |||||||| |||||||  ||||||||| ||| |
Db  8940 GAGATTGCTGGTATCCGGGGTTTCCCCTCTCTCCCCCTTTCATATGGGGTGTTACAT 8999

Qy  9003 CAATTGGATTTCACAAGCCAGAGAGTGAATTAGGGAG 9062
         |||||||||||||||||| ||||||||||||| ||||
Db  9000 CAATTGGATTTCACAAGCCAGAGAGTGAATCAGCGAGTTAAGGAG 9059

Qy  9063 ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGGCAAGGTCCGTGACTGATC 9122
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Db    9060 ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGGCAAGGTCTGGTGACTGATC 9119
                 ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||

Qy    9123 ATCACTGGAGGAGGTTCCCGCCCTCCCGCCCCAGGGGTCTCCCCGCCTGGGTAAAAAGGG 9182
                 ||||  ||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db    9120 ATCACCGGAGGAGGTTCCCGCCCTCCCGCCCCAGGGGTCTCCCCGCCTGGGTAAAAAGGG 9179

Qy    9183 CCCGGCCTTGGGAGGCATGGTTGGTTACTACTAACCCCTGGCAGGGTCAAAGCCTGATGGTGC 9242
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9180 CCCGGCCTTGGGAGGCATGGTTACTACTAACCCCCTGGCAGGGTCAAAGCCTGATGGTGC 9239

Qy    9243 TAATGCACTGCCACTTCGGTGCGGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC 9302
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9240 TAATGCACTGCCACTTCGGTGCGGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC 9299

Qy    9303 TGCTCCGCAGAGCCCTCCCCGGATGGGGCACACTGACTGTGATCTGAAGGGGTGCACCCC 9362
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9300 TGCTCCGCAGAGCCCTCCCCGGATGGGGCACACTGACTGTGATCTGAAGGGGTGCACCCC 9359

Qy    9363 GGTAAGAGCTCGGCCCAAAGGCCGGTTCTACT 9395
                 ||  |||||||||||||||||||||||||||:||||||
Db    9360 GGGAAGAGCTCGGCCCCGAAGGCCGGTTCTACT 9392
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Query Match         84.9%;  Score 7979;  DB 2;  Length 9392;
Best Local Similarity  90.7%;  Pred. No. 0;
Matches 8515;  Conservative  1;  Mismatches  876;  Indels  1;  Gaps  1:

Qy    3 ACGTGGGGGGTTGATCCCCCCCCCGGCACTGGGTGCAAGCCCATAAACCGACGCCT 62
           ||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db    1 ACGTGGGGGAGTTGATCCCCCCCCCGGCACTGGGTCAAGCCCAGAAACCGACGCCT 60

Qy   63 ATCTAAGTAGACGCAATGACTCGGCGGCCGACTCGGCGACCGGCCAAAAGGTGGTGGATGG 122
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   61 ATCTAAGTAGACGCAATGACTCGGCGGCCGACTCGGCGACCGGCCAAAAGGTGGTGGATGG 120

Qy  123 GTGGTGACAGGGTTGGTAGGTCGTAAATCCGGTCATCCTGGTAGCCACTATAGGTGGGT 182
           ||| ||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db  121 GTGATGACAGGGTTGGTAGGTCGTAAATCCGGTCACCTTGGTAGCCACTATAGGTGGGT 180

Qy  183 CTTAAGAGAAGGTCAAGACTCCTTGTGCCTGCCGGAGACCGCGACGGTCCACAGGT 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CTTAAGAGAAGGTTAAGATTCCTTGTGCCTGCCGGAGACCGCGACGGTCCACAGGT 240

Qy  243 GCTGGCCCTACCGGTGTGAATAAGGCCGACGTCAGGCTCGTCGTTAAACCGAGCCCGT 302
           ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GTTGGCCCTACCGGTGGGAATAAGGCCGACGTCAGGCTCGTCGTTAAACCGAGCCCGT 300

Qy  303 CACCCACCTGGGCAAACGAGCGCCACGTAGCGTCCACGTGCCCCCTTCCACATGTCTCTTG 362
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 TACCCACCTGGGCAAACGAGCGCCACGTACGCGTCCACGTGCCCCCTTCCACATGTCTCTTG 360

Qy  363 ACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAGTGGGGCGCGGGGTTATGGGGAAG 422
           ||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db  361 ACCAATAGGCGTAGCCCGCGAGTTGACAAGGACCAGTGGGGCGCGGGGCT-TGGAGAGG 419

Qy  423 GACCCCAAAACCTGCCCTTCCGCCCTTCCCGGTGGGCCGGCGAAATGCATGGGCCACCCAGCTCCGCG 482
           |||||||| ||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db  420 GACTCCAAGTCCCGCACCCTTCCCGGTGGGCCGGCGAAATGCATGGGCCACCCAGCTCCGCG 479

Qy  483 GCGGCCTGCAGCCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGGCCATTTCTT 542
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  480 GCGGCCTGCAGCCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGGCCATTTCCTTT 539

Qy  543 TTCTATACCATCATGGCAGTCTTCCTCTCCTTCTGTGGTTGAGCCGGCCATTCTG 602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  540 TTCTATACCATCATGGCAGTCTTCCTCTCCTTCTGTGGTTGAGCCGGCCATTCTG 599

Qy  603 GCCCCGCCGCCACCCACCGCTTGTCGAGCAATGACTCCTCACAAATTGCTGCC 662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  600 GCCCCGCCGCCACCCACCGCTTGTCGAGCAATGGCAATATTTCCTCACAAATTGTTGTGCC 659

Qy  663 CCGGAAGAGCATCGGGTTCTGCCCTGGAAGGCCGGATGCCTGGTGCGCCCTGGGGTGCACGGTT 722
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Qy  660                      ||||| |||||||||||||||| |||||||||||||||| ||                          719
Db       CCGGAGGACATCGGGTTCTGCCTTGGAGGGTTGGATGCCTGGTCGCCCTGGGGTGCACGATT

Qy  723  TGCACCGACCGGTTCGTCGGCCACTCTATCAGGCGGGTTTGCTGTGCGGCCTGGCAAGTCC  782
Db  720  TGCACTGACCAAATGCTGGCCACTCTATCAGGCGGGTTTGCTGTGCGGCCTGGCAAGTCC   779

Qy  783  GCGCCCAGCTCGTTGGGGAACTGGGCAGCCTGTACGGGCCTTGTCGGTCTCGGCTTAC     842
Db  780  GCGCCCAACTGGTGGGGGAGCTGGGTAGCCTATACGGGCCCCTGTCGGTCTCGGCCTAT    839

Qy  843  GTAGCCGGGATCCTGGGTCTGGGCGGAGGTTACTCCGGGGTTCCTGACAGTTGGTGTTGCG  902
Db  840  GTGGCTGGGATCCTGGGCCTGGGTGAGGTGTACTCGCGGTGTCCTAACGGTGGGAGTCGCG  899

Qy  903  TTGAGGGCGCGGGTCACCTGGGTCGAAGTCCCCAATCGGAGGTGTGCAGTAGAAGTGACGTTAAG  962
Db  900  TTGACGGCGCCGGGTCGCCGGGTCGAAGTCCCCAACTGCCTGCAGTCGAGCAGTCGCAGAGCTAAAG  959

Qy  963  TGGGAAGTGAGTTTTGGAGATGTTGCAAGGCGCCCCGCCTCCCGTTTGGGTCCCGCCCCTTTGAA  1022
Db  960  TGGGAAAGTGAGTTTTGGAGATGGACTGGAAGCCGAAATCCGGTTTGTCCGGGGTTTGCATGGCTCTCTTCG  1019

Qy  1023 TACCTTTGGAAAGTCCCATTTGAATTTTGGAGGAGTTGATGAGCCTGACCCCTCTGTTG      1082
Db  1020 TACCTCTCGAAGTGCGCCCATTTGATTTCTTGGAGAGGCGTGATAAGCCTGACCCCTTGTTG    1079

Qy  1083 GTTTGGGTGGCCCCGCCATTGCTTTCGCACGCTCTTGTGTTTCCTGCTGGTG          1142
Db  1080 GTTTGCGTTGGCCCCGCCATTGCTTGCGCTCCTGCGCGGAACGTTACGGTTCATGGTCTTCCTGTTCCTGGTG  1139

Qy  1143 ACGATGGGCGGGGATGTTGCAAGGCGCGCCCCGCCTCCCGTTTTGGGTCGCCGTCCGCCCTTTGAC  1202
Db  1140 ACGATGGGCGGGATGTTGCCAAGGCGCGCCCCGTTTGGGTGCACGCCCCTTTGAC         1199

Qy  1203 TACGGGTTGAAGTGGCAGTGCAGTCATGCTCCTGCTGAGGAGGTCGCGTATTCCCACTGGG  1262
Db  1200 TACGGGTTGACTTGGCAGACCTGCTCTGCTGCAGGGCCAACGGTTCGCGTTTTTGACTGGG  1259

Qy  1263 GAGAGGGTGTGGGATGCAGAGGAATGTCACGCTCTTGTTGACTGCCCCAACGGCGCCCCTG  1322
Db  1260 GAGAAGGTGTGGCAGACGTTGGGAACGTTACGCTTCAGTGCGCTTCAGTGTGACTGCCCCTAACGCCCCTG  1319

Qy  1323 GTTTGGGTCCCGCCTTTTGCCAGGCGGTTGGGTGGGCGACCCCATCACCCATTGGAGC    1382
Db  1320 GTGTGGGTCCCGCCTTTTGCCAGCAATGGGTCTGGGGGTGACCCCATCACTTATTGGAGC   1379

Qy  1383 CACGGGACAAAAACCAGTGGCGTGCTGGTGTGAGCGGTCGGTCTCATGTGTGTCCGTA      1442
Db  1380 CACGGGCAAAATCAGTGGCCCCTTCATGCCCCTGGGGAATCCCGTGCCTCGTGTACAGTC   1439

Qy  1443 ACGTGCGTGGGGTTCCCGTGTCTTGGTTGCCTCGACCGGCGTCGTGATTCGAAGATC     1502
Db  1440 ACTTGCGTGGGGTTCCCGTTCTTGGTTGCCTTGCCTCCCACCAGTGGTCCGACTCGAAGATA   1499

Qy  1503 GATGTGTGCGAGTTTGGTCCCGGTTGGGATCCTGCCAGCTGCACCACCGCCTCCTAGGGTCA  1562
Db  1500 GATGTGTGGAGTTTAGTGCCAGTTGGCCTCTGGCCCACCATCACTTATTGGATCA        1559

Qy  1563 TCGGATCCGGACACGGGTTCCGTGTCCGAGCTGTCGTGGGGAGTCCCGCCTGCCTAAGCTGTATT  1622
Db  1560 TCGGATCCGGACACGGGTTCCGTGTCCGAGCTGCTCCGAGTGTGGGAATCCCGTGCCTGCTGGTAACGTGTT  1619

Qy  1623 CTGGACCGTCGGGCCTGCTTCATGTGGCCACCTGTGCGGCACTGTGTCGGCCGAAACCGGG    1682
Db  1620 CTGGACCGTCGGGCCTGCCTTCGCGCCTCCGGCACCTGTGCGGCACTGCTCTGGCCCGGAGACCGGG  1679

Qy  1683 TCGGTTAGATTCCCTTCCATCGTGCGGCACGTGCGGCACGGGGCCTCGGCTTGACAAAGGACTTGGAA  1742
Db  1680 TCGGTTAGGTTCCCCATTCCATTGTGCGGCGGGCCTTGGCCTCGGCTTGACAAAGGACTTGGAA  1739

Qy  1743 GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATTAAGGGGCCCCTGGGCCAACCAG  1802
Db       ||||||||||||||||||||||| ||||| |||||| |||||||| ||||||||||||
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Db  1740  GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGCCCCTGGCAACCAG      1799
Qy  1803  GGGAGAGGCAACCCGGTCGGTCGCGGGTTCGCTGTGCGGCCTGGCACCATGACCAAGATC  1862
Db  1800  GGCCGGAGGCAACCCGGTCGGTCGCGGGTTTGGGTCTCCATGACCACGGATC          1859

Qy  1863  CGGGATTCCCTGCATTGGTGAAATGTCCCACACAGCCATAGAGCCTCCGACTGGAACG     1922
Db  1860  CGAGATACCCTACATCTGGTGAGTGTCCCACACCATTGAGCCTCCCACCGGACG        1919

Qy  1923  TTCGGGGTTCTTCCCCGAGTCCCGGCCATTAACAACTGCATGCCGCTAGGCACGGAAGTG  1982
Db  1920  TTTGGGGTTCTTCCCGGACGCGCCCTCAACAACTCATGCATGGCTCTGGCACGGAAC     1979

Qy  1983  TCTGAGGCATTGGGCGGAGCTGGGCTGGCCTTACGGACGGGGTTCTACGAGCCTCGGTTCGCAGG  2042
Db  1980  TCCGAGGCACTTGGGCGGGGGTGGCCTGGCTTCATGAACCCCTGTGCCCAGG          2039

Qy  2043  TGTTCGGAGCTGATGGGGACGCCGAAATCCGGTTGCCCGGGTACGCATGGCTGTGTCCTCT  2102
Db  2040  TGTTCGAAGCTGATGGGGAAGCCGAAATCCGGTTTGTCCGGGGTTTGCATGGCTCTCTTCG  2099

Qy  2103  GGTAGACCTGACGGGTTCATCACAGTGGGTCCAGGGCACCTGCAGGAGGTGGATGCGGGCAAC  2162
Db  2100  GGCAGGTCGTGATGGGTTTATACAGTGTCAGGGTCACGTGCAGGGGTGGATGCGGCAGGCAAC  2159

Qy  2163  TTCATCCCTCCTCCACGCTGGTTGCTCTTGGAGATTTTGTAGTTTGTCCCTGCTATCTGATG  2222
Db  2160  TTCATCACCCGCCCCGCCGTCTGTGTCTTGGGACTTTGTATTTTGTCCCTGTTATACCTGATG  2219

Qy  2223  AAGCTGCTGAGGCACGGTTGGTCTCGTGATCTTGGTGGTCTCGTGTGGTGGTGGTGAAC   2282
Db  2220  AAGCTGCTGAGGCACGGTTGGTCTCGCTGATCTTGCTGCTTGGTGGTGTGGGTGGTGAAC  2279

Qy  2283  CAGTTGGCGGTTCTAGGACTCGCCGGGCTGTGTGGACGCTGCCGGTGCCGGTGAAGTTTTGCG  2342
Db  2280  CAGCTGCAGTCGCAGTCCTAGGGCGTGTGGAAGCCCCCGTGTGCAGGTGAGGTGCTTGCCGCG  2339

Qy  2343  GGCCCCTTGCTGTCGTGTTTGGGCCTTCGCAGTGATGATACTAGTCTAGCA            2402
Db  2340  GGCCCTTGCCCTGTCGTGTCTTTCGGGACTCCCGTCGTCAGTGTGATGATGATGTGGCA     2399

Qy  2403  AACCTGTGTTGTACTTTCGGTGGATGGCCCTCAGCGCCTGTGATGGGCCTCCGTGTTGTGTG  2462
Db  2400  AACCTGGTCGTGTACTTTAGATGGTTGGGACCCCAACGGCCACCTGATGTTTCCTGTTGTGTGG  2459

Qy  2463  AAGCTCGCTCGGGGAGCTTTCCCGCTGGCACTTTTGATGGGGGCGATTTCGGCGACCCCGCGGG  2522
Db  2460  AAGCTTGCTCGGGGAGCTTTCCCGCTGGCCCCTTGATGGGGGATTTCGGCGACCCGCGGGG  2519

Qy  2523  CGCACCTTGCTCTGCGCGGCCCGAGTTCGCTTCGATGCGATGTCACATTCACCTTTTGTTCG  2582
Db  2520  CGCACTTGCTCTGCGCGGCCCGAGTTCGCTTCGATGCTCGATGCTGGACACTTCG        2579

Qy  2583  GTGTTGGGCTGGTGGGTGGGCCAGCGTGGTGGCCATAGCGCTTCCTGAGCTCAATG        2642
Db  2580  GTGTTGGGCTGGTGGGTGGGCCAGTGTGGTGGCCATTGCGCCTCCTGAGCTGATG       2639

Qy  2643  AGCGCAGGGGGTGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCAG      2702
Db  2640  AGCGCAGGGGGTGGAGCGCACAAAGCCGTGATCTATAGGACGTGGTAAGGGGTACCAG     2699

Qy  2703  GCTGTGCCCAGAGGGTGGTGCGGAGCCCCCGTCGGGAGGGCGGTCCTACCAAGCTTCTG   2762
Db  2700  GCAATCCGTCAAAAGGTGGTGAGGAGCCCCCGTCGGGGAGGGCGGCCGCCCAAACCCCCTG   2759

Qy  2763  ACGTTCGCCTGTCTGCTTGCCCTCATCATCTCGGCCCGATGCGTTGATGATGGTGGTGTG   2822
Db  2760  ACCTTTTGCCTGTCGCTTGCCCTCGTACATCGTCCGCCACAGATGCGTGATGATGGTGGTGTT  2819

Qy  2823  GCCTTGGTCGTCCTCCTTCTCTTTTTGGGCCTGTTGCGACGCGTTGCGATTGGGCCTGTGGGAGAGCTCCTG  2882
Db  2820  GCCCTTGGTCCTCCTTCTCTTCTTTTTGGGCCTTGTTGCGACGCGTTGCGATTGGGCCTTGGAGGAGGATCTTG  2879
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Left column (positions 2883–3962):

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Qy  2883 GTCTCCCGGCCCTCGTTACGGCGACTGGCACGGTGCTGTTGACTGCTGTGTGATGGCCGGC 2942
         || ||||||||||| |||| ||| |||||||||||||||||||||||| || |||||||||
Db  2880 GTGTCCCGGCCCTCGTTGCGCGACTGGCACGGTGCTCGGCGTGGTTGAGTGCTGTGGCGGGT 2939

Qy  2943 GAGAAGGCCACCACCATCCGACTGGTCTCCAAGATGTGCCAAGAGGGCGCCTACCTGTTT 3002
         ||||||||| ||| ||||||||||||||||||||||||||||||| || ||||||| |||
Db  2940 GAGAAGGCCACAACCGTCCGGCTGGTCTCCAAGATGTGCGCAGAGGAGCTTATTGTCTTC 2999

Qy  3003 GACCACATGGGCTCTTTCTCGCGCGTGTCAAGGAGGACGCCTTGTTGGAATGGGACCGGCT 3062
         || || |||||||||||| |||||| |||||||||||| |||||||||||||||||| |||
Db  3000 GATCATATGGGCTCTTTTTCGCGGTCTCGTCAAGGAGGAGCCCTGTTGGAATGGGACCAGCT 3059

Qy  3063 TTGGAGGCCCTTGTCATTCACTAGGACGGACTGCTCGCATCATCAGACGATGCCCGAGGACC 3122
         |   || |||||||||||||||||||||||||||||||| ||| ||| ||||||||||||
Db  3060 CTTGAACCTCTGTCATTCACTAGGACGGACTGCTCGCATCATCAGACGATGCCCGAGGACT 3119

Qy  3123 CTGTCCTGCGGACAGTGCGTCATGGGTTACCGTGTAGCACGGCGGCGGTGATGAGGTT 3182
         |||||||| |||||||||||||||||||||  ||| ||||||||||| ||||||||||
Db  3120 TTGTCCTGCGGACAGTGCGTCATGGGTTACCGTGTGCCGCCCGTGGTGATGAGGTT 3179

Qy  3183 CTCATCGGCGTCTTTCAGGATGTGAATCATTTGCCTCCCGGGTTGTCCCGACTGCACCA 3242
         ||||||||||||||||||||||||||||||||||||| ||||||||| |||||||||||
Db  3180 CTCATCGGCGTCTTCCAGGATGTGAATCATTTGCCTCCCGGGTTTGTTCCGACCGCCCT 3239

Qy  3243 GTTGTCATCCGGTGCCGAAAGGGCTTCCTGGGGTCACGAAGGCAGCCTTGACAGGT 3302
         ||||||||||||||||||||||||||||||||||||| ||||||| |||||||||
Db  3240 GTTGTCATCCGACGGTGCCGAAAGGGCTTCACGAAGGCTGCCCTTGCTTGACAGGT 3299

Qy  3303 AGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTTGGGGACGTCACGGTCACGAAGC 3362
         || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3300 CGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTTGGGGACGTCACGGTCGCGAAGC 3359

Qy  3363 ATGGGCACATGCTGATTAGATCCGACGGGCCTTGTTGTTGTTCACAACTTTGCCATGGCTT 3422
         |||||||||||||| |||||||||||||||||||||||||| ||||| |||||||||||||
Db  3360 ATGGGCACATGCTTGAACGGCCTGTCTTGCACACCTTCACAGTGTGTTCACCATTCCGAACC 3419

Qy  3423 ATCGGCCACGCCCGTGGGGGCCCTGGCCCTTAATCCACCAGGTGTGTCAGCCAGTGATGACGTCACG 3482
         |||||||||||||||| || ||||||||| ||||||| |||||||||||||||||||||||| ||||
Db  3420 ATCGGCCACACCCGTGGGGGCCCTGGCCCTTAATCCACAGTGTGTCAGCCAGTGATGATGTCACG 3479

Qy  3483 GTGTACCCGCTTCCAGATGGGGCAACTTCGTTGACGGCCTTGCCACTTGCCAGGCGGAGTCC 3542
         |||||| || ||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  3480 GTGTATCCACTCCCGGATGGGGCTACTTCGTTCAACACCTTGCCTGCTTGCCAGGCTGAGTCC 3539

Qy  3543 TGTTGGGTTATTAGATCCGACGGGGCCTTTGTGCCATGGCTTGAGCAAGGGGACAAGGTT 3602
         ||| ||||| | || || ||||| |||||||||||||||| ||||||||||||| |||||
Db  3540 TGTTGGGTCATCAGATCCGACGGGGCCTATGCCATGGCTTGAGCAAGGGGACAAGGTG 3599

Qy  3603 GAGCTGGATGTGGCCATGGGCAAAAGGAGTTTTCAAGGAGGCCCCGTTGTCTGTTTATGCCTACG 3662
         |||||||||||||||||||||||||| |||||||||||||||||||| |||||||||||||||||
Db  3600 GAGCTGGATGTGGCCATGGGCAAAAGGAGTCTCTGTTCGTCTGTCTGTTTATGCCTACG 3659

Qy  3663 TGCGACAAAGGGCACGCAGTAAGAAATGCCGCTCCCACTCTGGCCTGCGGCAGGGT 3722
         || |||  |||||||||||||||||||||| ||||||| ||| ||| || ||||||
Db  3660 TGTGACGAAGGGCACGCAGTAAGAATGCCTCCGTGTCTGTTCACTCCGGTGGTAGGGTC 3719

Qy  3723 ACTGCCGGCGGATTCACTAGGCCGTGACTCAAGATGCCAAGATACCACA 3782
         ||| ||||||||||| ||| |||||||||||| ||| |||||||||||||| |||||||
Db  3720 ACCGGCGGCACGGTTCACTAGGCCGTGACTGCCAACCAGATGCCAAAAACCACTACT 3779

Qy  3783 GAACCCCCTCCGGTGCCGCAAAAGGAGTTTTCAAGGAGGCCCCGTTGTTTTGTTTATGCCTACG 3842
         ||||||| | |||||||||||||||||| ||||||||||||||||||||||||| |||||||||
Db  3780 GAACCGCCACGTGCCGCCGGGAAAGAGCCCCGTTGTTGTTTTGTTTATGCCTTTA 3839

Qy  3843 GGGGGCCGGGAAAGAGAGCACCCGCTACCGCGCGTACCGTGAGTACGGCCACACAAGGTCTTG 3902
         |||| ||||||||||||||||||||||| |||||||||||||||||||||||||||||| |||
Db  3840 GGAGCTGGGAAAGACTGCCCCATCGGCCCATCGGCTACCGTGAGTACGGCCACACAAGGTCTTTA 3899

Qy  3903 ATCTTGAACCCCTACAGCTCGGTAGCTACCGTGCGGGGCCGGCTGGGCG 3962
         ||||||||||||| |||||||||||||||||||||||||||| ||||||
Db  3900 ATCTTGAACCCCATCAGCTCGGTGGGGCCCGTGCCCCCTACAGTGGGCCGCTGGGCG 3959
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Right column (positions 3963–5102):

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Qy  3963 GGGAAAACACCCCAGTATTACTGTGGCCATGACGACCACTGCTTTCACAAGGATCACTGAC 4022
         | ||||| || |||||||||| | ||||  |  || |||||||||||||||||||||||||
Db  3960 GGTAAACATCCAAGTATATACTGTGGGCATGACATACAACTGCTTTCACAAGGATCACTGAC 4019

Qy  4023 TCGCCCCTTACGTATTCCACTTACGGACGAAGGTTTTTGGCCAACCCTAGGCAGATGCTGAGG 4082
         |||||||| |||||||| ||||  ||||| ||||||| || |||||||||||||||| |||||
Db  4020 TCCCCCGCTGCGTATTCAACCTATGGGACGAAGGTTTTTGGCCAACCCTAGGCAGATGCTACGG 4079

Qy  4083 GGTGTGTCGGTGGTCATTGTGACGAGTGCCACAGTCATGACTCAACTGTGTTGTTGGGC 4142
         || ||||||||||| ||||||| |||||| ||||| ||||||||||||| || |||||||
Db  4080 GGCGTTTCGGTGGTCATTGTGATGAGTGCCAGTGATCATCAACCTGCTGTGACTGTTAGGC 4139

Qy  4143 ATTGGGCGTGTCAGGGAGCTGCGCGAGGATGTGGAGTGCAATTGGTGCTCTACGCCACT 4202
         ||||||| | || |||||||  || ||||||| |||| ||||||| ||||||| ||||||
Db  4140 ATTGGGAGAGTCCAGGGAGCTGCGCGGTGCTGCGCGGGTGCAACTAGTGCTCTACGCCACC 4199

Qy  4203 GCACCCCCCGGATCCCAGACCCCGGATGACCCAGCACCATCAATCATTGAGACAAAACTGGAC 4262
         |||||||||||||||| ||| ||||| |||||||||||||| ||  |||| || ||| |||||
Db  4200 GCTACACCTCCCGGATCCCCATGACGCAGCAGCACCCCTTCCATAATTGAGACAAAATTGGAC 4259

Qy  4263 GTGGGAGAGATCCCTTCTATGGCATGGCATGGACGATGCGGAGGGACCGGAAGG 4322
         ||||| |||||||| |  |||| |||| ||||||||||| ||| |||||| ||||
Db  4260 GTGGGCGAGATCCCTTTTATGGGCATGGACGATGCGGAGGGACCGGAAGG 4319

Qy  4323 CATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGCGCCTGCGCGGGCCAGTTTTCGGCT 4382
         ||  |||| ||||||||||||||||||||| |||||||| |||||||||||||| | |||||
Db  4320 CACCTCGTGTTCTGCCATTCTAAGGCTGAGTGCGAGCGCCTGCTCGGCCAGTTCTCTCCGCT 4379

Qy  4383 AGGGGGTAAATGCCATCGCCTATTACAGGGGGAAAGACAGTTCTATCATCAAAGATGGA 4442
         ||| ||| |||||| ||||||| | || ||||||| ||||| ||| || | |||||| ||
Db  4380 AGGGGGTCAATGCCATCGCCTATTATAGGGGTAAAGACAGTTCTATCATCAAGGATGGG 4439

Qy  4443 GACCTGGTGGTGTGCTACAGACGCGACTCACTGGGAACTTCGATTCT 4502
         ||||||||||| ||||||||||| |||| ||||||| | |||||||||
Db  4440 GACCTGGTGGTCTGTGTGTACAGACGCGCTTGGACTCACTGGGTACACTGGAAATTTCGACTCC 4499

Qy  4503 GTCACCGATTGTGTGGGTTAGTGTCGAGGAGCGTCGTCGAGGTGACCCTGATCCCACCATT 4562
         ||||||||||||||| ||| || ||||| |||||||||| ||||| || ||||||||||||
Db  4500 GTCACCGACTGTGTGATTAGTGGTTGGTGGGAGGTGCTGCGTCGTCGTGATCCCACCATT 4559

Qy  4563 ACCATCTCCCTGCGCGACAGGTGCCGGCTGAACTGTCGATGCAGCGGCGGAGGACGCGC 4622
         ||||| |||||||||||||| ||| |||||| ||||| |||| |||||| ||||||| ||
Db  4560 ACCATCTCCCTGCGGACAGTGCCGCTGAACTGTGATGCAGCGGCGGAGGACGCGC 4619

Qy  4623 ACGGGTAGGGGCAGGTCTCGGGCGGCTCAGACGCTACTACGGCGGGCCCCTGCCGTGT 4682
         ||||||||||| |||||||||||| ||| ||||| ||||||||||||| ||||  ||||
Db  4620 ACGGGTAGGGGCAGGTCTCGGGCGTCTTGACGCTACTACGGCGGGCCCCTGCCTGGGT 4679

Qy  4683 GTGGTGCCTCAGTCCTTGTCGTGTGAAGCCGGTGTGACCTGGTACGGAATG 4742
         ||||||||||||||||||| |||||| ||||| ||||| |||||||||||||
Db  4680 GTGGTGCCTCAGTCGTCCTTGTCGTGTGAAGCCGGTGTGACTGGAGTGACTGGTACGGAATG 4739

Qy  4743 GAACCTGACCTGACAGCAACTACTGACAACTTTACGACCACTTCCCTTCACACCCGAGCC 4802
         |||||||||||||| ||  |||| ||| ||||| ||||| |||||||||||||||||||
Db  4740 GAACCTGACCTGACAGTTGACAGCTAACCTACTGACGACTTTTACGACGACTGCCCGCGCC 4799

Qy  4803 GTCGCAGCTGACCATTGGGGAAGCCCGTCGTGTTCTTTTCGCGGGGTTGCCCCGGTTGAGGATG 4862
         || || ||||||||| ||  ||||| |||||||| ||| || ||||||||||||| |||||||
Db  4800 GTCGCGGCTGATATCGGAGAAGCCGTCGTTCTTCTCTGGGCCTCGCCCCATTGAGGATG 4859

Qy  4863 CATCCCGATGTTAGCTGGGCCCCCGGTTGTTTTGTCGCGGCCAACTGGCCCCGCTCGGTGGGTGTT 4922
         |||||| |||| |  ||||| ||| ||||||||||| |||||||||||| |||| |||||||||
Db  4860 CACCCTGATGTCAGCTGGGCAAAGTTCGCGGCCAATCGGCCCATCGGTGGGTGTT 4919

Qy  4923 CAGCGGACCATGTGCCCGGGAAACACTGTCTCCCGGATGCGCCAGTGGCA 4982
         ||||| ||||||||||| ||||| ||||||||||||||| |||||||||| ||
Db  4920 CAGCGGACCATGTGCCCGGGAAACACTGTCTCCCCACTCCTGCTGAGGTGCGGCAATGATTTACCATCT 4979

Qy  4983 GGTCTGAAGGCCCGAATCCTGTCCCACTCCTGCTGAGGTGGGGCAATGATTTACCATCT 5042
         |||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db  4980 GGTCTGAAGGGCCCAAATCCTGTCCCACTCCTGCTGAGGTGGGGCAATGATTTACCATCT 5039

Qy  5043 AAAGTGCCGGCCCATCACATGTGACGACGTGGTCCGTAGGCTGGGTCGGGGTGGCGGAGGGT 5102
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Db         ||||||||||||  ||||    |||||||||||||||   |||| ||||||||||
     5040  AAAGTGGCCGGCCACCATAGTGGACGACCTGGTCCGAGACTCGGTGTGGCCGAGGGGT  5099

Qy   5103  TACGTCCGCTGGGATGCGGGACCCATCTTGATGGTGGCCTATTGCGGGGGGCCATG      5162
           |||||||||||||| ||  || ||  |||||||||  || ||
Db   5100  TACGTCCGCTGCGACGCTGGGCCGATCTTGATGATCCGTAGCTATCGCGGGGGGAATG    5159

Qy   5163  ATCTATGCGTCATACACCGGGTCTCTCGTCGTGGTGGTTACAGACTGGGATGTGAAGGGGGGT  5222
           |||||||||||||||||||||||||  ||||  |||  ||| ||||||||||
Db   5160  ATCTACCGTCATACACCGGGTCGCTAGTGGTCGTCAGAGCATGGATGTGGAGGGGGGT    5219

Qy   5223  GGCAGCCCTTTATCGGCATGGAGAGACCAGGCCACGCCCCACGTTGTGCAGGTCCCC     5282
           ||  ||||||||||||||||||| ||   ||||||| ||||||||||||||
Db   5220  GGCGCCCCCCTTTATCGGCATGGAGAGACCAGGCCACGCCGGTGTGCAGGTCGTCAAAGAA  5279

Qy   5283  CCGGTAGACCATCGGCCGCCGGGGAGAGTCTGCGCCATCGGATGCCAACACAGTGACAGAT  5342
           |||||||||||||||||||||||||||||||||||||||||||||
Db   5280  CCGGTAGACCATCGGCCGCCGGGGGGGTGAATCAGCACCATCGGATGCGGTAGCACAGAT   5339

Qy   5343  GCGCTGCGGCCATCCAGTTGCGATTGCTCAGTGTCAGTCAGTCCCTGTCGATCGGGGAA   5402
           |||  || ||||||||||||| |||  ||||| |||  |||||||||||
Db   5340  GCGCTGCAGCCGATTGGAGCTCAGGGGCCGGCTGCTCGGTGTCGATCTGTCGATCGGGAGAA  5399

Qy   5403  GTGGCTGCCTCCTTGGCCCAGGCTAAGAGGGGGACGGCGGGCGTCCCCACTCGTTGACAAGCTCTTC  5462
           ||| ||||||||||||||||||||||||||  ||||||||||||  ||
Db   5400  GTGTTGCCTGCTATACGGGGACCGGCGGCGGGCCGAGCGTCCCACTTGTTGACAAGCTGCTC  5459

Qy   5463  GCTGGCTGCTACACGGGACGGGCGGCACGCGTCCCCACTGTTCAATTGTTGACAAGCTCTTC  5522
           ||||||||| |||||||||||||||||||||||||||  |||||||||||
Db   5460  GCTGGCTGCTATACGGGACGGGCGTGGCCACTCGTGTCTATCCATTGTTGACAAGCTCTTC  5519

Qy   5523  GCCGGGGGCTGGGCGGCGGCACGCGTCGTAGGCCATTGCCACAGTGTAATAGCTGCGGCCAGTGGCG  5582
           ||||||||||||||||||||||||||  |||||||||||||||  ||| |||
Db   5520  GCCGGAGGGGCTGGGCGGCGGCCAGGTGTGTCCAGCCGTGATTGCCACAGCGTGCTGGCGGCCAGTGGCG  5579

Qy   5583  GCCTATGGGGCGTTCTAGGAGCCCTCCATTGCTGCTCCGCGGTTCCGCGTACCGTACCTCATGGGGGCTT  5642
           ||||||  || ||||| ||||  ||||||||||||||| |||||
Db   5580  GCCTACGGGGCGTTCAAGGAGCCCCGTTGCGCCGCGGCTTCCTACCTACCTCCTGATGGGGGTT  5639

Qy   5643  GGGAATGGGCTCGGAGGCAACGCGCAAACCCGCTAGCCGTTATGCGCTGGGGGCTGCGGTGG  5702
           ||||||||||| |||| ||||||||||||||||||||||||
Db   5640  GGCGTTGGAGGCAACGCTCAGAGCGCCTGGCGCGCCGCTGGGGCTGCGGTGGA  5699

Qy   5703  ACCGGTCTCGGCACGCGTGTCGTGTGGGTTAACCAGTGCCGGCCGTTCATGGGCAAGTGCT  5762
           ||||||  ||||||||||||||||||  |||||||||||||||  || ||||||||||
Db   5700  ACCGGCCTTGGGGCACTCGTCGTGTCGTGTGGGTTCATGCCGGGGATCCTTCATGGGGGGCC  5759

Qy   5763  AGCGTCTCCCCCCCTCCTTGGTCACCATTTACTGGGGGCCGTGGGGGCGGTCGGAGGGCGG  5822
           ||   ||||| | ||||||||||||||| ||| |||  ||||||||
Db   5760  AGTGTCTCCCCCCCTCCTTGGTCACCATTTTATTGGGGGCCGTGGGAGGTTGGGAGGGGTGTT  5819

Qy   5823  GTGAATGCCAAGGTCCTAGCCTTGTCTTCAGGCGCGGGGAAATATCATCAGAGATCTG     5882
           ||  ||| || ||||||||||||| |||  |||||| ||  ||||||||||||||
Db   5820  GTCAACGGCCAAGGTCTTCAGACTTCTTCAACTGGCGGGAAACTTTCATCAGAAGATCTG   5879

Qy   5883  TGGTATGCCATCCCAGTGCTAACCAGTGCGGGGCAGGACTTGCCTGGGGGATCGCCCTCGGG  5942
           ||||||||||||||||||||||||||| ||  ||||||||||||||||||
Db   5880  TGGTATGCCATCCCAGTACTCGGGGGTTCGGGGGTCAGGACTTGCCTGCGCGGGGATCCTCTCGGG  5939

Qy   5943  TTGGTGTGTACTCAGCTAACAACTCGGCCTAACACCACTTGTTGAACCGTCTGCTGACT    6002
           |||  || |||  |||  |||||||||||||| |||||||||| |||
Db   5940  TTGGTTTTGTATTCAGCTAACAACTCGGCCTAACACCACTTGTTGAACCGTCTGCTGACT   5999

Qy   6003  ACAGCCAAGGTCCTAGCCATCCCGACTTACTTCAGCAGCCGATTACTGTGAC         6062
           ||  || |||||| |||||||||||||||||||||||| | ||||||
Db   6000  ACGTTACCAAGGTCTTCAGCCCTCCATCCCGACACGTTACTTGACTATTGCGAC       6059

Qy   6063  AAGGTCTTCAGTCTGTCTCCACTGCGGTCCTCGACCGTGGTTGCCCTGGTCAAC        6122
           |||||| || ||||| |||  |||||||||| |||||||||||||||||||
Db   6060  AAGGTCTTCAGCCCTCGCCGGGCCCTCAGCCGCACCCGCACAGTGGTTGCCCTGGTCAAC  6119

Qy   6123  AGGGAGGCCTAAGGTCGATGGATGAGTTCAGGTTCAGGTTGTTGTGGGACTTGTGGAGTGGATC  6182
           ||||||||||||||||||||||||||||||||||||||||||||
Db         AGGGAGGCCTAAGGTGGATGAGGTACAGGTGGGTATGTCTGGGACCTGTGGGAGTGGATC  6179
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Qy   6183  ATGCGTCAAGTGGCCCATGGTGATGGCCAGACTTGGGGCCCTCTGCCCCGGTGTGTCATTA  6242
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Db   6180  ATGCGGCCAAGTGCGGCGGTGTGCTATTGCGGCCTATCGCGGCCCTCAGGGGTGTCACTA   6239

Qy   6243  CCCTTATGGCACTCGCGGGAGGGGGTTGGTCCGGAGAATGGTGTTGGACGGCCATGTTGAG  6302
           |||||||||||||||| || |||  ||||  ||  ||| ||||||||||
Db   6240  CCCTTGTGGCATTGCGGGGAGGGGTGCCGGGCAGATGGTTGCTTGACGGTCATGTTGAG    6299

Qy   6303  AGTCGTTGTCTTTGTTGCGTGTCCTGGCTGCGTGATCACCGGTGATGTTTTGAATGGCAACTCAAAGAT  6362
           |||||  ||| || |||||| |||||||||||  | | ||| |||||||||||
Db   6300  AGTCGTCGCCCTCTGTCTGGCTGCGTGATCACTCAGTGCGTTCTGAATGGGCAACTCAAAGAA  6359

Qy   6363  CCAGTTACTTACTGTGCCACCAAGTCTGCCAGGGGAGCATTATTGGATGGGGACAGTCCTGTGAACATG  6422
           |||||||||||||||||||||||||||||||||||||||||||||
Db   6360  CCAGTTACTTCTCTACCCAAGTCTGCCCACTATTGGATGGGGACTGTCCCTGTGAACATG     6419

Qy   6423  CTGGGCTATGGCGGAGACGTCGCCCTTGCTCAGCACCCCACCCCAGTTGTGACCCTCAGCCCTTTAC  6482
           ||||||||| |||||||||| || || |||||| | |  ||||||||||||
Db   6420  CTGGGTACGGTGCAGCGTCGCTGGGCTGGGCTGAGTGTGACCACCACCCAGTGTAATCAGGAA  6479

Qy   6483  GGGACGTGTGGGTGGGCTGAGTGGTGGTGACCCTGTCGCGTGCTGTTGCTGTGAGCCCTTATTAC  6542
           ||||||||||  |||  || || || |||||||||||||||||||||||||||
Db   6480  GGGACGTGTGGGTGGGCTGGGTGAGGTGGTGACCACCACGTGTAATCAGGAGCCCTACTAC    6539

Qy   6543  TCCCCTACAAACTACTTCAATTGTTTCAATTGTTGACAAGCTCTGTTGCGTGTTGTGCTGTTATTAC  6602
           ||||||||| |||||||| ||||||  |||||| |||||||||||||
Db   6540  TCCGCCTATAAAGTGCTGCTGGTCTGTCATTGTTGACAAGCTGGTGCTGTAGCTGTGACTTACTAC  6599

Qy   6603  GTCACGGGCATACCGGTCTCATGGGATGGACGCGGACGGGCCGTCCCGCCCCTGCCCTTCAGCCCTATGGCTATTAC  6662
           ||||||||||||||  |||||||||||||||||||||||||||||  ||||||||||
Db   6600  GTCACGGGCATTCCCGGTCTCATGGGATGGACGCGGACGGGCCGTCGTGCGCCCGCCCCTGCCCATGTTATGGC  6659

Qy   6663  CCTGGCAAAGTGTCCACCATTGACGGGGAACGCTACACCCTTCCGCATCCAACTGCGGCTT  6722
           ||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   6660  CCTGGCAAAGTGTTACCATTGACGGGGAGCGCTACACCTGCCTCCATCCATCGAGGGGCTC   6719

Qy   6723  AGGAATGTGGCGCCCTGTCATTGGACATTGGACATTGGACCGGAGACTACCCCGAGACT  6782
           |||||||||||||| || ||||||||||  || | || |||||||||||||||||
Db   6720  AGGAATGTGGCACCCTCATTTCATCCGAGGTCGCCAGGTGTCCATGGGACGAAGACACT    6779

Qy   6783  GAAGACTCAGAACTGACTGAGGCCCTTCCCCGCCGGCCTTCAGCCCTTATC          6842
           |||||||||||||||||||||||  ||  ||||| || |||||||| |||||
Db   6780  GAAGACTCAGAACTGACTGAGGCCGATCCGCCGCCCGCTCCAGCGATC            6839

Qy   6843  GAGAATGCTGCGAGAATTCTTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTACA    6902
           ||||||||||||||||||||||||  || || |||||||||||||||||||||||
Db   6840  GAGAATGCTGCGAGATTCTTGAACCGCACATTGATGTCATCATCGGAGGACTGCAGTACA   6899

Qy   6903  CCCTCTCTTGTGTGGCTAGCCGAGAGATGGCCTGTCATCGGGAGAAGACATACCCCGCACT  6962
           ||||  |||  ||||||  |||||| ||| || || |||  ||||| |||||||||| ||
Db   6900  CCCTCTCTTTGTGTGGTAGCCGAGATGCCTGTTCATGGGAGAAGACATGCCCCGTACT     6959

Qy   6963  CCATCGCCAGCACTTATCTCGGTTACTCGGTTAAGATGTCATCGGTGTTGAGAAGAGC     7022
           ||||||||||||| ||||||||| || || |||||||||||||| ||||||||||||
Db   6960  CCATCGCCAGCACTTATCTCGGTTACTCGGTTAAGATGTCATCGGTGTTGAAAGAGC     7019

Qy   7023  TCTTCCTCCGCAGGGAGGATACCCCGTCTTCATTGACTCTTGCTGACT           7082
           |||||||||||||||||||||||||||||||||||||||||||||
Db   7020  TCCTCCGCAGGGAGGATACCCCGTCTTCATTGACTCTTGCTGACT               7079

Qy   7083  ACAGCCGAGGGGAGGGGAAAGCGTCTCAACGTGCTCTTCCGTTACTAAAAGCCTTGTTT   7142
           |||||||||||||||||||||||||||||||||| ||| |||||||||||
Db   7080  ACAGCCGAGGGGAGGGGAAAGCGTCTTCAACGTGCTCTTTCCGTTATTAAAAGCCTTTATTT  7139

Qy   7143  CCACAGAGGCGATGCCACAGAAAGCTTACCGTGTTAAGATGTCATCGGTGTTGAGAAGAGC  7202
           ||||||||||||||||||||||||||||||||||||||||||  ||||  |||
Db   7140  CCACAGAGGCGATGCCGACCAGGAAAGCTTACCGTTACCGTTGCGTTGCGTTGAAAAGAGC  7199

Qy   7203  GTAACACGGCTTCTTTTCTCATTGGGGTTGCGGGGACTTGCGTGTGGAGTGGATG       7262
           ||| || ||||||||||  ||||||||||||||||||||||||||
Db   7200  GTCACGGCGCCTTTTTTTTCTCATTGGGGTTGCGGGGTGCTGATGTTGCTGTGTGAGATG  7259
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Qy  7263  GAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCCACTCCGCTTGAATTGCAGGTT  7322
          ||||||| |||||||||||||||||||| |||||| || ||||||||||||||||||||
Db  7260  GAAATCCAGAACCATACAGCCTATTGTGACCAGGTGCGCACTCCGCTTGAATTGCAGGTT  7319

Qy  7323  GGGTGCTTGTGTGGGCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAGAG  7382
          |||||||||||||||| ||| ||||||||| ||||||| |||||||||||||||||||||
Db  7320  GGGTGCTTGTGTGGGCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAGAG  7379

Qy  7383  ACCTTGGCTTCCTTCTCTTACAATTGGTCTGGGGTGCCACTGACGAGGGCCACTCCGGCC  7442
          |||||||| |||||||||||||||||||||||||||||| |||||||||||||| ||||
Db  7380  ACCTTGGCCTCCTTCTCTTACAATTGGTCTGGGGTGCCGCTGACGAGGGCCACGCCGGCC  7439

Qy  7443  AAGCCCCTGTGGTGAGGCCGGTTGGCTCTTGCTTGGCTCTTGCTGCCGACACCAAGGTGTAT  7502
          ||||||||||||| ||||||||||||| ||||||| |||||| ||||||||||||||| |||
Db  7440  AAGCCCCTCCCGTGGTGAGGCCGGTTGGCTCTTGCTTGGCTCTTGCTGACGACACTAAGGTGTAT  7499

Qy  7503  GTCACCAACCCGGACAATGTTGGGAGAGAGTTGACAAGTTCACCTTCTCGGCGTGCCCCCT  7562
          || |||||||||||||||||||||| | ||||| |||||| | ||||||||||||||||
Db  7500  GTTACCAATCCAGACAATGTGGGACGAGGGTGACAAGTTCATGTTCTGGCGTGCCCCCT  7559

Qy  7563  AGGGTTCATGACAAATTCCTGTGGACTCCATAGAGCGGCAATAAGGACTGTAAGGCCACATGCTGCC  7622
          ||| |||||| |||||||||| |||||||| |||||||||||| |||| ||||||||||||| |||
Db  7560  AGGGTTCATGATAAGACTACCTCGTGGACTCTATTGCGCCCGTCATTGAGGGCCGCGCAAGCC  7619

Qy  7623  TGCCTTAAGCATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCC  7682
          ||||||||||||||||||||||||||||||| | ||| |||||||||| |||||||||||
Db  7620  TGCCTTAAGCATGGGTTACACTTATGAGGAGCAATAAGGACTGTAAGGCCACATGCTGCC  7679

Qy  7683  ATGGGCTGGGGATCTAAGGTGTCGGTCAGGACCTCGCCACCCCTGCGGGGGAAGATGGCT  7742
          |||||||||||||||||||||||| |||||| |||| |||||| ||| |||||||||||
Db  7680  ATGGGCTGGGGATCTAAGGTGTCGGTTAAGGACTTAGCCACCCCGCGGGGGAAGATGGCC  7739

Qy  7743  GTCCATGACCGGCTCCAGGAGATACTTGAAGGACGCCAGTCCCTTTACTCTTACTGTGTG  7802
          |||||||||||||||||||||||||||||| | ||||| |||| |||||||||||||||
Db  7740  GTCCATGACCGGCTTCAGGAGATACTTGAAGGAGACTCCCGTCCCCTTTACTCTTACTGTGTG  7799

Qy  7803  AAAAAGGAAGTGTTCTTCAAAGACCGAAAGAGAAGAAGCCCCGCCCCTCATTGTGTTC  7862
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  7800  AAAAAGGAGGTGTTCTTCAAAGACCGAGAGAGAAGAAGCCCCGCCCCTCATTGTGTTC  7859

Qy  7863  CCCCCCTGACTTCGGATAGTCGAAAAGCTTATTCTGGGAGACCCTGGACGCCGGTAGCC  7922
          ||||| || ||| ||||||||||||||||| |||| |||||||||| |||||||||||
Db  7860  CCCCCCTGACTTCGGATAGTCGATAAGCTCATCTCGTGGGAGACCCTGGACGCCGGTAGCC  7919

Qy  7923  AAGGCGGTGTGGGGGGGCCTACGCCTTCCAGTAGACACCCCAAATCAGCGAATTAGGGAG  7982
          ||||||||||| ||||||||||| |||||||| |||||||||||| ||||||||||||||
Db  7920  AAGGCGGTGTGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAGTTAAGGAG  7979

Qy  7983  ATGCTCAAACTGTGGAATCAAAGAAGAAGACACCACCATGCGCCTGAGACAGGCCACATGC  8042
          ||||||||||||||||| |||||||||||| |||||||||||||||||| |||||||||
Db  7980  ATGCTCAAGCTGTGGAATCAAAGAAGAAGACACCACCATGCGCCTGTGTGACAGGCCACCTGC  8039

Qy  8043  TTCGACAGTAGCATAACTGAAGAGACGTGGCGCTGACGTTGGCTTTATGCCTGGCT  8102
          ||||||||||||||||||||| |||||||| ||| |||||||| |||||||||| |
Db  8040  TTCGACAGTAGCATAACTGAAGAGACGTGGCTTTGGCTTTATACGCTCTGGCC  8099

Qy  8103  TCAGACCATCCAGAAATGGGTGCGTGCCCTGGGAAATACTGCTTCTGGCACAAATGGTA  8162
          ||||||| |||||||||||||| |||||||||||||| ||||| ||||||| ||||| |
Db  8100  TCTGACCATCCAGAATGGGTGCGTGCCCTGGGAAATACTATGCCTCCAGGCACCATGGTC  8159

Qy  8163  ACCCCCGAGGGGTGTCCAGTGGTTGAGAGTATTGTGATCTCTCAGGGTCTTGACCACC  8222
          |||||||||||||||||||||| |||||| |||| |||||| ||||||||| | |||||
Db  8160  ACCCCGGAGGGGTGTCCAGTGGTCGCGGGTATTGTGATCCTCGGGGTGTCCAACAACT  8219

Qy  8223  AGTGCGAGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCCCGCCGCCGCCGCGGGGT  8282
          || || ||||| ||||| || ||||||| |||||||| |||||| ||||| |||||||
Db  8220  AGCGCGAGCAACTGCTTGACCTTGCTATATCAAGGTGAAAGCCCGCCGCGCCGCGGGG  8279

Qy  8283  CTGAAAAATGTCTCGCTCCATCCGCGATGACTGTTTGATCATATGCGAACGGCT  8342
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Db  8280  CTGAAAAATGTCTCTCTTCTCCATAGCCGGGATGACTGTGCTTGATCATATGTGAGCGGCCA  8339
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Qy  8343  GTGTGCGGATCCTAGCGACGCCTTGGGCAGAGCCCTGGCAGAGCCCTACGGGGTACGCATGCGAG  8402
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Db  8340  GTGTGCGGACCCCAAGCGACGACGCCTTTGGGCAGAGCCCTGGTACGCATGCGAG  8399

Qy  8403  CCTTCGTATCATGCGATCACTGGACACGCCCCCTTCTGCTCCACTTGGCTAGCTGAGTGC  8462
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Db  8400  CCCTCATATCATGCGATCACTTGGACACGCCCCCTTCTGCTCCACTTGGCTTGCTGAGTGC  8459

Qy  8463  AATGCAGATGGGAAACGCCATTTCTTCCTGACCACGGACTTTCGGAGGCCCCTCCGCTCGC  8522
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Db  8460  AATGCAGATGGGAAGCGCCATTTCTTCCTGACCACGGACTTCCGGAGGCCGCTCCGCTCGC  8519

Qy  8523  ATGTCGAGCGAGTACAGTGACCCAATGCTTCGGCCATCATCCGGTTACATCCTCCTATACCCT  8582
          ||||||||| |||| |||||||||||| |||||| ||||||| |||||||| || |||||
Db  8520  ATGTCGAGTGAGTAGTGACCCGATGCTTCGGCGATCATCCGGTTACATCCTCCTTTATCCT  8579

Qy  8583  TGGCATCCTATCACACGTGGTGGTCATCATCCCTCACGTGTCTCACCTGCGCGTTTAGGGGT  8642
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Db  8580  TGGCACCCCATCACACGGTGGGTCATCGTCATCGTCCTCGTGTCTCACGTGCGCCATTCAGGGGT  8639

Qy  8643  GGTGCACACCGTCGATCCTGTGTGGTGCCGCCTCCACGGACCCAGCAGCGTTGAGGGTTACC  8702
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Db  8640  GGAGGCCACACCGTCTGATCCCGTTTGGTGCCGCCTCCACGGACCCAGCAGCGTTGAGGGTTACC  8699

Qy  8703  CTGGACAAACTGCCTAACATCATCGTGGCCCTCTGGCCCTCCGGACCAGCCCAGGTTACC  8762
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Db  8700  CTGGACAAACTGCCTAACATCATCGTGGCCCTTGGCCCTGTTGGCCCGGACCAGCCCAGGTTACC  8759

Qy  8763  GCAGACAACTAAGACAAAATGGAGGCTGGCAAGTGCTGGCGACCTCAAGCTCCCT  8822
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Db  8760  GCAGACAACTAAGACAACTAAAACAAAGATGAGGCTGGTAAGGTTCGAGCGACCTCAAGCTCCCT  8819

Qy  8823  GGCCTAGCACGTCCACCGGGGCAGGAGAAGGCGGGGCATTGCGGAACCGGTATGCTCCGGTCGCGC  8882
          ||| |||||||| |||| |||||| ||||||| |||| || ||||||| |||||||| ||||||
Db  8820  GGCTTAGCAGTGCCACCGGGGCAGGAGAAGGCCGGGGCATTGCGGAACACGCCGTTGCGAACACGCTCCGGCGC  8879

Qy  8883  GGTTGGGCTGAGTTGGCTAGGGGCTGTGTTGGCGTCCCCCTTCCCCCCCTATAGGGGTGGTTCCG  8942
          ||||||||||||||||||||||||| |||||||| |||||| |||| |||||||||||||||||
Db  8880  GGTTGGGCTGAGTTGGCTAGGGGCTTGGTGTTGGCGTCCCCCTTCCTCTCCCCT  8939

Qy  8943  GAGATTGCTGTATCCCCGGGGGTTCCCCCTATGGGGTGGTTCAT  9002
          |||||||||||| ||||||||||| || |||||||||||||| ||
Db  8940  GAGATTGCTGTGTATCCCCGGGGGTTCCCCCTATATGGGGTGGTGTACAT  8999

Qy  9003  CAATTGGATTTCACAAGCCAGAGAGTCGCCGGTGGTTGGGTTCTTAGCCGTCTC  9062
          |||||||||| |||||||||||||||||||||||||||||| |||||||||||||
Db  9000  CAATTGGATTTCACAAGCCAGAGAGTCGCCGGTGGTTGGGTTCTTAGCCCGTGCTC  9059

Qy  9063  ATCGTAGCCCTCTTGCGGGTGAACTAAATTCATCTGTGCGCCCCCCCCAGGGGTCGACTGATC  9122
          |||||||||||||| ||| |||||||| |||||||||| |||||| |||||||||||||||||
Db  9060  ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTGCGCCCCCCCAGGGGTCTGTCGACTGATC  9119

Qy  9123  CCCGCCTTGGGAGGCATGGGTTCCCCGCGTCTACAACCCCCGGTCAAAGCTCAAAGGTGTGC  9182
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Db  9120  CCCGCCTTGGGAGGCATGGGTTCCCCGCGTCTACAACCCCCGGTCAAAGCTCAAAGGTGTGC  9179

Qy  9183  CCCGGCCTTGGGAGGCATGGGTGGTTACTAACCCCCGTACCGGTAATCCGTGACTACGGGC  9242
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Db  9180  CCCGGCCTTGGGAGGCATGGGTGGTTACTAACCCCCGTACCGGTCAAAGCTCGATGGTGC  9239

Qy  9243  TAATGCACTGCCACTTCGGTGGCGGGTCGCTAGCGTAATCCGTGACTACGGGC  9302
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Db  9240  TAATGCACTGCCACTTCGGTGGCGGGTCGCTAGCGTAATCCGTGACTACGGGC  9299

Qy  9303  TGCTCGCGAGCAACTGCTTGACTTGCTATATCAAGGTGAGAGGGTGCACCCCC  9362
          ||||| |||||||||||||||| ||||||||||||||| ||||||||||||||
Db  9300  TGCTCGCAGCAACTGCTTGACCTTGCTATATCAAGGTGAGAGGGTGCACCCCC  9359

Qy  9363  GGTAAGAGCTCGGCCCCAAAGCCCGGTTCTACT  9395
          || |||||||||||| ||||||| ::||||||||
Db  9360  GGGAAGAGCTCGGCCCCGAAGCCCGGSTTCTACT  9392
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RESULT 5
US-08-485-910-14
; Sequence 14, Application US/08485910
; Patent No. 5874563
;   GENERAL INFORMATION:
;      APPLICANT: Kim, Jungsuh P.
;      APPLICANT: Wages, John
;      APPLICANT: Young, LaVonne M.
;      APPLICANT: Fry, Kirk E.
;      APPLICANT: Linnen, Jeffrey M.
;      TITLE OF INVENTION: Hepatitis G Virus and Molecular
;      TITLE OF INVENTION: Cloning Thereof
;      NUMBER OF SEQUENCES: 277
;      CORRESPONDENCE ADDRESS:
;         ADDRESSEE: Dehlinger & Associates
;         STREET: 350 Cambridge Ave., Suite 250
;         CITY: Palo Alto
;         STATE: CA
;         COUNTRY: USA
;         ZIP: 94306
;      COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/08/485,910
;         FILING DATE:
;         CLASSIFICATION: 435
;      PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 08/389,886
;         FILING DATE: 15-FEB-1995
;      PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 08/357,509
;         FILING DATE: 16-DEC-1994
;      PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 08/329,729
;         FILING DATE: 26-OCT-1994
;      PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 08/344,271
;         FILING DATE: 23-NOV-1994
;      PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 08/285,558
;         FILING DATE: 03-AUG-1994
;      PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 08/285,543
;         FILING DATE: 03-AUG-1994
;      PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 08/246,985
;         FILING DATE: 20-MAY-1994
;      ATTORNEY/AGENT INFORMATION:
;         NAME: Fabian, Gary R.
;         REGISTRATION NUMBER: 33,875
;         REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
;      TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (415) 324-0880
;         TELEFAX: (415) 324-0960
;   INFORMATION FOR SEQ ID NO: 14:
;      SEQUENCE CHARACTERISTICS:
;         LENGTH: 9392 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: double
;         TOPOLOGY: unknown
;      MOLECULE TYPE: cDNA
;      HYPOTHETICAL: NO
;      ANTI-SENSE: NO
;      ORIGINAL SOURCE:
;         INDIVIDUAL ISOLATE: HGV-PNF 2161 Variant
;      FEATURE:
;         NAME/KEY: CDS
;         LOCATION: 459..9077
US-08-485-910-14
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Query Match             84.9%;  Score 7979;  DB 2;  Length 9392;
Best Local Similarity   90.7%;
  Matches 8515;   Conservative    1;  Mismatches  876;  Indels    1;  Gaps    1;

Qy      3 ACGTGGGGGGTTGATCCCCCCCCCGCACTGGGTGCAAGCCCCATAAACCGACGCCT 62
            |||||||| |||||||||||||||||||||||||||||||| |||||| |||||
Db      1 ACGTGGGGGAGTTGATCCCCCCCCCGCACTGGGTGCAAGCCCCAGAAACCGACGCCT 60

Qy     63 ATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCGCCGACCGGCCAAAAGGTGGTGGATGG 122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCGCCGACCGGCCAAAAGGTGGTGGATGG 120

Qy    123 GTGGTGACAGGGTTGGTAGTCGTAAATCCGGTCATCCTGGTAGCCACTATAGGTGGGT 182
            ||| ||||||||||||||| ||||||||||||| |||||||||||||||||||||||
Db    121 GTGATGACAGGGTTGGTAGGTCGTAAATCCGGTCACCTTGGTAGCCACTATAGGTGGGT 180

Qy    183 CTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTGCCGGGCGAGACCGCACGGTCCACAGT 242
            ||||||||||||| |||| ||| ||||||||||||||||||||||||||||||||||
Db    181 CTTAAGAGAAGGTAAGATTCCTTGTGCCTGCCGGGCGAGACCGCACGGTCCACAGT 240

Qy    243 GCTGCCCTACCGGTGTGAATAAGGCCCGACGTCAGGCTCGTCGTTAAACCGAGCCCGT 302
            |||||||||||||| || |||||||||||||||||||| |||||||| |||||||||
Db    241 GTTGGCCCTACCGGTGGGAATAAGGCCCGACGTCAGGCTCGTCGTTAAACCGAGCCCGT 300

Qy    303 CACCCACTGGGCAAACGACGCCCACGTACGGTCCGCACGTCCGCCCTTCAATGTCTCTG 362
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TACCCACTGGGCAAACGACGCCCACGTACGGTCCGCACGTCCGCCCTTCAATGTCTCTG 360

Qy    363 ACCAATAGGTTTATCCGGCAGTTGACAAGGACCAGTGGGGCCGGGGGGTTATGGGAAG 422
            |||||||||| ||||||||||||||||||||||||||||||||||||| ||||||||
Db    361 ACCAATAGGCGTAGCCGGCGGAGTTGACAAGGACCAGTGGGGGCCGGGGGGCT-TGGAGAGG 419

Qy    423 GACCCCAAACCTGCCCTTCCCGGTGGGCCGGGAAATGCATGGGGCCACCCAGCTCCCG 482
            |||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GACTCCAAGTCCCGCCCTTCCCGGTGGGCCGGGAAATGCATGGGGCCACCCAGCTCCCG 479

Qy    483 GCGGCCTGCAGCCGGGGTAGCCCAAGAATCTTCGGGTGAGGGCGGGTGGCATTTCTCTT 542
            |||||||| ||||||||||||||||||||||||||||||||||||||||||||||| |
Db    480 GCGGGCCTGCAGCCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGGCATTTCCTTT 539

Qy    543 TTCTATACCATCATGGCAGTCCTTCTGCTCCTCGTGGTTCGGTGCCGGGGCCATTCTG 602
            |||||||||||||||||||||||||||||||||| |||| |||||||||||||||||
Db    540 TTCTATACCATCATGGCAGTCCTTCTGCTCCTCGTGGTTGCGGTGCCGGGGCCATTCTG 599

Qy    603 GCCCCGGCCACCCACGCTTGTCGAGCGAATGGCAATATTCCTCACAAATTGCTGTGCC 662
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    600 GCCCCGGCCACCCACGCTTGTCGAGCGAATGGCAATATTCCTCACAAATTGTTGTGCC 659

Qy    663 CCGGAAGACATCGGGTTCTGCCCTGGAAGGCGGATGCCTGGTGCCTGGGGTGCACGGT 722
            ||||| ||||||||||||||||||||||||||| ||||||||||||||||||||||| |
Db    660 CCGGAGGACATCGGGTTCTGCCCTGGGAGGGTGGATGCCTGGTGCCTGGGGTGCACGATT 719

Qy    723 TGCACCGACCGTTGCTGCCCACTGTATCAGGCGGTTTGCCTGTGCGCCTGCCAAGTCC 782
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    720 TGCACTGACCAATGCTGCCCACTGTATCAGGCGGTTTGCCTGTGCGCCTGCCAAGTCC 779

Qy    783 GCGGCCCAGTCGTTGGGGAACTGGGGAGCCTGTACGGGCCCGTATAGCCCGTCTCGGCTTAC 842
            ||||||||||||||||||| ||| | ||| |||||||||||| ||||||||||||||||
Db    780 GCGGCCCAACTGGTGGGGGAGCTGGGTAGCCCTATACGGGCCCCTATAGCCCGTCTCGGCCTAT 839

Qy    843 GTAGCCGGGATCTGGGTCTGGGCGGAGGTTTACTCCGGGTCTGACAGTTGGTTGCCG 902
            || | ||||||||||| ||||| ||| |||||| ||||||||||||||||||||||||
Db    840 GTGGCTGGGATCCTGGGTCTGGGGTGAGGTGTACTCGGGGTGTCCTAACCGGTGGGAGTCGCG 899

Qy    903 TTGAGGGCCCGGGTCTACCTGAATGCCCAAACCTGAAGTGTGCAGTAGAATGTGACGTTAAG 962
            ||||||||||||| || ||||| |||| |||||||||||||||||||||||||||||||
Db    900 TTGACGCCCGGGTGCTACCCGGTGCCTCAACCTGACGTGCGCGTGTGAGCTAAAG 959

Qy    963 TGGGGAAGTGAGTTTGGAGATGCAGCTGCTCCATTACTGGATTTTGGAA 1022
            ||| | |||||||||||| ||||||||||||| ||| ||| |||||||
Db    960 TGGGAAGTGAGTTTGGAGATGGACTGAACAGCTGCCTCCAACTACTGGAATTCTGGAA 1019

Qy   1023 TACCTTTGGAAGTCCCATTTGAATTTTGGAGAGGAGTTGATGAGCCCTGACCCCCTCTGTTG 1082
US-08-485-910-14
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Db  2100 GGCAGGCCTGATGGGTTTATACATGTCCAGGTCACTTGCGAGGAGTGGATGCAGGCAAC 2159
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Qy  2163 TTCATCCCTCCTCCACGCTGGTTGCTGCTTGGATTTGTATTTGTATTTGTCCTGCTCTATCTGATG 2222
              ||||||||||| ||| ||||| |||||||||||| |  | |  ||| |||||  | |
Db  2160 TTCATCCCGCCCCGCCGGCTGGTTGCTGCTGCTTGGACTTGCTGTTGCTGTTATACCTGATG 2219

Qy  2223 AAGCTGGCTGAGGCACGACGCGGTTGGTCCCGTGATCTTGCTCTCGTGTTGGTGGTGAAC 2282
              |||||||||||||| |||||||||||||||||| ||||| ||||||||||||||||||
Db  2220 AAGCTGGCTGAGGCACGACGCGGTTGGTCCCGTGATCTTGCTCTCGCATGGTGGTGGTGAAC 2279

Qy  2283 CAGTTGGCGGTTCTTAGGACTGCCCGTGTGGACTGCCCTGCGGTGGGTGAAGTTTTGCG 2342
              || || ||||||||  || |||  |||||||| |||| ||||||||||||| ||  ||
Db  2280 CAGCTGGCAGTCCTAGGGCGCTGCCGCGTGTGGAAGCCGCCCGGCAGGTGAGGTCTTCGCG 2339

Qy  2343 GGCCCTGCCTTGTCATGGTGTGTTTGGGCCTTCCCCACTGTCCAGTCAGTATGATACTAGGTCTAGCA 2402
              ||||| ||| ||||||||||   ||||||  |||||||| || ||||||||||| | |  |
Db  2340 GGCCCTGCCCTGTCCTGTGTCTCGGGACTTCCCGGTCGTCAGTCAGTATGATATTGGGTTTGGCA 2399

Qy  2403 AACCTGGTGTGTACTTTCCGTGGATGGGCCTCAGCGCGCCTCATGTTCCTCGTGTTGTGG 2462
              |||||||||| |||||  ||||| | || | ||||  | |||  |||||||||||||||
Db  2400 AACCTGGTGCTGTACTTTAGGATGGTTGGGACCCCAACGCCTGATGTTCCTCGTGTTGTGG 2459

Qy  2463 AAGCTCGCTCGGGGAGCTTTCCCCGCTGGACTTTTGATGGGGATTTCGGCGACCCGCGGG 2522
              |||||||||| |||||| || ||||  |||  | |  ||| || |||| ||| | ||||
Db  2460 AAGCTTGCTCGGGGAGCTTTCCCGCTGGGCGCTGGGGATTCGGCGACCTGAGCGTCGATG 2519

Qy  2523 CGCACCTCTGTGCTCCGGGGCCGAGTTCTGCTTCGTGATTCGAAGATC 2582
              ||||||| || |||||||| |||||| |||||| ||||||| || |||||
Db  2520 CGCACCCCAGTGCTTCGGGGCCGAGTTCTGCTTCGTGATGCTACATTCGAGGTGGACACTTCG 2579

Qy  2583 GTGTTGGGCTGGTGGTGGCCAGCCGGTGCTTGGCGTGCTCCTGAGCTCAATG 2642
              ||| ||||||||||||||  |||| ||||||||||  ||| ||||||||||
Db  2580 GTGTTGGGCTGGTGGTGGCCAGTCGGTAGCTTGGCGCATTGCGCTCCTCGAGCTCGATG 2639

Qy  2643 AGGCCAGGGGGTGAAGCACAAGCCGTGATCTATAGGACGTGTGTAAAGGTACCAG 2702
              |||||||||||||| ||||||||||||| |||| |||||||| |||||||||||
Db  2640 AGGCGCAGGGGGTGAGGCGCACAAAGCCGTGATCTATAGGACGTGTGTAAGGGTACCAG 2699

Qy  2703 GCTGTGCGCCAGAGGGTGGTGCGGAGCCCCCTCGGGGAGGGGCGCCTCCACAAGCTTCTG 2762
              || || |||| ||||||||||| |  |||  |||||||||| ||| |  |||||||||||
Db  2700 GCAATCCGTCAAAGGTGGTGAGGAGCAGGGCCTGCCGCCCAAACCCCTG 2759

Qy  2763 ACGTTCGCCTGGTGCTTGGCCTCATACATCTGGCCGGATGGTGGTGGTG 2822
              |  |  | ||||| || |||||  |||||||||| |||||| |||||| ||
Db  2760 ACCTTTGCCGTGGTGCTTGGCCGCCGTACATCTGGCCAGATGCGTGATGATGGTGTGTTGTT 2819

Qy  2823 GCCTTGGTCCTCCTCTTCCGGCCTGTTGACGCACTGGACTGGGCCCTGGGAGAGCTCTG 2882
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Db  2820 GCCTTGGTCCTTCTCTTTCGGCCTGTTGCGACGCGGTTGGATTGGGCCTTGGAGGAGATCTTG 2879

Qy  2883 GTCTCCCGGCCCTCGACTACGGCGACGGGGTGGTTGAGTGTGTGATGGCGGGC 2942
              || |  |||| || ||||||| |||||| |||||||||||||||||| || ||
Db  2880 GTGTCCGGCCCTCGACTACGGCGTTGGCGTTGGCTGGTCAGTGCGTGTCAGTGCGGGGT 2939

Qy  2943 GAGAAGGCCACCAACCATCCGACTGGTCTCCAAGAGTGCGCAAGAGGGGCTACCTGTTT 3002
              ||||||||||||| |||||||||||||||||||||||| ||  |||||||| ||| ||
Db  2940 GAGAAGGCCACAACCGTCCGGTCTCCAAGAGTGTGCGAGAGGAGCTTATTTGTTC 2999

Qy  3003 GACCACATGGCTCTTTCTCGCGGACGTCCATCATCAGAGATGCGGAGGACC 3062
              ||| |  ||| || ||||  |||||||||||||||||||||| |||| |||
Db  3000 GATCATATGGGCTCTTTTCGCGTGCTGTCATCATACGGGATGCCGCGAGGAGCT 3059

Qy  3063 TTGGAGCCCTTGCATTCACTAGGACGACTGTCCATCATCAGAGATGCCGCAGG 3122
              |  ||  |  || |  | ||  |||||  |||||||||||||| ||||||| ||
Db  3060 CTTGAACCTCTGTCATTCACTAACGACGACTGTCCATCATACGGGATGCCGCGAGGACT 3119

Qy  3123 CTGTCCTGCGGACAGTGCGTCATGGGTTTACCCGTGGTAGCACGGCCGCGTGATGAGGTT 3182
              ||||  |||||| |||||| |||||||  |||||||||  |||||| ||| ||||||||
Db  3120 TTGTCCTGCGGGCAGTGCGTCATGGGTTTACCCGTGGTTGCGCCCGTGGTCGTGATGAGGTT 3179

Qy  3183 CTCATCGGCGTCTTTCAGGATGTGAATCATTTGCCTCCCGACTGCACCA 3242
              |||||| |||| |||| ||||||| |||||||||||| |||| ||||||
Db  3180 CTCATCGGCGTCTTCCAGGATGTGAATCATTTGCCTCCCGGGTTTGTTCCGACCGCCT 3239
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Db  1020 TACCCTGGAAGGTGCCCGCCATTTGAATTCTGGAGGAGGCTGATAAGCCTGACCCCCTTGTTG 1079
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Qy  1083 GTTTGGGTGCCCGGCATTGCTTTTGCTGGAGCAACGGATTGTCATGGTTTCCTGCTGGTG 1142
              |||| |||||||  || |||||||| | ||||  || || ||| |||||| ||||||| |
Db  1080 GTTTGCGTGGCCGCCGCCATTGCTGCTTGAGCAGCGGATTGTCATGGTTTCCTGCTGTGTGGTG 1139

Qy  1143 ACGATGGGGGATGTTGCCAAGGCGCCCCGCCTCCGTTTGGGGTCCCGCCCTTTGAC 1202
              |||||| | |||| | | |||| | ||| ||| || || || ||||| ||||||||
Db  1140 ACGATGGGCAGGTCGCAAGGGCGCCCCTGCCCTCCGTTTGGGGTCACGCCCTTTGAC 1199

Qy  1203 TACGGGTTGAAGTGGCAGTGGCATGCATGCTCGCGTATTCCCACTGGG 1262
              ||||||||  || || | |  ||| || |||||||  || |||||||
Db  1200 TACGGGTTGACTTGGCAGACCTGCTCGCAGCCGGTTTCGCCGGTTCGGACTGGG 1259

Qy  1263 GAGAGGGTGGGATGCGAGGGAATGTCACGCTCTTGTGTGACTGCCCCACGGCCCCTG 1322
              ||||||||||||  ||||||| || ||| || |||| | || |||||| || |||||
Db  1260 GAGAAGGTGTGGAACGTTACGCTTCAGTGCATGTTCAGTCCCTAACGGCCGCCCCTG 1319

Qy  1323 GTTTGGGGTCCCGGCCTTTGCCAGGCGGTTGGGCGGCGACCCCATCACCCATTGGAGC 1382
              ||||||||||  |||||||||||||| | | ||| || | |||||| | ||||||| |
Db  1320 GTGTGGGGTCCCGGCCTTTGCCAGCAATCGGCGGGTGGGACCCCATCACTTATTGGGAC 1379

Qy  1383 CACGGACAAAAACCAGTGGCCCCCATCATGCCCCAATATGTCATGGGTCTGTGTCCGTA 1442
              |||||||||| |  ||||||||  ||||| ||||||| |||  |||||||| | |||
Db  1380 CACGGACAAATCAGTGGCCCCTTTCATGCCCCCAGTATGTCTATGGGTCTGCTACAGTC 1439

Qy  1443 ACGTGCGTGTGGGGTTCCCGTGTCTTGGTTGCCTCGACCGGCGTGATTCGAAGATC 1502
              || |  ||||| |||| |||||| |||||||||| ||||  |||  | |||||||
Db  .1440 ACTTGCGTGTGGGGTTCCCGTGTCTTTGGTTGCCTCCACCAGTGGTCGCGGAAGATA 1499

Qy  1503 GATGTGGAGTTGGTGCCGGTTGGATCGCTGCCAGCTGCACCATAGCCGCTTAGGGTCA 1562
              |||||||||||||||| || |||| |||||||||| |||||||||||||| | |||
Db  1500 GATGTGGAGTTTAGTGCCAGTTGGCTCTGCCACCTGCACCATAGCCCACTTATTGGAA 1559

Qy  1563 TCGGATCGGCACACGGTGGTTGAGCTCTTCCGAGTGGGGAGTCCCGTGCCTAACGTGTATT 1622
              |||| |||||||||||| | |  ||||||||||||| |||||  ||||| || |||||| |
Db  1560 TCGGATCGGCACACGGTGCTGCTGGCTCTCCGAGTGGGGAATCCCGTGCGTGACGTGTGTT 1619

Qy  1623 CTGGACCGGTCGGCCTGCTTCATGTGCACCTGTCTGCGGACTGTGCTGGCCCGAAACCCGGG 1682
              ||||| ||||||||||| |||  | ||| || |||||||| ||| |  ||||||  |||||
Db  1620 CTGGACCGGTCGGCCTGCTTCCTGCGGCACCTGTGTGAGGGACCGTTGGCCCGGAGACCGGG 1679

Qy  1683 TCGGTTAGATTCCCTTTCCATCGGTGCGGCACGGGCCTCGGCTGACAAAGGACTTGGAA 1742
              ||||||| ||| || |||||| ||||||| ||||||| ||||||| ||||||||||||
Db  1680 TCGGTTAGGTTCCATTCCATCGGTGCGGCACGGGCCTCGGCTGACAAAGGACTTGGAA 1739

Qy  1743 GCTGTGCCCTTGTCAACAGGACAACTCCCTTCACCATAAGGGGCCCCCTGGGCAACCAG 1802
              || | ||||  |||| |||| |||||||| ||||| ||||  |||||||  ||||||||
Db  1740 GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGCCCCTGGGCAACCAG 1799

Qy  1803 GGGAGAGGCAACCCGGTGCGGTCGGCCTACGGGGTTTGGGTCCTACACCATGACCAAGATC 1862
              |||| ||||||||  |||| |||||  |  |||||| ||||| ||||||||||||||||
Db  1800 GGCCAGGCAACCCGGTGCGGTCGGCCTCCGGGGTTTCATGGTCCTACACCATGACCAGGATC 1859

Qy  1863 CGGGATTCCCTGCATTTGTGAAAATGTCCACACCAGCCTCGACTGGAACG 1922
              |||| |  || ||||| ||| |||||||||| |||||| |||||||||| |
Db  1860 CGAGATACCCTACATCTGTGGAGTCCCCATTAACAACTGCATCCCACCGGGACG 1919

Qy  1923 TTCGGGTCTTCCCCGAGTCCCGCCCATTAACAAACTGCATGCCTCTAGGCACGGAAGTG 1982
              |  ||||| || |||   |||||||| |  |||||| ||||| |||||||||||||||
Db  1920 TTTGGGTTCTTTCCCCGGGACCCGCCCATTAACAACTGCATGCTTCTTGGGCACGGAAGTG 1979

Qy  1983 TCTGAGGCATTGGGCGGAGCTGGGGTTCTACCAGCCTCGGTTCGCAGG 2042
              || |  | |||| | |||||||||| |||  |  |||| ||||| |||
Db  1980 TCCGAGGCACTTGGGCGGAGCTGGGGTTCTCATGAACCCCTGGTTGCGCAGG 2039

Qy  2043 TGTTCGGAGCTGATGGGACGCCGAAATCCGGTTTGCCCGGGTACGCATGGCTGTCCTCT 2102
              |||||||||| ||||| | | |||||  || || |||| ||||||  ||||| ||  |
Db  2040 TGTTCCGGGCAGTGGGCGTCATGGGTTTACCCGTGGTTGCGCCCGTGGTCGTGATGGCTCTTCG 2099

Qy  2103 GGTAGACCTGACGCGGTTCATAACGTCCAGGGCCACCTGCAGGAGGTGGATGCGGGCAAC 2162
              || | |||||||| |||||||  ||||||| | ||| ||||| ||||| |||| |||||
Db  2100 GGCAGGCCTGATGGGTTTATACATGTCCAGGTCACTTGCGAGGAGTGGATGCAGGCAAC 2159
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Qy 3243 GTTGTCATCCGTCCGGTCGGTGCGGGAAAGGGCTTCCTGGGGTTCACGAAGGCAGCCTTGACAGGT 3302
          ||||| |||||| |||||| ||||||| ||||||| ||||| ||||||||||||| ||||||||||
Db 3240 GTTGTCATCCGACGGTGCGGGAAAGGGCGCTTCCTGGGGTTCACGAAGGCTTCCTGGGGTTCACGAAGGCTTCCTGCCTTGACAGGT 3299

Qy 3303 AGGGATCCTGACTTACATCCAGGGAACGTCATGGTTGGGACGCCTACGTCACGGAAGC 3362
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db 3300 CGGGATCCTGACTTACATCCAGGGAACGTCATTGGGACGTCATGGGTCATGGGGTCATGGGGTTGGGACGCCTACGTCGCGGAAGC 3359

Qy 3363 ATGGGCCACATGTCGAATGGCCTGCTGTTCACAACTTTCGTCATCCCGAACC 3422
          ||||| |||||||||||||||||||||||||||||||||||||||||||||
Db 3360 ATGGGAACATGTTGAACGGCCTGCTGTTCACAACTTTCGTCATCCCGAACC 3419

Qy 3423 ATCGCCACGCCCTGGGGGCCCTTAATCCCAGTGTGGTGTCAGCCAGTTGTCAGCGATGACGTCACG 3482
          |||||||||||||||||||||| |||||||||||||| ||||||||| |||||||||||||||||
Db 3420 ATCGCCACACACCCCGGGGGCCCTTAATCCCAGTGTGGTGTCAGCCAGTTGTCAGCGATGATGTCACG 3479

Qy 3483 GTGTACCCGCTTCCAGATGGGGCAACTTCGTTGACGACCTGCACTTGCCCAGGCCGGAGTCC 3542
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Db 3480 GTGTATCCACTCCCCGGATGGGGCAACTTCGTTAACCACCTTGTACTTTGCTCCAGGCCTGAGTCC 3539

Qy 3543 TGTTTGGGTTATTAGATCCGACGGGCTTGTGCCATGGCTTGAGCAAGGGGACAAGGTT 3602
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Db 3540 TGTTTGGGTTCATCAGATCCGACGGGCTTGTGCCATGGCTTGAGCAAGGGGACAAGGTG 3599

Qy 3603 GAGCTGATGTGCGCCATGGAGGTCTCTGACTTCCGTGTTCGTCTCTCT 3662
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Db 3600 GAGCTGGATGTGCGCCATGGAGGTCTCTGACTTCCGTGTCGTCTCGTCTCGCTGCCTCACCGGTCCTA 3659

Qy 3663 TGCCGACAAAGGGCACGCAGTAAGAATGCTCGTGTCAGTGCTCCACTCTGGCCGTGGCCGCAGGGTT 3722
          || |||||||| |||||| |||||||||||||||| ||||||| |||||| ||||
Db 3660 TGTGTGACGAAGGGCACGCAGTAGGAATGCTCGTGTCTGTGCTTCACTCCGGTTGTGGTAGGGTC 3719

Qy 3723 ACTGCGGCGGCGATTCACTAGGCCGTGGACTCAAGTACCAAGACTACCACA 3782
          || ||||||| ||||| ||||||||||| |||||||||||||||||| |
Db 3720 ACCGCGGCGGCGATTCACTAGGCCGTGGACTCAAGTGCCAACAGATGCCAAGACACCAAACCACTACT 3779

Qy 3783 GAACCCCCTCCCGGGTCCGTGCCGCAAAAGGAGTTTTCAAGGAGCCCCGTTGTTATGCCTACG 3842
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Db 3780 GAACCCCCTCCCGGGGTCCGTGCCGCCAAAGGAGTTTTCAAAGAGCCCCGTTGTTATGCCTACG 3839

Qy 3843 GGGAAACACCCCAGTATTTACTTACGTGCCCGTACCGTTGGAGTACGGCCAACATGGGCCACAAGGTCTTG 3902
          |||| || |||| |||||||| |||||||||| ||||||||||||||| |||||||||||||
Db 3840 GGAGCGGGAAAGAGACACTCGCCGTCCCGTGAGTACGGCGACAACATGGGCACCAAGGTCTTA 3899

Qy 3903 ATCTTGAACCCGTCGCAGTAGTCCGTGGCCATGGAGCCGCTGCG 3962
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Db 3900 ATCTTGAACCCCGTCGAGTAGTCCGGGCCACTGTGCGGGGCTGCCG 3959

Qy 3963 GGGAAACACCCCAGTATTACTTACTGTGGCCATGACCACCACTGCTTTCACAAGGATCACTGAC 4022
          |||| || ||||| ||||||||| ||||||||||||||| |||||||||||||||||||
Db 3960 GGTAAACATCCAAGTATCGTGGCCATGACACCACCACTGCTTTCACAAGGATCACTGAC 4019

Qy 4023 TCGCCCCTTAACGTATTCCACTTACGGAAGGTTTTTGGCCAACCCTAGGCCAGTGCTGAGG 4082
          || |||||| |||||||||||| |||||| ||||| ||||||| |||||||||| ||||
Db 4020 TCCCCCCTGACGTATTCAACCTATGGAAGGTTTTTGGCCAACCCCTAGGCCAGTAGCTACGG 4079

Qy 4083 GGTGTGTCGGGTGTCATTTGTGACGAGTGCATTGTTGTTCGGC 4142
          ||||||| |||| ||| ||||| ||||| |||| || |||||
Db 4080 GGCGTTTCGGGTCATTTGTGACGAGTGCATGGACTGTGCCACAGTGTGTTAGGC 4139

Qy 4143 ATTGGGGCTGTCAGGGAGGTGGCGAGGATGTGGCACCCACTGTGCTCTACGCCACT 4202
          ||||||||| || |||| ||| |||||| |||| ||||| ||||||||||||||
Db 4140 ATTGGGGAGTCCAAGGAGGTCAACTAGTGTCTTTCACAAGGATCACTGAC 4199

Qy 4203 GCCACCCCCCGGATCCCGGGTGGAGGCATGGGCCACCATCAATCATTGAGACAAAAACTGGAC 4262
          ||||||||||||||||| ||| |||||| |||||||||||||||||| ||||||||||||||
Db 4200 GCTACACCTCCCGGATCCCCATGACCCCAGTCCAGTGCTAATAATTGAGAACAAAATTGGAC 4259

Qy 4263 GTGGGAGAGATCCCTTCTATGGCATGGGATGCGGACCGGAAGG 4322
          |||| |||||| ||||| | |||||||||||||||||||||||
Db 4260 GTGGGCGAGATTCCCTTTTATGGCATGGGATGCGGAGCGGAAGG 4319

Qy 4323 CATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGGCGCCTGGCGGCGCCAGTTTCGGCT 4382
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Db 4320 CACCTCGTGTTCTGCTCCATTCTAAGGCTCTAAGGCTGAGTGCTGCCGCCTTGCTGGCCTTCTCCGCT 4379

Qy 4383 AGGGGGTAAATGCCATCCGCCTATTACAGGGGGAAAGACAGTTCTATCATCAAAGATGGA 4442
          ||||| |||| ||||||| ||| | ||| || |||||||||| |||||||||||||||
Db 4380 AGGGGGGTCAATGCCATTCCCTATTATAGGGTCAAAGACAGTTCTATCATCAAGGATGGG 4439

Qy 4443 GACCTGGTGGTGTCGCTACAGAGCCACTATCCACTGGGTACACTGGGAACTTCGATTCT 4502
          |||||||||||||||| |||||| ||||||||||||||||||| ||||||||||| ||
Db 4440 GACCTGGTGCTGTCGCTACGACGCGCCTTTCCACTGGGTACACTGGGGAAATTTCGACTCC 4499

Qy 4503 GTCACCGATTGTGGTTAGTGTGGTGAGGAGTCGTCGAGGTGACCCTTGATCCCACCATT 4562
          |||||||| ||||||| || |||||| ||||||||| ||||| |||||||||||||
Db 4500 GTCACCGACTGTGGATTAGTGTGGTGAGGAGTCGTTGAGGTGACCCTTGATCCCACCATT 4559

Qy 4563 ACCATCTCCCTGCGCACGGTGCCCGCTGCGTCTGGCTGACTGTGTGATGCAAACGAGGACGC 4622
          ||||||||||| ||||||||| |||||| ||||||||||||||||||| ||||||| |||
Db 4560 ACCATCTCCCTGCGCACAGTGCCTGACGTGCCTGCAGTGCCTGCAGTGTCGATGCAAACGAGGACACGC 4619

Qy 4623 ACGGGTAGGGCCAGGTCTGAGCTGGCGCTACTACGGGGGTCGGCCAAGGCGCCCCTGCTGGT 4682
          |||||||||||||||||||||||||||| ||| |||| ||||||||| |||||| |||||
Db 4620 ACGGGTAGGGCCAGGTCTGAGCTGGCGCTACTACGGGGGTGGGCCAAAGCGCCCCTGCTGGGGT 4679

Qy 4683 GTGGTGCGCTCAGGTCCTGTCGGTCGGCGGTGGAAGCCGGTTGACCTGTACGGAATG 4742
          ||||||||||||||| ||||||||||| ||||| ||| |||| |||||||||||||
Db 4680 GTGGTGCGCTCAGGTCCTGTCGGTCGGCGGTGGAGTGGAGTGACCTGGTACGGAATG 4739

Qy 4743 GAACCTGACGACAGCAGACAAACCTACTGAGACTTTACGACAACTGCCCTTACACCGCAGCC 4802
          |||||||| ||||| ||| |||||| |||||| |||| |||||| ||||||||||||||
Db 4740 GAACCTGACTGACAGCAGCTAACCTACTGAGACTTTACGACGACTTTACGACACCCGCAGCC 4799

Qy 4803 GTCCAGTGACATTGGGAAGCCCGGTTGTTCTTTCGTTCCCGTTGCCCGTTGGCTGGAGGATG 4862
          |||||||||||||||||| |||||||| ||| ||||||| |||| |||| |||||| ||||
Db 4800 GTCGCGGGCTGATATCGGAGAAGCCCGGTGTCTCTCCCACTCCTGCTGGCTCGCTCGGGGGAAGGATG 4859

Qy 4863 CATCCCGATGTTAGCTGCGGGCAAAAGTTCGCGGCGTCAACTGGCCCCTTCCTGTGGGTGTT 4922
          ||| ||||||| ||| || |||||||| ||||||||||||||| ||||| ||| |||||||
Db 4860 CACCCTGATGTCAGCTGCGGGCAAAAGTTCGCGGCGTCAACTGGCCCCTTCTTGTGGGTGTT 4919

Qy 4923 CAGCGGACCATGTGCCGGGAAACACTGTCTCCCGCCAATCGGATGACCCCAGTGGGCA 4982
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Db 4920 CAGCCGGACCATGTTCCGGCGATCTTCGTCGCGGCTGAAATCGGATGACCCCAATGGGCA 4979

Qy 4983 GGTCTGAAGGGCCCGAATCCTGTCTCCCACTCCTGAGTGTGGGCAATGATTTACCATCT 5042
          ||||| ||||||| ||||||||| ||||||||||||||||| ||||||| ||||||||
Db 4980 GGTCTGAAGGGCCCAAATCCTGTCTCCCACTCCTGAGTGTGGGCAATGATTTACCATCT 5039

Qy 5043 AAAGTGGCCGGCCATCACATCGTGACGACATCACACAGGGATCACTGAC 5102
          |||||||||||||| ||||||||||||| ||||||| ||||||| ||||
Db 5040 AAAGTGGCCGGCCATCACCACCACTAGTGACGACTGTCAGCCGTGTGGCGAGGGGT 5099

Qy 5103 TACGTCCGTGCGATGCGGCTGGCCGATCTTGATGTGGCCTATTGCGGGGGCATG 5162
          ||||| |||||||| ||||| ||||||||||||| |||| ||||||||||||||
Db 5100 TACGTTCCGCTGCGACGCGTGGCGATCTTGATGTGGCTGTCATCGGGGGGGGAATG 5159

Qy 5163 ATCTATGCGTCATACACCGGTCGGATGGATGTGGTTGTTACAGACTGGGATGTGAAGGGGGGT 5222
          |||| ||||| ||||||||| || ||||| || | ||| |||||| ||||||||||| |||
Db 5160 ATCTACGCGTCATCACACCGGGTCGGATGGATGTGGTGCAGCAGTAGCAGCAGTGACAGAGT 5219

Qy 5223 GGCAGCCCCTTTATCGCACCGGTTGTGTCGCAGGGTCCCCC 5282
          ||| ||||||| ||||||||||||||| |||||||| ||||
Db 5220 GGCGCCGCCCCCTTTATCGCAGCCATCCAGCCTTCAGCGATGTTCAGCCATCCAGCCTTCAGCGGGGGT 5279

Qy 5283 CCGGTAGACCCATCGGCGATGACCGGGGGAGTGCTTGCGCGCAACACAGTGACAGAT 5342
          ||||| ||| |||||| ||||| ||| |||||| |||||||| ||||||||||||||
Db 5280 CCGGTAGAACCATCGGCGATGACCGGGGTGAATCAGCCAAGCAGCAGTGACAGTGACAGAT 5339

Qy 5343 GCGGTGCCGCCATCCAGTCCAGTTGGTGCCAATTGGTCAGTGTCGATCCGGGGAA 5402
          |||| |||||||||| ||| |||| ||||||||| ||||||||||||||||||||
Db 5340 GCGGTGCAGCCATCCAGTCCAGTTGGACTGCGATTCATGAGCTGCTGTCGTCGATGCGGGGAGA 5399

Qy 5403 GTGCGTGCCTTGGCCCAGCTAAGACGGCCTAAGAGCCGGTCGGGAGCTTCACCACGCACGGCTT 5462
          |||| ||||||| ||| |||||||||| ||| ||||| ||||||||||| ||| |||||||||||
Db 5400 GTGGGCGAGATTCCCTTTTATGGCATGGCATGGGATGCGGAGCGGAAGG 5462

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Db  6480 GGGACGTCTGGCTGGGCTGAGGTGGTGTGACCACTACCCACCTGGTAATCAGGAGGACC 6539
Qy  6543 TCCGCCTACAAACTGCTGCGCCAGCAAATCTGTCGGCTGCGTTGCTGAGCCCTATTAC 6602
         ||||||| | | |||||||||||| ||  |||||||||||||||||||||| |||||||
Db  6540 TCCGCCTATAAGCTGCTGCGCCAGCAAATCCTATGCGGCTGCGTAGCTGAGCCCTACTAC 6599

Qy  6603 GTCGACGGCATACCGGTCTCATGGGACGCGGACGCGGACGCCTGCCGTCCATGGCTATGGC 6662
Db  6600 GTCGACGGCATTCCGGTCTCATGGGACGCGGACGCGGACGCCCCCGCCATGGTCTATGGC 6659

Qy  6663 CCTGGGCAAAGTGTCACCATTGACGGGGAACGCTACACCCCTTCCGATCAACTGCGGCTT 6722
Db  6660 CCTGGGCAAAGTGTTACCATTGACGGGGAGCGCTACACCCCTTGCCTCATCAACTGAGGCTC 6719

Qy  6723 AGGAATGTGGCGCCCCTGAGGTGTCATCCGAGGTGTCCATTGACATTGGGACGACGAGACT 6782
Db  6720 AGGAATGTGGCACCCCTGAGGTTTCATCCGAGGTGTCCATTGACATTGGGACGACGGAGACT 6779

Qy  6783 GAAGACTCAGAACTGACTGAGGCCGACCTGCCGCGGCCTGCAGCCTTCAGCCTATC 6842
Db  6780 GAAGACTCAGAACTGACTGAGGCCGACCTGCCGCGGCCTGCTGCTCTCCAAGCGATC 6839

Qy  6843 GAGAATGCTGCCGAGAATTCTTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTACA 6902
Db  6840 GAGAATGCTGCCGAGGATTCTTGAACCGCACATTGATGTCATCATGGAGGACTGCAGTACA 6899

Qy  6903 CCCTCTCTTGTGGGAGTAGCCGAGAGATGCCTGTGTGGGAGAAGACATACCCCGCACT 6962
Db  6900 CCCTCTCTTTGTGGTAGTAGCCGAGAGATGCCTGTATGGGAGAAGAACATCCCCGTACT 6959

Qy  6963 CCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCCAGATGAGAGAGACCCGTCGGTG 7022
Db  6960 CCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCCAGATGAGAGAGACCCGTCGGTG 7019

Qy  7023 TCTTCCTCGCAGGAGGATACCCCGTCTTCTGACTCATTCGAGCTCATCCAAGAGTCCGAG 7082
Db  7020 TCTTCCTCGCAGGAGGATACCCCGTCTTCTGACTCATTCGAGCTCATCCAAGAGTCCGAG 7079

Qy  7083 ACAGCCAAGGGGAGGAAAGCGTCTTCAACGTGGCTCTTTCCGTACTAAAAGCCTTGTTT 7142
Db  7080 ACAGCCGAAGGGGGAGGAAAGTGTCTTCAACGTGGCTCTTTCCGTATTAAAAGCCTTATTT 7139

Qy  7143 CCACAGAGCGATGCCACCAAGAAAGCTTACCGTTAAGATGTCATGCTGTGTTGAGAAGAGC 7202
Db  7140 CCACAGAGCGACGCGACCAGGAAGCTTACCGTTAAGATGTCGTGCTGTTGAAAAGAGC 7199

Qy  7203 GTAACACGCTTCTTTCTCTTTCATTGGATTGGACGGTCGCTGACGTCGTGTGAGATG 7262
Db  7200 GTCACGCGGCTTTTTCTCATTGGGTTGGACGGTCGCTGATGTTGCTAGCCTGTGTGAGATG 7259

Qy  7263 GAAATTCAGAACCATACAGCCTATTGTGACAAGGTGGCCACTCCGCTTGAATTGCAGTT 7322
Db  7260 GAAATTCAGAACCATACAGCCTATTGTGACAAGGTGGCCACTCCGCTTGAATTGCAGTT 7319

Qy  7323 GGGTGCTTGGTGTGGGCAATGAACTTACCTTTGACAAGTGTGAGGCTAGGCAAGAG 7382
Db  7320 GGGTGCTTGGTGTGGGCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAGAA 7379

Qy  7383 ACCTTGGCTTCCTTCTCTTACATTTGGTCTGGGGTGCCACTCCGCC 7442
Db  7380 ACCTTGGCCTCCTTCTCTTACATTTGGTCTGGGGTGCCACGCGCCGCC 7439

Qy  7443 AAGCCCCTGTGTGAGGCCGGTTGTGAGGCCGCACCACCAAGGTGTAT 7502
Db  7440 AAGCCCTCCCGTTGGTGAGGCCGGTTCTCGTTGTTAGTGGCCGACACTACTAAGGTGTAT 7499

Qy  7503 GTCACCAACCCGACAATGTTGGGAGAAGAGTTGACAAGTTACCTTCTGGCCGTGCCCCT 7562
Db  7500 GTTACCAATCCAGACAATGTGGGACGACGGTGGACAAGGTGGACAAGTTGACCTTCTGGCCGTGCTCCT 7559

Qy  7563 AGGGTTCATGACAAATTCCTCTGGACTCTATTGAGCCGTAAGAGCGGCCAGCTCAAGCC 7622
Db  7560 AGGGTTCATGATGATAAGCTACCTCGTGGACTCTATTGAGCCGTAAGAGCGGCCCTCAAGCC 7619
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Db  5400 GTGTTGTCCTTGGCTGCACGGGAGCTCAGGCTGGCTAAGACGGCCGAGGCCTACACAGCAGCAGGCCTACACAGCAGGCCAAGTTGGCTC 5459

Qy  5463 GCTGGCTGCTACACGGGGAACCGGCGGGCCGTCCCACTGTTTCAATTGTTGACAAGCTCTTC 5522
Db  5460 GCTGGCTGCTATACGGGGGAGCCGGCGGGCCCGGTTCCCACTGTATCCATTGTTGACAAGTCTTC 5519

Qy  5523 GCCGGGGGGCTGGGCGCGGTGTAGGCCATTGCCACAGTGTAATAGTGCGGCGCAGTGGCG 5582
Db  5520 GCCGGAGGGTGGGCGCGGTGTGGGCCATTGCCACAGCGTGCGTTCATGGGGCGGTGGGCC 5579

Qy  5583 GCCTATGGGGCTTCGTAGGAGCCCTTCCATTGCTGCTGCCGCCTTCCTACCTTCATGGGGTTG 5642
Db  5580 GCCTACGGGGCTTCAAGGAGCCCGCGGCTTCCTACCTTGATGGGGTTG 5639

Qy  5643 GGGCTCGGAGGCAACCGCGCAAACCCCGCTTAGCCTTCCGCTCCCTACTAGGGGCCGCTGGG 5702
Db  5640 GGGCGTTGGAGGCAACGCGCAGAACGGCCCTCGAGACGCGCCGCGTCTCCGCTGGCGTCTGGA 5699

Qy  5703 ACCGGTCTCTGGGCACGCCTCGTCGTGGGGCGCGTTCATGGGAAGTGCT 5762
Db  5700 ACCGGCCTGGGCACTCCTCGTCGTGGGGCGCCCATGCGCAGGTGCGTTCATGGGGGGGCC 5759

Qy  5763 AGCGTCTCCCCCTCCTTGGTCACCATTTTACTGGGGCCGTGGGGGGCGTGGGGAGGGGCGTG 5822
Db  5760 AGTGTCTCCCCCTCCTTGGTCACCATTTTATTGGGGCCGTCGGGAGGTTGGGGAGGGTGTT 5819

Qy  5823 GTGAATGCGGCTAGCCTTGTCTTCGACTTTATGGCGGGGAAACTATCATCAGAAGATCTG 5882
Db  5820 GTCAACGGCTCTTCATGGCCGGGTAGTCTTTGACTTTCATGGCCCGGGAAACTTTCATCAGAAGATCTG 5879

Qy  5883 TGGTATGCCATCCAGTGCTAACCAGTGCGGGGATCGCCCTCGGG 5942
Db  5880 TGGTATGCCATCCAGTGCTAACCAGTGCGGGGATCGCCCTCGGG 5939

Qy  5943 TTGGTGTTGTACTCAGCTAACAACTCGGCACTACCACTTGGTTGAACCGTCGCTGCTGACT 6002
Db  5940 TTGGTTTGTATTCAGCTAACAACTCGGCACTACCACTTGGTTGAACCGTCGCTGCTGACT 5999

Qy  6003 ACATTGCCAAGGTCCTCATGCATCCCTGACAGTTACTTTCAGCAGGCCGATTACTGTGAC 6062
Db  6000 ACGTTACCCAAGGTCTTCATGCGCCGTTACTTTGACTAGTTGCGAC 6059

Qy  6063 AAGGTCTCAGCTGTGCTCCGACGTTGAGCCTCGCACCGTGTTGCCCTGGTCAAC 6122
Db  6060 AAGGTCTCAGCTGCTCCGGGCCCTCGAGCCTCACCCGCAGTGGTTGCCCTGGTCAAC 6119

Qy  6123 AGGGACCTAAGGTGATGAGGTTCAGGTGGGACTTGTGGGAGTGGATC 6182
Db  6120 AGGGAGCCTAAGGTGATGAGGTACAGGTGGGGACTGGGTATGCTCTGGGAGTGGATC 6179

Qy  6183 ATGCGTCAAGGTGCCGATGGTGATGGCCAGACTTCGGGCCCTCTGCCCCGTGGTGTCATTA 6242
Db  6180 ATGCGCCAAGGTGCCGATGGTGATGGCCAGACTCAGGGCCCTCTGCCCCGTGGTGTCACTA 6239

Qy  6243 CCCTTATGGACTGCCGGGGAGGGGTGTTGTTGGACGCCATGTTGAG 6302
Db  6240 CCCTTGTGGCTATGGGCCAATTGGATGGGGAATGGTTGCTTCGACGTCATGTTGAG 6299

Qy  6303 AGTCGTTGTGTTGTGGTGCGTGAGTGATGTTTTGAAATGGGCAACTCAAAGAT 6362
Db  6300 AGTCGCTCGTGTGTGGTTGCGTCGATCACTGGTGACGTTTCTGAAATGGGCAACTCAAAGAA 6359

Qy  6363 CCAGTTTACTTCTACCAAGCTGTCCAGGCATTATTGGGATGGGGGACAGTCCCCTGTGAACATG 6422
Db  6360 CCAGTTTACTTCTACCAAGCTGTGCCCGGGCACTATTGGGATGGGGGACAGTCCCTGTGAACATG 6419

Qy  6423 CTGGGTCTATGGCGAGACGTCCCCTTTGCTCGCCTCAGAACACCCCGAAGGTGTACCAATTC 6482
Db  6420 CTGGGTTACGTGGTGAAAACGTGCCCTCCCCCGAAGGTTGTGCCCTTC 6479

Qy  6483 GGGACGTCTGGGCTGCTGAGGTGGTGATCAGAGGCCCTACCCACGTGTGATCAGGCCGAACA 6542
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Qy   7623  TGCCTAAGCATGGGTACACTTATGAGGAGCAATAAGGACTGTAAGGCCACATGCTGCC  7682
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Db   7620  TGCCTAAGCATGGGTACACTTATGAGGAGCAATAAGGACTGTAAGGCCACATGCTGCC  7679

Qy   7683  ATGGGCTGGGGATCTTAAGGTGTCGGTCAAGGACCTGCCACCCTGCGGGGAAGATGGCT  7742
           ||||||||||||||||||||||||||| ||||||| |||||||| ||||||||||||||
Db   7680  ATGGGCTGGGGATCTTAAGGTGTCGGTTAAGGACTTAGCCACCCCGGGGGAAGATGGCC  7739

Qy   7743  GTCCATGACCGGCTCCAGGAGATACTTGAAGGGACACCCAGTCCCCTTTACTTCTTACTGTG  7802
           ||||||||||||||||||||||| |||||||||||| || ||||||||||||||||||||||
Db   7740  GTCCATGACCGGCTTCAGGAGATACTTGAAGGGACTTGAAGGGACTCCGGTCCCCTTTACTTCTTACTGTG  7799

Qy   7803  AAAAGGAAGTGTTCTTCAAGAACCGAAAGAAGAGGAAGGCCCCCGCCCTCATTGTGTTC  7862
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   7800  AAAAGGAGGTGTTCTTCAAGAACCGAAAGAAGAGGAAGGCCCCCGCCCTCATTGTGTTC  7859

Qy   7863  CCCCCCTGGACTTCCGGATAGCTGAAAAGCTTATTCTGGAGGACCTGGACGGGGTAGCC  7922
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   7860  CCCCCCTGGACTTCCGGATAGCTGAAAAGCTCATCTTGGAGGACCTGGACGGGGTAGCC  7919

Qy   7923  AAGGCCGTGTTGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGGAATTAGGGAG  7982
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   7920  AAGGCCGTGTTGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAGTTAAGGAG  7979

Qy   7983  ATGCTCAAACTGTGGGAATCAAAGAAGACACCATCTGTGTGGACGCCCACATGC  8042
           |||||||| ||||||||| || |||||| ||||||||||| |||||||||||||
Db   7980  ATGCTCAAGCCCTCTGGGAGTCTAAGAAGTCTGTGTGGACGCCCACCTGC  8039

Qy   8043  TTCGACAGTAGCATAACTGAAGAGACGTGCCGTGGCGCCTGAGACAGAGCTTTATGCCCTGGCT  8102
           |||||||||||||||||||||||||||||| ||||||| || |||||||||||||||| ||||||
Db   8040  TTCGACAGTAGCATAACTGAAGAGACGTGCGTGGCGCCTGGGGAGACAGAGCTGTTTGGGTAAAAAGGG  8099

Qy   8103  TCAGACCATCCAGAATGGGTCGCGTGCCCTGGGAAATACTATGCCTCCTGGCACAATGGTA  8162
           ||||| |||||||||||||||| || |||||| ||||||||||| |||||||||||||||| |
Db   8100  TCTGACCATCCAGAATGGGTCGCGTGCCCACTTGGGAAATACTATCCTCCAGGCACCATGGTC  8159

Qy   8163  ACCCCCGAGGGGTCCGTTGGAGGTGGTCATCCTCAGGGGTCTTGACCACC  8222
           ||||| || ||||||||| ||||||| ||| |||||||||| |||||||||
Db   8160  ACCCCGAGGGGTGCCGTTGGAGGTGGTCATTGCGAGATCCTCGGGGTGTCTAACAACT  8219

Qy   8223  AGTGGCGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCCGCCGCTGTGAGAGGGTGGGG  8282
           |||||||||||||||||||||||||||||||||| || ||||||||||||||| ||||||||
Db   8220  AGCGGCGCAGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCTGCCTGTGAGAGAGTGGGG  8279

Qy   8283  CTGAAAAATGTCTCGCCTCTCATCCGCTTGGGCAGAGCCCTTGGGCAGAGCGCCT  8342
           ||||||||||||||||| ||||||||||||||||| ||||||||||||||| ||||
Db   8280  CTGAAAAATGTCTCCTCTCTCATCCGCTTGACCTGCGGGCCGGGCAGAGCGAGGGCCGCA  8339

Qy   8343  GTGTGCGATCCTAGCCGACGCGTTTGGGCAGAGCCCTGGCGAGCTACGGCGTGCCGAG  8402
           |||||| ||||||||||||| ||||||||| |||||||||||||| |||| ||||||||
Db   8340  GTGTGCGACCCCAAGCCACGCGCTTGGGCAGAGCCCTGGGCGTAGGGTACGGCGTGCCGAG  8399

Qy   8403  CCTTCGTCCTATCATCACTGGACGTGGGCGACACGGACCCCCCTCGCTCGCCACTTGGCTGGCTGAGTGC  8462
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Db   8400  CCCTCCATATCACATCATGGACACGGACCCCCCTCGTCCACTTGGCTCCACTTGGCTGCTCGAGTGC  8459

Qy   8463  AATGCAGATGGGAAACGCCATTTCTTCCTGACCACCGGAAACGCCATTTCCGGAGGCCCCTCGCGC  8522
           ||||||| ||| |||||||||||||||||| |||||||||||||||||| |||||||||| ||||||
Db   8460  AATGCAGATGGGAAAGCCATTTCTTCCTGACCACCGGGAAGCCATTTCCGGAGGCCCCTCGCGC  8519

Qy   8523  ATGTCAGCGAGTCAGTAGCAGTGCCATGGCTTCGGCCAGTTCATCCTCTAATCCCTACTCCTATACCCT  8582
           |||||||||||||||||||| || |||||||||||||||| ||||||||| |||||||||| |||||||||
Db   8520  ATGTCCAGTGAGTAGTCAGTGTATGGCGTTACGCTCCTTTATTCCTTTATTCCT  8579

Qy   8583  TGGCATCCTATCACACGGTGGGCATCATCATCCCTACGCTGCCACCTGCGCCGCCGTTTAGGGGT  8642
           || |||| |||||||||| ||||||| ||||||||||||||||||| |||| ||||||||||||||
Db   8580  TGGCACCCCATCACACGGTGGGTCATCATCATCCCTCCATTGGCTGCCATTGTGCTAACGTGCCATTCAGGGGT  8639

Qy   8643  GGTGGCGCCACCGGTCTGATCCGTGTGTGTCCAGGTAACATGGTAATTACTACTAACAAGTTTCCA  8702
           || || ||||||||||| ||||||||||||| |||||||||||| |||||||||||||||||||||
Db   8640  GGAGGCCACACCGGTCTGATCCGTTTGTGTGCCAGGTAACATGGTGGTGTTGTGCCAGGTAACTAACTACAAGTTTCCA  8699
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Qy   8703  CTGGACAAACTGCCTAACACATCATCGTGGCCCTCCACGGACCAGCAGCGTTGAGGGTTACC  8762
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Db   8700  CTGGACAAACTGCCTAACACATCATCGTGGCCCTCCACGGACCAGCAGCGTTGAGGGTTACC  8759

Qy   8763  GCAGACAACTAAGACAAAAATGGAGGCTGGGACCTGCTGAGCGACCTCAAGCTCCCT  8822
           |||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||
Db   8760  GCAGACACAACTAAAACAAAGATGGAGGCTGGTAAGGTTCTGACGCGACCTCAAGCTCCCT  8819

Qy   8823  GGCCTAGCAGTCCACCGGAAGAAGGCCGGGGCACGGGACCATGGTTGCGGGTCCAGGTCCCGGGC  8882
           ||   |||||||||||||||||||||||| |||||||||||| ||||||||||||||||||||||
Db   8820  GGCTTAGCAGTCCACCGGAAAGAAGGCCGGGGCGTTGCGAACACGCATGCTCCGGCTCCGCGC  8879

Qy   8883  GGTTGGGCTGAGTTGGCTAGGGGCGTGTTGTGTGGGCTCAGGTCCAGGCCTTGCCCGTTCCCCCTCG  8942
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   8880  GGTTGGGCTGAGTTGGCTAGGGGCGTTGTGTGTGGGCCTCACCGGCCTTCCTCCAGGCCTTCCTCCCCCT  8939

Qy   8943  GAGATTGCTGGTATCCCGGGGGTTTCCCCCTTTCCCCCCTATATGGGGTGGTTCAT  9002
           ||||||||||||||||||||| |||||||||||||||||||| |||||||||||||
Db   8940  GAGATTGCTGGTATCCCGGGGGTTCCCCCTGTCTCCCTCCCCCTATATGGGGTGGTACAT  8999

Qy   9003  CAATTGGATTTCACAAGCCAGAGGAGTCGCTGCGGGTCGTGGTTCTTAGCCCTGCTC  9062
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9000  CAATTGGATTTCACAAGCCAGAGGAGTCGCTGCGGGTCGTGGTTCTTAGCCCTGCTGC  9059

Qy   9063  ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCGTTGCGGCAAGGTCCGGTGACTGATC  9122
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   9060  ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCGTTGCGGCAAGGTCTGGTGACTGATC  9119

Qy   9123  ATCACTGAGGAGGTTCCCGCCTCCCCCCCCCAGGGGTCTCCCCCGCTGGGTAAAAAGGG  9182
           |||||||||||||||||||| |||||||||||||||||||||||| |||||||||||||
Db   9120  ATCACCGGAGGAGGTTCCCGCCTCCCCCCCCCAGGGGTCTCCCCCGCTGGGTAAAAAGGG  9179

Qy   9183  CCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCCTGTGGTCAAAGCCTGATGGGTGC  9242
           ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   9180  CCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCCTGGTGGTCAAAGCCTGATGGGTGC  9239

Qy   9243  TAATGCACTGCCACTTCCGGTGCGGGTCCTCACTTATAGGCGTATCCTGACTACGGGGC  9302
           ||||||||||||||||||||||||||||||| |||||||||||| |||||||||||||||
Db   9240  TAATGCACTGCCACTTCCGGTGCGGGTCCTCCTACCTTATAGGCGTAATCCTGACTACGGGGC  9299

Qy   9303  TGCTCGCAGAGCCCTCCCCCCGGATGGGGCACTGTGATCTGATGGGTGCACCCC  9362
           ||||||||||||||||||||| |||||||||||| |||||||||||||||||||
Db   9300  TGCTCGCAGAGCCCTCCCCCCGGATGGGGCACTGTGATCTGATGGGTGCACCCC  9359

Qy   9363  GGTAAGAGCTCGGCCCAAAGGCCGGGTTCTACT  9395
           || ||||||||||||||  ||||||::||||||
Db   9360  GGGAAGAGCTCGGCCCGAAGGCCGGGTTCTACT  9392
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RESULT 6
US-08-638-911A-1

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      CLASSIFICATION: 435
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Evans, Susan T.
;       REGISTRATION NUMBER: 38,443
;       REFERENCE/DOCKET NUMBER: 4600-0124
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (415) 324-0880
;       TELEFAX: (415) 324-0960
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 9391 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE: PNF-2161 genome
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 459..9077

US-08-638-911A-1

Query Match     84.9%;  Score 7971.8;  DB 1;  Length 9391;
Best Local Similarity   90.6%;  Pred. No. 0;
Matches 8509; Conservative    0; Mismatches  877; Indels    1; Gaps    1;
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(Sequence alignment data — Qy/Db rows, positions 3–722 on left column and 723–1799 on right column)

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Qy  1803 GGGAGAGGCAACCCGTGCGTCGCCCCTGGTTTGGTTCCTACACCATGACCAAGATC 1862
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Db  1800 GGCCCAGGCAACCCGTGCGTCGCCCTTGGGTTTGGTTCCTACACGCCATGACCAGGATC 1859

Qy  1863 CGGATTCCCTGCATTTGGTGAAATGTCCCACACAGCCATAGAGCCTCCGACTGGAACG 1922
         |||||||| |||| |||| || ||||||||| ||||  ||||||| ||| |||  ||||
Db  1860 CGAGATACCCTACATCTGGTGGAGTGTCCCACCAGCCATTGAGCCTCCCACACCGGACG 1919

Qy  1923 TTCGGGTTCTTCCCCGGAGTCCCGCCCATTAACAACTGCATGCATGCGCCTAGGCAGGAAGTG 1982
         || ||||||||  ||||  |||| |||| | |||| |||||| | ||| ||| |||||||||
Db  1920 TTTGGGTTCTTCCCCGGACGCCGCCGCCTCAACACTGCTTGGGCACCCGGCACGGAAGTG 1979

Qy  1983 TCTGAGGCATTGGCGGGAGCTGGGGTTCACGGGGTTCTACGAGCCTCTGGTTCGCAGG 2042
         ||  |||| ||| || || |||  || |||||||||| ||||||| |||||| ||||||
Db  1980 TCCGGCACTTGGGGCGCTGGGCTGGGGTTCTATGAACCCCTGGTGCTGCGCAGG 2039

Qy  2043 TGTTCGGAGCTGATGGACGCGGAAATCCGTTGCCCGGGGTACGCATGGCTGTCCTCT 2102
         ||||||||||||||| |||||  ||||||||||||||||  ||| ||||| ||||||
Db  2040 TGTTCGAAGCTGATGGGAGAACCGGAAATCCGTTGTCCGGGGTTTCGCGGCTCTCTCG 2099

Qy  2103 GGTAGACCTGACGGGGTTCATACAGTCCAGGGGCACCTGCCAGGAGGTGGATGCGGGCAAC 2162
         ||  ||||| |||| ||| || || ||||| | |||||||||||| |||||| ||||||||
Db  2100 GGCAGGCCTGATGGGGTTTATACATGTCCAGGGGTCACTTGCCAGGAGGTGCACAGGCAAC 2159

Qy  2163 TTCATCCCCTCCACGCTGGTTGCCTTGATTTTGTATTTGTCCTGCTCTATCTGATG 2222
         |||||| ||  ||| |||| | ||  |||| || | || ||||| |||  ||||||
Db  2160 TTCATCCCCGACGGTGCCTGGTTCTTAGATGGTTGTCCTGTTATACCTGATG 2219

Qy  2223 AAGGATGGCTGGACGGTTGGTCCCGTTGATCTTGCTTGCTGTTGGTGTGGTGAAC 2282
         ||||||||||||||||||| ||||||| |||||| |||||| ||||||||||||||
Db  2220 AAGCTGGCTGGACGGTTGGTCCCGCTGATCCTGCTTGCTGTCGTGCTATGTGGGTGAAC 2279

Qy  2283 CAGTTGGCGGTTCTAGGACTGCCGGCGTGTGCAGCCTGTGCCGTGGCGAAGTTTTTGCG 2342
         |||||||| ||||||||||||| ||||||||||||| ||||| |||||||||| |||||
Db  2280 CAGCTGGCAGTTCTCGGGGACTTGCTGGGCGTGTGCAGGTGAGGTCTTCGCG 2339

Qy  2343 GGCCCTGCCTTGTCATGGTGTTGGGGCCTTCCCACTGTCAGTATGATACTAGGTCTAGCA 2402
         |||||||||||  |||||  |||||||||||  |||||||||| ||||| ||||||| ||
Db  2340 GGCCCTGCCTCCGTCGTGGGGCCTTCCCACTGTCAGTATGATATTGGGTTTTGGCA 2399

Qy  2403 AACCTGGTGTGTTGTACTTTCGGTGATGGGCCTCAGCGCCTTCATGTTCCTCGTGTTGTGG 2462
         |||||||||| |||||| || |||||||| ||  ||  |||| |  ||||| ||||||||
Db  2400 AACCTGGTGCGTCTGTTTTTAGATGGTTGGGACCCCAACGCCTGTGTTCCTCGTGTTGTGG 2459

Qy  2463 AAGCTCGCTCGGGGAGCTTTCCCCCTGGCACTTTTGATGGGAGATTTCGGCGACACCCGGGG 2522
         ||||| ||||||||||||||| |||| |||| | |||| |||||| | |||||||||||||
Db  2460 AAGCTTGCTCGGGGAGCTTTCCCCGCTGGCCCTTGATGGGGATTTCGGCGACACCCGGGG 2519

Qy  2523 CGCACCCTGTGTCGCGGGGGCCAGAGGGTGGTGCGGAGGGGGCGTCCTACCCAGAGTTCG 2582
         ||||||||| ||||||||||||||| ||||||||| |||||||||| ||||||| |||||
Db  2520 CGCAATCCGTCAAAGGGGTGGTGAGGAGGGGGCGCCCCAAACCCCTG 2579

Qy  2583 GTGTTGGGGTGGGGTGTGGCGGTGGCGGTGGCTGGCCATATCATAGAGACGTGGTGTAAAGGGTACCAG 2642
         |||||||||| |||||||| ||||| || |||| |||| ||| ||||| |||| ||||||||||||||
Db  2580 GTGTTGGGGTGGGGTGTGGCGGTGGCGGTGGCTGGCCATATCATAGGGTGGTCTATAGGGTGTAAAGGGTACCAG 2639

Qy  2643 AGCCAGGGGGGTGAAGCAGCAAGGGCGTGATCTATAGGGACGTGGTGTAAAGGGTACCAG 2702
         ||||||||  |||||||| |||||||||| |||||||||||| ||| |||||||||||||
Db  2640 AGCCAGGGGGGTGAGGCTGGGCACAAGCCGTGATCTATAGGGACGTGGTGTAAGGGGTACCAG 2699

Qy  2703 GCTGTGCCAGAGGGGTGGTGCGGAGGGGGCGTCCTACCCAGAGTTTTCTG 2762
         ||||||||||||||||||| |||||||||||||||| ||||||||| ||
Db  2700 GCAATCGGTCAAAGGGGTGAGGAGGGGGCGCCCCAGAGGCGCCGGCCAAACCCCTG 2759

Qy  2763 ACGTTCGCCTGGTCGTGCTCATCGGACTCCGGCCTCATACATCTGGCCTGATGATGGTGGTG 2822
         ||  ||||||| |||| ||  |||| ||||||||| |||| || ||| |||||||| |||||
Db  2760 ACCTTTCGCCTTGGCCTTGGCCTTCCGGACTGCTGGCCAGATGCTGTCGATGATGGTGGGTT 2819

Qy  2823 GCCTTGGTCGTCCTCCTCTTCGGACCTCGTTCCGCCGACTGGGCCTCCTG 2882
         ||||||||| |||||||||||| |||| |||||||| ||||| |||||||
Db  2820 GCCTTGGTCCTCCTTCTTCTTTGGACGCGTGTTGGGATTGGGCCTTGGTGTG 2879

Qy  2883 GTCTCCCGGACGCTCGTTACGGCGACTGGCCAGCTGGCACGGGGTGGTTGAGTGCTGTGATGGCGGGGGC 2942
         |||||||| | |||||||| ||||| |||||||| ||| ||||| ||||||||||||||||||
Db  2880 GTGTCCCGGCCCTCGTTGCGGCGTTGGCCGTTGCGCTGGGTGGTTGAGTGCTGTGATGGCGGGGGT 2939
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Qy  2943 GAGAAGGCCACCACCATCCGACTGGTCTCCACAAGTGCGCAAGAGGGCCTACCTGTTT 3002
         ||||||||||||| |||||||||||| || |||||||| |||||||||||| ||| ||
Db  2940 GAGAGTGCCAACCGTCCGGCTGGTCTCCAAGATGTGCGAGAGGAGCTGTTTATTTGTTC 2999

Qy  3003 GACCACATGGGCTCTTTCTCCGCGCGTCGTCAAGGAGGCCTTGTTGGAATGGACGCGCGCT 3062
         ||| ||| ||||| |||| |||| ||| ||||  ||||||| ||||  ||||| ||||||
Db  3000 GATCATATGGGCTCTTTTCGGCGTCGTCAAGGAGGCCCTGGGAATGGACGGACGCACGCT 3059

Qy  3063 TTGGAGCCCTGTCATTCACTAGGACGACTGTCGCATCATCACAGAGATGCCGAGACC 3122
         ||  ||||| ||||||| |||| |||| ||| |||| ||| || ||||||| ||||||
Db  3060 CTTGAACCTCTGTCATTCACTAGGACGACTGTCCGCATCATCACGGATCATACCGGAGACT 3119

Qy  3123 CTGTCCTGCGGACAGTGGTCATGGTGCATGGGTTACCCGGGGTTGCCTCCCGGGTTTGTCCCGACTGCACCA 3182
         || ||||| |||||||| |||||||| |||||||||||| |||||||| || ||||| | ||||||||||||
Db  3120 TTGTCCTGCGGACAGTGGTCATGGTGCATGGGTTACCCGGGTTGCCGCCCGGGTTTGTTCCGACCGCGCCT 3179

Qy  3183 CTCATCGGCGTCTTTCAGGATGTGAATCATTTGCCTCCCGGGGTTCACGAAGGCCTTGACAGGT 3242
         ||||||||||||||| |||||||||||||||||||| ||||||||||| ||||||||||||||
Db  3180 CTCATCCCGACGGTGCGGAAGGGTGCCGAAAGGGTTCACGAAGGGTCACAAAGGTGCCTTGACAGGT 3239

Qy  3243 GTTGTCATCCCGGTGCGGAAACGTCATGGGGACGGCCTCATGGGGTCACGGGGACGCTACGTCACGAGGC 3302
         |||||||||| ||||||||| || ||||||||||||| ||||| ||||| ||||||||| |||||||||
Db  3240 GTTGTCATCCGACGGTGCGGAAGGGTGCCGAAAGGGTTCCTTGGGGTCACAAAGGTGCCTTGACAGGT 3299

Qy  3303 AGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTTGGGGACGCTACGTCACGAAGC 3362
         |||||||||||||  ||||||||||||| ||||||||||| |||||| |||||||||||
Db  3300 CGGGATCCTGACTTACATCCAGGGAACGTCATGGGTTGGGGACGCTACGTCACGTCGCGAAGC 3359

Qy  3363 ATGGGCACATGTCTGAATGGCCTGCTGTTCACAACTTTCCATGGCTTTCATCCCGAACCC 3422
         ||||| || |||||||| ||||||||| ||||| ||||||| |||||||||||||||||||
Db  3360 ATGGGAACATGTCTCAGATCCGACGGGTTGTTCACGACCTTCCATGGCTTCATCCCGAACCC 3419

Qy  3423 ATCGCCACGCCCGTGGGGGCCCTGGGGGCCCTTAATCCCAGTGGTGGTCAGCCAGTGATGACGTCACG 3482
         ||||||||| |||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||
Db  3420 ATCGCCACACCCGTGGGGGCCCTGGGGGCCCTTAATCCCAGTGGTGGTCAGCCAGTGATGTGACGTCACG 3479

Qy  3483 GTGTACCCCGCTTCGACAGTGGGCAACTTCGTTGACGGCCGGAGTCC 3542
         |||||||||| || || ||| ||||||||||||| ||||||||||||
Db  3480 GTGTATCCCCGATGGGCGTACTTGCTTGGTTAACACCTTGGTCTCGTGAGTCC 3539

Qy  3543 TGTTGGGTTATTAGATCCGACGGGCTTTGTCCCATGCTTGAGCAAGGGGACAAGGTT 3602
         |||||||| |||||| |||||||||| | |||| || |||||| ||||||| ||| |
Db  3540 TGTTGGGTCATCAGATCCGACGGGCTTTGTGAGCTCCGTCGTGACTTGCAGCAAGGTG 3599

Qy  3603 GAGCTGGATGTGGCCATGGCCGTCTCGGAGTTCCGTGACTTCCGTGGTCTGCTGTTCACCGGCTCCTT 3662
         ||||||||||||||||||||||||| ||||||||| ||||| |||||||||||||||||| ||||| |
Db  3600 GAGCTGGATGTGGCCATGGCCGTCTCTGGAGTTCCGTGGACTTCCGTGGTCTGCTGTTCACCGGTTCCTA 3659

Qy  3663 TGCGACAAAGGGCACGCAGCTAAGCAATGCTCGTGTCAGTGTCGTCCAACAGAGTGCAAGGGGACCAAGGTT 3722
         |||||||||||||| || ||| |||||||||| ||  |||| ||||||||||| | |||| ||||||||
Db  3660 TGTGACGAAGGGCACCGACACTGGGGAAGTCGTGTGGTGTCGTGTCGTGTCACTCCGGTGGTGGTAGGGTC 3719

Qy  3723 ACTGCCGCGCGATTCACTAGCCGTGATCTATAGGGACGTGGTCAAGACTACCACA 3782
         || ||||| || |||||||||| |||||||||||||| | |||| |||||||||||
Db  3720 ACCGCGCACGGTTCACTAGCCGTGATCTATAGGGACGTGGTCAAATGCCAAAACCACTACT 3779

Qy  3783 GAACCCCTCCCGGTGCGCCGGGCGTCCTACCCAGAGTTTTCAAGGAGTTTATGCCTACG 3842
         |||||||| |||||||||||| |||| ||||| |||||| ||||||| |||||| ||||
Db  3780 GAACCCCGTCCCGGGCGCCGGGCGTCCACCCGGTTTTTTATGCCTACG 3839

Qy  3843 GGGCGGGAAAGAGCACCCGTACCGTTGGAGTACGGCAACATGGCCACAAGGTCTTG 3902
         ||||| ||||||||||| ||| |||||||  ||||||| |||||||||||||| ||
Db  3840 GGAGCGGGAAAGAGCACTGGGGAGTACGATAAACATGGGCCACCAAGGTCTTA 3899

Qy  3903 ATCTTGAACCGTCGGTAGCTACCGTTACCATGGAGCGGCTGCGCG 3962
         ||||||||||||||||| ||||| ||||| |||||||||||||||
Db  3900 ATCTTGAACCCCTCAGTGCCCACTGTGCGCCCGTCACATGGCGCCCGCTACATGGAGCGGCTGCGCG 3959

Qy  3963 GGGAAACACCCCAGTATTTACTGGTGCGTCATGCACACCACTGCTTCACAAGGATCACTGAC 4022
         ||  ||||  ||   | ||||| || ||||||| | ||||||||||||||||||||||||||
Db  3963
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Qy  5103 TACGTCCCGCTGCGATGCGATGCG------------TTGATGTGGTGGGCCTCGCTATTGCGGGGGGCATG 5162
         ||||| ||| |||||| ||  ||             ||  ||||| |||||||||||||||||  |||||||
Db  5100 TACGTCCGCTGCGACGCGTGGCCCGATCTTGATGATCTTGATGATCGGTCAGCTATCGCGGGGGGGGAATG 5159

Qy  5163 ATCTATGGCGTCATACACCCGGTCTCTCGTGGTGTTACAGACTGGGATGTGAACGGGGGT 5222
         |||| ||||||||| ||||||||||||| |||||  ||||  |||||| ||||||||||
Db  5160 ATCTACGGCGTCATCACACCCGGTCTCTCGTGGTGGTACAGACTGGGATGTGAAGGGGGGT 5219

Qy  5223 GGCAGCCCCTTATCGGCATGGGACAGCCGCCACGCCCCCAGCCCGGTGTGCCAGGTCCCC 5282
         |||  |||| ||||||||||| ||||||| |  ||||||||||||  |||||| |  |||
Db  5220 GGCCCCCCTTTATCGGCATGGGACGAGCCGCCACGCCCCAGCCCGGTGTGCCAGGTTCCT 5279

Qy  5283 CCGTAGACCATCGGCCGCGGGGGGAGAGTCTGCGCCATCGGATGCGCAACACAGTGACAGAT 5342
         ||| |||| ||||||||||||||||||||| ||||||| |||| ||||| |||||||||||
Db  5280 CCGGTAGACATCGGCGCGCGGGGGGTGAATCAGCAGCCATCAGATGCGCAAGCAGTGACAGAT 5339

Qy  5343 GCGGTGGCGCCATCCAGTGGATTGCGATTGGTCAGTCATGACCCTGTCGATCGGGAA 5402
         ||||||||  |||||||||||  || |||||||| || |||||| ||| ||||| ||
Db  5340 GCGGTGGCAGCCATCCAGTGGACTGACGATTGGTCAGTCATGACTGACTCGTCGATCGGAGAA 5399

Qy  5403 GTGCTGTCCTTGGCCCAGCTAAGACGGCCGAGCCGTCGGCCAGTTTTCGGCT 5462
         ||| |||||||||| ||||||||||||||||||||| |||||||  ||||||
Db  5400 GTGTTGTCCTTGGCTCAGGCTAAGACGGCCTAAGACGCCCTACAACGCCAAGTGGCTC 5459

Qy  5463 GCTGCTGCTACACGGGGACGCGGCGCCGTCCCACTGTTCAATTGTTGACAAGCTCTTC 5522
         |||||||| |  ||||||||| |||||||||||| ||| ||| |||||||||||| ||
Db  5460 GCTGGCTGTATACGGGGACGCGGCGCCGTCCCACTGTATCCATTGTTGACAAGCTCTTC 5519

Qy  5523 GCCGGGGGCTGGGCGGCGGTAGGCCATTGCCACAGTGTAATAGCTCGGCAGTGGCG 5582
         |||||| || |||||||||| |||||| ||||| || || |||||||| ||||||
Db  5520 GCCGGAGGTGGCGGCGGCTGTGGTTGGCTTCCATTGCCACAGCGTGATTGCTCGGCGGTGGGCG 5579

Qy  5583 GCCTATGGGGGGCTTCTAGGAGCCTTCGCGGCCTTGATCCCACCATT 5642
         |||| |||||||||||| || |||||| |||||||| |||||||||
Db  5580 GCCTACGGGGGGCTTCAAGGAGCCTTCAGCGGCCTTCTTATTGCCACCATT 5639

Qy  5643 GGGGTCGGAGGCAACCGCCAAACCCGCTTAGCCTTCCGCTCTCCTACTAGGGCCGCTGGG 5702
         ||||| ||| ||||| ||  ||||| ||||||| || ||||| |||| |||||| |||
Db  5640 GGGCGTTGGAGGCAACGCGCTCAGACGCGCCTCCTGGCGTCCGCCTCTCTCATTGGGGCGGCTGCTGA 5699

Qy  5703 ACCGCTCTGGGCACGCGCCTGCGTCGTGGGTTCATGGGAAGTGCT 5762
         ||||| ||||||||||| || ||||| |||||| |||||||||||
Db  5700 ACCCGCCTGGGCACCCGTCGTGGTTCGTGGGTTCGGGGGGGGGGGC 5759

Qy  5763 AGGGTCTCCCCCTCCTTGGTCACCATTTTACTGGGGGCCGTTG 5822
         || |||||||||||||||||||||||||| ||||||||||||  ||
Db  5760 AGTGTCTCCCCCTCCTTGGTCACCATTTTATTGGGGGCCGTCGAGGGGTGTT 5819

Qy  5823 GTGAATGCGGCTAGCCTTGTCTTCGACTTTATGGCGGGAAACTATCATCAGAAGATCTG 5882
         ||  |  |||| |||| |||| |||||| || |||||||||||| ||||||| ||| |||
Db  5820 GTCAACGCGGCGAGCCTAGTCTTTGACTTCTTCATGGCGGGGAAACTTTCATCAGAAGATCTG 5879

Qy  5883 TGGTATGGCCATCCCAGTGCTGTAACCAGTGCGGGGATCGCCCTCGGG 5942
         |||||||||||||||||| || ||||| ||||||||| ||||| |||
Db  5880 TGGTATGGCCATCCCAGTACTGACCAGTGCCCTTGCGGGGATCGCTCTCGGG 5939

Qy  5943 TTGGTGTGTACTCAGCTAACAACTCTGCTGCATCCCTGACAGCAGGCAGATTACTGTGAC 6002
         ||| | |||| |||||||||||||| |  |||||| ||||||| |||||| | ||||||
Db  5940 TTGTTTTGTATTCAGCTAACAACTCTGACTCAGCATCCCTGACAGCAGTTGACTATTGCGAC 5999

Qy  6003 ACATTGCCAAGGTCCCATGCATCCCTGACAGTCTGTACTTGTGGGAGTGGATCTGTGAC 6062
         || |||||||||||| ||| |||||| ||||| |||| ||| ||||| |||| | ||||
Db  6000 ACGTTACCAAGGTCTTCATGATCCCGACAGTGGTATCTTGGGAGGTTGACTATTGCGAC 6059

Qy  6063 AAGGTCTCAGCTGTCTCCGACGTTGTCCCTGTCAAC 6122
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Db  6060 AAGTCTCAGCCTCAGCCGAGCCGCACCCGCACCAGTGGTTGCCCGTGTCAAC 6119

Qy  6123 AGGGAGCCTAAGGTGGATGGGTACGTCTGTGGGAGTGGATC 6182
         ||||||||||||||||||||||  | |||||| ||| |||||
Db  6120 AGGGAGCCTAAGGTGGATGGTAGTCTGGGGACCTGTGGGGACTATTGCGAT 6179

Db  3960 GGTAAACATCCAAGTATATACTGTGGGCATGATGATACAACTGCTTCACAAGGATCACTGAC 4019

Qy  4023 TCGCCCCTTACGTATTCCACTTACGGAGGTTTTGGCCAACCCTAGGCAGATGCTGAGG 4082
         ||||| ||| |||||| |  ||  || |||||||| |||||| ||  ||||||||||
Db  4020 TCCCCCTTGACGTATTCAACCTATGGAGGTTTTGGCCAACCCTAGGCAGATGCTACGG 4079

Qy  4083 GGTGTGTCGGTGGTCATTGTGACGAGTGCCACAGTCATGACTCAACTGTGTTGTTGGGC 4142
         || | |||| ||| ||||||| |||||||||||||| ||||| |||  |||  |||||
Db  4080 GGCGTTTGCGGTTGTCATTGTGATGAGTGCCACAGTCATGACTCAACCGTGTTAGGC 4139

Qy  4143 ATTGGGCGTGTCAGGGAGCTGGCCGAGGATGTTGGAGTGCAATTGGTTTCTCTACGGCCACT 4202
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Db  4140 ATTGGGAGAGTCCGGGAGCTGGCCGCGCGTGCGGGGTGCAACTAGTGCTCTACGCACACC 4199

Qy  4203 GCCACCCCCGGGGATGACCCGAGACCCAGCCAGCAAACCCATCAATGAGACAAAACTGAC 4262
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Db  4200 GCTACACCTCCGGATCCCTCATTGACGCAGCAGCACCCTTCCATAATTGAGACAAAATTGGAC 4259

Qy  4263 GTGGGAGAGATCCCTTCTATGGCATGCATCACCTCTTGAGCGGATGTCGGACCGGAAGG 4322
         |||||||| |||||||| |||  ||||  ||||  ||||| ||||| || ||||||||
Db  4260 GTGGGCGAGATTCCCTTTTATGCCATGGGATGGAGTACCCTTCGAGCGGCGGAGTCGAACCGGAAGG 4319

Qy  4323 CATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGCCGCTGGCGCCCAGTTTTCGGCT 4382
         |||||| ||||||||||| |  ||||||| ||||| |||||| |||| |||| ||||||
Db  4320 CACCTCGTGTTCTGCCATTCTAAGGCTGGAGTGCGAGCCGCTGGCGCCAGTTCTCTCGCT 4379

Qy  4383 AGGGGGTAAATGCCATCCCATTACCTATTACGGGGGAAAGACAGTTCTATCATCAAAGATGGA 4442
         ||||||||||| ||||||||| |||  || ||| ||||||  || |||| |||| ||||||
Db  4380 AGGGGGGTCAATGCCATTCCCATTATTAGGGATTAAGGATGGGAAAGACCAGTTCTATTCATCAAGGATGGG 4439

Qy  4443 GACCTGGTGGTGTGTACGACGCCACTATCCACTGGGAACTTCGATTCT 4502
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Db  4440 GACCTGGTGGTGTCTGCGACGCGCTACTACGCCGGGATCTGGGAAAATTTCGACTCC 4499

Qy  4503 GTCACCGATTGTGTAGGTGGTAGTGGTGGAGGAGGTCGTCGAGGTGACCCTTGATCCCACCACCATT 4562
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Db  4500 CACCTCGTGTTCTGCCATTCTAAGGCTGTGGAGGTGCGTCGTTGAGGTGACCCTTGATCCCACCATT 4559

Qy  4563 ACCATCTCCCTGCGCACGGTGCCGCGCGTCGGCTGAACTGTCGACGCGGCGAGGACGC 4622
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Db  4560 ACCATCTCCCTGCGACAGTGCCTGCCGTCGGCTGAACTGTCGATGCGCAAAGACCAGGACGC 4619

Qy  4623 ACGGGTAGGGGCAGGTCTGGGGCGCCGCTACTACGCGGGGTCGCCCAAGGCCCCTGCTGGT 4682
         |||||| ||||||||| ||||| ||| |||||||| || ||| ||||| || || ||  |
Db  4620 ACGGGTAGGGGCAGGTCTGGGGCGCCACTACTACGCGGGTCCGCCCAAGGCCCCGTTGGGT 4679

Qy  4683 GTGGTGGCCTCAGGTCCTCGTGTCGGCGGTGGAAGCCGGTGACCTGGTACGGAATG 4742
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Db  4680 GTGGTGCGCGTCAGGTCCTCGTGTCGGCGGTGGGAAGCTGGAGTGACCTGGTACGGAATG 4739

Qy  4743 GAACCTGACCTGACAGCAAACTACGAGACTTTACGACCACCGAGCGC 4802
         |||| |||| |||||||| |||| |||||||||||| ||||||||| |
Db  4740 GAACCTGACTTGACAGCTTAACCTACTGAGACTTTACGACGACTGCCCTTACACCGCAGCGC 4799

Qy  4803 GTCCAGCTGACAATTGGGGAAGCCCCCGGTGTCTTTTTCCGGGGGCTTGACGGAATG 4862
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Db  4800 GTCCAGCTGACTTGATATCGGGAAGCCGCGGTGTCTTCTTCTTTCCGGGGCTCAACGGAGATG 4859

Qy  4863 CATCCGATGTTAGCTGGCAAAAGTCGGCAAAAGTTCGGCGACCTGGTGGGTGTT 4922
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Db  4860 CACCCGATGTGGGATCGGTCAGCTGGCAAAAGTTCGGCGACCTCGTGGGTGTGT 4919

Qy  4923 CAGCGGACCATGTGCCCGAACCTGTCTCCCCACTCCTGCTCCCGATGACCCCCAGTGGGCA 4982
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Db  4920 CAGCGGACCATGTGCCCGAAACCTGTCTCCCACTCCTGCTCCCGATGACCCCCAATGGGCA 4979

Qy  4983 GGTCTGAAAGGGCCCCGAATCCTGCTCCCACTCCTGCTGAGCCTTGCCAATGATTACCATCT 5042
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Db  4980 GGTCTGAAAGGGCCCCAAATCCTGCTCCCACTCCTGCTGAGCCTCGCCAATGATTACCATCT 5039

Qy  5043 AAAGTGGCCGGCCGCCATCACCATGGGCCGGACGACCTGGTCCTCCGAGCTGGCGCCAGGGGT 5102
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Db  5040 AAAGTGGCCGGCCGCCATCACCATGGGACGACCTGGTCGGTGTCCGGAGAGCTGGGGAGTGGGAGGGT 5099
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;  Sequence 14, Application PC/TUS9506266
;  GENERAL INFORMATION:
;  APPLICANT:
;  TITLE OF INVENTION:   Detection of Viral Antigens Coded
;  TITLE OF INVENTION:   by Reverse Reading Frames
;  NUMBER OF SEQUENCES:  157
;  CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Dehlinger & Associates
;     STREET:  350 Cambridge Avenue, Suite 250
;     CITY:  Palo Alto
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  94306
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US95/06266
;     FILING DATE:
;     CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/246,985
;     FILING DATE:  20-MAY-1994
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/285,561
;     FILING DATE:  03-AUG-1994
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/329,729
;     FILING DATE:  26-OCT-1994
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/344,271
;     FILING DATE:  23-NOV-1994
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/357,509
;     FILING DATE:  16-DEC-1994
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/389,886
;     FILING DATE:  15-FEB-1995
;  ATTORNEY/AGENT INFORMATION:
;     NAME:  Fabian, Gary R.
;     REGISTRATION NUMBER:  33,875
;     REFERENCE/DOCKET NUMBER:  4600-0202.41
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 324-0880
;     TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO: 14:
;  SEQUENCE CHARACTERISTICS:
;     LENGTH:  9391 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  unknown
;  MOLECULE TYPE:  DNA (genomic)
;  HYPOTHETICAL:  NO
;  ANTI-SENSE:  NO
;  ORIGINAL SOURCE:
;     INDIVIDUAL ISOLATE:  HGV-PNF 2161 Variant
;  FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  459..9077
PCT-US95-06266-14

Query Match             84.9%;  Score 7971.8;  DB 5;  Length 9391;
Best Local Similarity   90.6%;  Pred. No. 0;
Matches 8509; Conservative 0;  Mismatches 877;  Indels 1;  Gaps 1;

Qy     3  ACGTGGGGGGGTTGATCCCCCCCCCGGCACTGGGTGCAAGCCCCCATAAACCGACGCCT 62
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ACGTGGGGGAGTTGATCCCCCCCCCGGCACTGGGTGCAAGCCCCCAGAAACCGACGCCT 60

Qy    63  ATCTAACTAGACGCAATGACTGCTCGGCGCCGCGACTCGCGCCCAAAAGGTGGTGGATGG 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   8340  GTGTGCGACCCAGCGACGCGCTTGGGCAGAGACCCTAGCGAGCTATGGTACGCGTGCCGAG 8399
           ||||||||||||| ||||||| ||||| |||||||||||||||||||||||||||||||||
Qy   8403  CCTTCGTATCATGCATCACTGGACACGGCGCCCCCTTCTGCTCCACTTGGCTAGCTGAGTGC 8462

Db   8400  CCCTCATATATCATGCATCATTGGACACGGCGCCCCCTTCTGCTCCACTTGGCTTGCTGAGTGC 8459

Qy   8463  AATGCAGATGGGAAACGCCATTTCTTCCTGACCACGGACTTTCGGAGGCCCCTCGCTCGC 8522
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8460  AATGCAGATGGGAAGGCGCCATTTCTTCCTGACCACGGACTTTCGGAGGCCCGCTCGCTCGC 8519

Qy   8523  ATGTCGAGCGAGTACAGTGACCCAATGGCTTCGGCCATCGGTTACATCCTCCTATACCCT 8582
           ||||||||||||||  |||||||||||||||||||||||||||||||||| ||| ||||
Db   8520  ATGTCGAGCGAGTGAGTATAGTGACCCGATGGCTTCGGCCATCGGTTACATCCTCCTTTATCCT 8579

Qy   8583  TGGCATCCTATCACACGGTGGTCATCATCCTCACGTGCTCACCTGGCGTTTAGGGGT 8642
           ||||| |||| ||| | |||||||||||||||||||||||||||||||||||||||||||
Db   8580  TGGCACCCCATCACACGGTGGTCATCATCCCTCATGTGCTAACGTGCGCATTCAGGGGT 8639

Qy   8643  GGTGGCACACCCTCTGATCCTGTGTGCCAGGTACATGGTAATTACTACAAGTTCCA 8702
           || ||||||||||||||| ||  ||||| || |||||||||||||||||||||||||
Db   8640  GGAGGCACACCCTCGATCCGGTTTGTGCCAGGTGCATGGTAATGTAACTACTACAAGTTCCA 8699

Qy   8703  CTGGACAAAACTGCCTAACATCATCGTTGGCCCTCCACGGACCAGCAGCGTTGAGGGTTACC 8762
           ||||||||||| ||||||||||||| |||||| |||||||||||||||||| ||||||||||
Db   8700  CTGGACAAACTGCCTTAACATCATCGTGGCCCTCCACGGACCAGCAGCGTTGAGGGTTACC 8759

Qy   8763  GCAGACACAACTAAGACAACAAAAATGGAGGCTGCTGCAAGGTGCTGAGGCGACCTCAAGCTCCCT 8822
           ||||||||||||| |||||||||| |||| || |||||||||||| ||||||||||||||
Db   8760  GCAGACACAACTAAAACAACAGAAGATGAGGCTTCTGAGCCGACCTCAAGCTCCCT 8819

Qy   8823  GGCCTAGCAGTCCACCGGAAGAAGGCCGGGCGCATTGCGAACGCGTATGCTCCGGTGCGCGC 8882
           ||| |||||||||||||||||||||||||| |  |||||||| | |||||||||||| |||
Db   8820  GGCTTAGCAGTCCACCGGAAAGAAGGCCGGGGCGTTGCGAACACGCATGTCTCCGCTCGCGC 8879

Qy   8883  GGTTGGGCTGAGTTGGCTAGGGGGTGTTGTTGGCGTTCCAGGCCTGCGGCCTTCCCCCTCCG 8942
           |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   8880  GGTTGGGCTGAGTTGGCTAGGGGGTTCATTGTTGTGCATCCAGGCCTACGGCCTTCCTCCCCCCT 8939

Qy   8943  GAGAGTTGCTGGTATCCCGGGGGTTCCCCCTTCCCCCCCTATATGGGGTGGTTCAT 9002
           |||||||||||||||||||||| |||||||||||| |||||||||||||||||| |||
Db   8940  GAGATTGCTGGTATCCCGGGGGTTCCCCTCTCCCCCCCTATATGGGGTGGTGGTTACAT 8999

Qy   9003  CAATTGGATTTCACAAGCGTCGCTGGCGAGTGCGCTGGCCGTGGGTTCTTAGCCCTGCTC 9062
           |||||||||||||||||||||||||| ||||||||||| | |||||||||||| |||||
Db   9000  CAATTGGATTTCACAAGCGTCGCTGGCGAGTGCGCTGGCCGTGGGTTCTTAGCCCGTGCTC 9059

Qy   9063  ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGGCAAGTCCGTGACTGATC 9122
           |||| ||||||| ||||||||||||||||||| |||||||| ||||| ||||||| |||
Db   9060  ATCACCGGAGGAGGTTCCCGCCCAGGGGTCTCCCCGCCCCAGGGGTCTCCCGCCCCTGGGTAAAAAGGG 9119

Qy   9123  ATCACTGGAGGAGGTTCCCGCCCAGGGTCGTTGTTACTAACCCCCTGGCAGGGTGGTGTGC 9182
           ||||| |||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   9120  ATCACCGGAGGAGGTTCCCGCCCCAGGGGTCTCCCGCCCCTGGGTAAAAAGGG 9179

Qy   9183  CCCGGGCCTTGGGAGGCATGGTGTTACTAACCCCCTGGCAGGGTCAAAGCCTGATGGTGC 9242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9180  CCCGGGCCTTGGGAGGCATGGTGTTACTAACCCCCTGGCAGGGTCAAAGCCTGATGGTGC 9239

Qy   9243  TAATGCACTGCCACTTCGGTGGCGGTCGCTGCACTGTGATCTGAAGGGGTGACTACGGGC 9302
           ||||| ||||||||||||||||||||||||||||||||| |||| |||||||||||||||
Db   9240  TAATGCACTGCCACTTCGGTGGCGGTCGCTGCACTGTGATCTGAAGGGGTGCACCGGGC 9299

Qy   9303  TGCTCCGCAGAGCCTCCCCAGATGGGGCACAGTGCACTGGGGTGCACCCC 9362
           |||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   9300  TGCTCCGCAGAGCCTCCCCGGATGGGGCACAGTGCACTGGGGTGCACCCC 9359

Qy   9363  GGTAAGAGAGCTCCGGCCCAAAGGCCGGGT 9389
           |||| |||||| || ||||||||||||||| |
Db   9360  GGGAAGAGCTCGGCCCCCAAGGCCGGGGTT 9386

RESULT 7
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Db    61  ATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCGGCCCAAAAGGTGGTGGATGG  120

Qy   123  GTGGTGACGAGGGTTGGTAGGTCGTAAATCCCGGTCATCCTGGTAGCCACTATAGGTGGGT  182
          ||| |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   121  GTGATGACGAGGGTTGGTAGGTCGTAAATCCCGGTCACCTGGTAGCCACTATAGGTGGGT  180

Qy   183  CTTAAGAGAAGTCAAGACTCCTCTTGTCGCGCGAGACCGGCACGCGTCCACAGGT  242
          |||||||||  ||||  |||||||||||||||||||||||||||||||||||||||
Db   181  CTTAAGAAGGTTAAGATTCCTCTTGTCGCGCGAGACCGGCGACGCGTCCACAGGT  240

Qy   243  GCTGGCCCTACCGGTGTGAATAAGGGCCGACAGTCAGCTCGTCGTTAAACCGAGCCCGT  302
          | ||||||||||| ||  || |||||||||| |||||||||| |||||||||||||||
Db   241  GTTGGGCCCTACCGGTGGGAATAAGGGCCGACAGTCAGCTCGTCGTTAAACCGAGCCCGT  300

Qy   303  CACCCACCTGGGCAAACAGCAGCACGTACGGTCCACGTACGGTCGCCGCCTTCAATGTCTCTTG  362
          ||||||||||||||||||  |||||||||||||||||||||  ||||||||||||||||||
Db   301  TACCCACCTGGGCAAAACGACGGCCACGTACGGTCCACGTACGGTCGCCGCCTTCAATGTCTCTTG  360

Qy   363  ACCAATAGGTTTATCCGGCGAGTGACAAGGACCAGTGGGGGCCGGGGGTTATGGGAAG  422
          ||||||||| ||  ||||||||||||||||||||||||| | ||  ||  ||||||||
Db   361  ACCAATAGGCGTAGCCGGCGAGTGACAAGGACCAGTGGGGGCCGGGGGGCT-TGGAGAGG  419

Qy   423  GACCCCAAAACCCTGCCCTTCCCGGTGGGCCGGGGAAATGCATGGGGCCACCCAGCTCCCG  482
          |||||||||| |||||||||  ||||||||||||||||||||||||||||||||||||||
Db   420  GACTCCAAGTCCCGTGGGCCGGGGAAATGCATGGGGCCACCCAGCTCCCCG  479

Qy   483  GCGGCCTGCAGCCCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGCAATTGCTGTGCC  542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480  GCGGCCTGCAGCCCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGCAATTGCTGTGCC  539

Qy   543  TTCTATACCATCATGGCAGTCCTTCCTGCCTCCTGGTTGGCCTGCGGCCTGGCAATTCTG  602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540  TTCTATACCATCATGGCAGTCCTGTCTCGGCGGGTTGGCCTGCGGCCTGGCAATTCTG  599

Qy   603  GCCCCGGCCACCCACGCTTGTGCGAGCCAATGGGCAATATTCCTCACAAATTGCTGTGCC  662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   600  GCCCCGGCCACCCACGCTTGTGCGAGCCAATGGGCAATATTCCTCACAAATTGTTGTGCC  659

Qy   663  CCGGAAGACATCGGGTTCGCTGGTGGGGGCGGAGTGGCGGCCTGTTACTCCGGGTGCACGGTT  722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   660  CCGGAGGACATCGGGTTCGCTGGTGGGGGCGGAGTGGCGGCCTGGTGCCTTGGGGTGCACGATT  719

Qy   723  TGCACCGACCGGTTGCTGGCCACTGTATCAGGCGGTTTGGCTGCGGCCTGGCAAGTCC  782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   720  TGCACTGACCAATGCTGGCCACTGTATCAGGCGGTTTGGCTGCGGCCTGGCAAGTCC  779

Qy   783  GCGGCCCCAGCTCGTCGTTGGGGAACTGGGGAGCCTGTGTACCGGCCTGTCGGTCTCGGCGTTAC  842
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   780  GCGGCCCCAACTGGTGGGGGAGCGTGGGCTGGGGTAGCCTATACGGGGCTGTCGGTCTCGGCGCCTAT  839

Qy   843  GTAGCCCGGGGATCCTGGGCTGGGGCGAGGGTTTACTCCGGGTGGTGTGTTGGCG  902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   840  GTGGCTGGGGATCCTGGGGTCTGCCTGGAGCGTGGGGTGGGAGTCGGCG  899

Qy   903  TTGAGGGCCCGGGGTCACCGGTGTCTGCTGGCCACTGACGATAGAATGTGACGTTAAG  962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   900  TTGACGGCGGCCCGGGGTCACCGGTGTCTGCTGGCCACTGACGATGGGTGTGCGTCGAGCCTAAAG  959

Qy   963  TGGGGAAGTGAGTTTTGGGCAGGAGTGACGCTGAGCAGTGGCCTCCAATTACTGGATTTTCTGGAA  1022
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   960  TGGGGAAGTGAGTTTTGGGCAGGAGTGACGCTGAGCAGTGGCCTCCAATTACTGGATTTTCTGGAA  1019

Qy  1023  TACCTTTGGAAAGTCCCATTTGAATTTGCTGGAGGAGTCCATTTGGAGAGAGTCCCCTTGTTGCG  1082
          ||||||| ||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db  1020  TACCTCTGGAAGGTCCGAATTCTGGAGAGGCGTGATAAGCCTGAGTCGACCCCCTTGTTG  1079

Qy  1083  GTTTGAGGTGGCCCCATTGCTTTTGCTGGCAACGGATTGTCATGGTTTTTCCTGCTGTG  1142
          ||||||||||||||||||  |||||||||||||||||||||||||||||||||||||
Db  1080  GTTTGCGGTGGCCCCATTGGTGCTGCTGGCAACGGATTGTCATGGTGTTCTTCCTGCTGTTGGTG  1139

Qy  1143  ACGATGGCGGGGATGTTGCAAGGCGCCCCCCTGCCTCCCCGGCCCCTTTGAC  1202
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140  ACGATGGCGGGGATGTTGCAAGGCGCCCCCCTGCCTCCCCGGCCCCTTTGAC  1199


Qy  1203  TACGGGTTGAAGTGGCAGTCATGCTCCTGCGCAGGCGTCATGTCCTCGCGGTATTCCCACTGGG  1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200  TACGGGTTGACTTGCGACCTGCTCTTGCGAGGCGCAACCGTTTTTCGGTTTCGACTGGG  1259

Qy  1263  GAGAGGGTGTGGGATCGCAGAGGGAAGTGTCAGCGTCCTGTGTGACTGACCGCACCGGCCCCTGG  1322
          ||| ||||||||||||||||||||| |||||||||  ||||||||||||||||||||||||
Db  1260  GAGAAGGGTGTGGGACCGGTGGGAACGTTAGCGTTCAGTGTGACTGACTGGGACCGCCCCCTGG  1319

Qy  1323  GTTTGGGTCCCGGCCTTTTGCCAGGCGGTCGGCGGTGGGGCGGCCACCCATCACCCATTGGAGC  1382
          |  ||| || ||||||||||||||||||||||||| || |||||||||| ||||||||||||
Db  1320  GTGTGTGGTGCCAGCCTTTTGCCAAGCAATCGGCGGTGGGGTGACCCCATCACCCATCACTTATTGGAGC  1379

Qy  1383  CACGGACAAAACCAGTGGCCCCTATCATGCCCCAATATGTCTCATGGGTCTGTGTCCCGTA  1442
          ||||||||||||||||||||||||||||||||||||||||||  ||||||||| |||||
Db  1380  CACGGGCAAAAATCAGTGGCCCCTTTCATGCCCCCAGTATGTCTCATGGGTCTCATGGGTCGTACAGTC  1439

Qy  1443  ACGTGCGTGTGGGGTTCCGTGTCTTGGTTTGCCTGCGACCCGCGGTCGTGATTCGGAAGATC  1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db  1440  ACTTGCGTGTGGGGTTCCGTGTCTTGGTTTGCCTTCCACCAGTGGTCGCGGACTCGAAGATA  1499

Qy  1503  GATGTGTGGAGTTTGTGCGTGATCGGCCACGTGCACCTGCACCATAGCCGTCTAGGGTCA  1562
          ||||||||||||||||||||||||||||| || || |||||| ||||||||||||||||
Db  1500  GATGTGTGGAGTTTAGTGCCTGCTGCCAGTTGCTTGCCACCACTTGCCACTTGGATCA  1559

Qy  1563  TCGGATCGCGACACGGTGTTGAGCTCTCCGAGTGGGGAGTCCCGTGCGTTAACGTGTGTATT  1622
          ||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
Db  1560  TCGGATCGCGACACGGTGCCGTGGGGTGGGAATCCCGTGGGACTGCCGTGCGTGACGTGTGTT  1619

Qy  1623  CTGGACCGTCTCGGCCGTCGCTGCTCTCATGTGGCACCGTGTGTGGGGGACTGTGCCCGAAACCGGG  1682
          |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db  1620  CTGGACCGTCGCGGCCGTGCCTGGCGGCGCCACCGTGTGAGGGACTGTCGCCGAGACCGGG  1679

Qy  1683  TCGGTTAGATTCCCTTCCATCGGTGCGGCCGCCTCGGTGACAAAGGACTTGGAA  1742
          ||||| |||  || |||||||||||||||||||  |||||||||| ||||||||
Db  1680  TCGGTTAGGTTCCCATTCCATCGGTGCGGCCGTGGGCTGACAAAGGACTTGGAA  1739

Qy  1743  GCTGTGCCCTTCGTCAAGCAGGACAACTCCCTTTCAACAGGACACTCCCCTGGGCAACCAG  1802
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1740  GCTGTGCCCCTTCGTCGTCGTCAACAGGACAACTCCCTTTCAACTTAGGGGCCACCAG  1799

Qy  1803  GGGAGAGGCAACCCGGTGGCCTGGGTGGGCTCCTACACCATGACCAAGATC  1862
          ||||||||||||||||| ||||||||||||||||||||| ||||||||||
Db  1800  GGCCCAGGCAACCCGGTGGCCTGGGTCCTCGTCCTACGTCCGTACCACCAGGATC  1859

Qy  1863  CGGGATTCCCTGCATTGGTGAAAATGTCCGTGTAGAGCCTCCGACTGGAACG  1922
          ||| ||  |||||||| |||||||| |||||||||||||||| ||||||||
Db  1860  CGAGATACCCTACATCTGTGGAGTGTCCCACCAGCCATTGAGCCTCCACCGGGACG  1919

Qy  1923  TTCGGGTCTTCCCGGAGCTCCCGCCATTAACAACTGCATGCGCGTGGCACCGGAAGTG  1982
          ||||||| ||||||||  |||||||||||||||||||||||| ||||||||||||||
Db  1920  TTTGGGTTCTCCCCGGACGCCGGCTCTTGGGGCTCTTGGGCACATGCACGGAAGTG  1979

Qy  1983  TCTCGAGGCATTGGGCGAGCTGGGCTGGGGGTTCTACGAGCCTCGGTTCGGTTCCCAGG  2042
          || ||||||||||||||||||||||||||  |||||||||||||||||||| ||||||
Db  1980  TCCCAGGCACTTGGGGGGGCGGGGTTCTCATGAACCCCCTGGTGTCGGTGTCCCAGG  2039

Qy  2043  TGTTCGGAGCTGATGGAGACGCCGGAAATCCGGTTGCCCGGGTACGGCTGCGTGCCTCT  2102
          ||||||||||||||||||  |||||||||||||||| | ||||| ||||||||||
Db  2040  TGTTCGGAGCTGATGGGAAGCCGGAAATCCGGTTTGTCCATGGCTCCTTCG  2099

Qy  2103  GGTAGACCTGACGGGTTCATCACGTTCAGGGGCGACTGATGGATGCGGGCAAC  2162
          |||||||| ||||||| ||| ||| ||||||||||||||||||||||||||||
Db  2100  GGCAGGCCTGATGGGGTTTATACATGTCACCGGTTCACTTGCAGGCGGCAGCCGCAAC  2159

Qy  2163  TTCATCCCTCCTCCCACGCTGGTTGCCTCTTGGATTTTGTATTTGTCCGCTGCTCTATCGATG  2222
          ||||||||||||||||||||  |||||||||||||||||||||||| |||||| ||||||
Db  2160  TTCATCCCGCCCCCGCCGGCTGGTTGCTTCTTGGACTTTGTATTTGTATTCCTTGTTGCTGCTGATG  2219

Qy  2223  AAGCTGGCTGAGGCACGGTTGGTCCCGGTTGATCTTGCTTCTGCTGTGGTGAAC  2282
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2220  AAGCTGGCTGAGGCACGGTTGGTCCCGGTTGATCTTGCTGTCTGCTGTGGTGGTGGAAC  2279
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Qy  2283  CAGTTGGCGGTTCTAGGACTGCCGGCTGTGGACGCTGCCGTGGCGGTGAAGTTTTGCG  2342
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Db  2280  CAGCTGCCAGTCCTAGGGCTGCCGGCTGCCCGGCTGTGGAAGCCGGCCGTGGAGGTCTTCGCG  2339

Qy  2343  GGCCCTGCCTTGTCATGGGTGTTTGGGCCTTCCCACTGTCAGTATGATATGATAGGTCTAGCA  2402
          |||||||||||||||||||||||||||| ||  |||||||||||||||||||||||||
Db  2340  GGCCCGAGCCTGCGCCCGTGTCCCGGGACTCCCGGGTGTCAGTATCGTCAGTATGATATTGGCA  2399

Qy  2403  AACCTGTTGTGTACTTCGGTGGATGGGCCCTCAGCGCCTCATGTTCCTCGTGTTGTGG  2462
          ||||||||||||| | ||| | |||||||||||||| |  ||||||||||| | |
Db  2400  AACCTGGTGCTGTTTAGATGGTTGGGACCCCAACGCCTGATGTTCCTCGTGTTGTGG  2459

Qy  2463  AAGCTCGCTCGGGGAGCTTTCCCGCTGGCCACTTTGATGGGGGATTTCGGCGACACTTCG  2522
          |||||||||||||||||| |||||||||||| |||| |||||||| |||||||||||||
Db  2460  AAGCTTGCTCGGGGGAGCTTTCCCGCTGGCCCTCTGTGATGGGGGATTTCGGCGACACCGGG  2519

Qy  2523  CGCACCTCGTGTCGGGGCCGAGTTCTGCTTGCGATGTCACATTCGAGGTGGACACTTCG  2582
          |||||||||||||||||||||||||| |||||| ||||||| ||||||||||||||||
Db  2520  CGCACCTCCAGTGCTCGGGGCCGAGTTCTGCGTGCTCGATGCTCGAGGTGGACACTTCG  2579

Qy  2583  GTGTTGGGCGTGGTGGTGCCAGCCGTGGTGGCCCATGAGCCTCGGCCCATCGAGCCTCAATG  2642
          | | ||||||||||||||||||||||||||||| |||||||||||||| |||||||||||
Db  2580  GTGTTGGGCGTGGTGGTGCCAGCTGTGGTGGCCCATGAGCCATTCGGCCTTCGAGCCTCGATG  2639

Qy  2643  AGCGCAGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACCGTGTGTAAAGGGTACCAG  2702
          |||||||||| |||||||||| ||||||||||||||| |  ||||||||||||||||||
Db  2640  AGCGCAGGGGAGGGGTGGAGGCACAAAGCCGTGATCTATAGGGGGTGTAAGGGGTACCAG  2699

Qy  2703  GCTGTGCCAGAGGTGGTGCGGAGCCCCCTCGGGGAGGGCGTCTACCAAGGTTCTG  2762
          |  ||| || ||||||||||||||||||||||||||||||| |||||||||||||
Db  2700  GCAATCCGTCAAAGGTGTGGCGGAGCCCCCTCGGGGAGGGCCCTGCCAAACCCCTG  2759

Qy  2763  ACGTTCGCCTGTGCTTGGCCTCATACATCTGGCCGATCTGTGTCGATGATGGTGGTG  2822
          |  ||||||||||||||||||| ||||||||  ||| |||||| |||||||||||||
Db  2760  ACCTTTGCCTGTGCTTGGCCTCTATACATCTGGCCAGATGCTGTGATGATGGTGGTT  2819

Qy  2823  GCCTTGGTCTCCTCCTTCGCGACGGCACTGGTTCGAGGAGCTCCTG  2882
          |  ||| || ||||||||||||||||| |||||||||||||||||
Db  2820  GCCTTGGTCTCTTTCGCGTGTCGTGTCCTTGGATTGGGAGGAGATCTTG  2879

Qy  2883  GTCTCCCGGCCCTCGTTACGGTGGCACGGGGCGTCGTGTGAGTGTGTGATGGCGGGC  2942
          | | ||||||||| |||  ||| ||||||| |  |||||||||||||||||||||||
Db  2880  GTGTCCCGGCCCTTGTTGGCGGTTGCGGTTGCCTCGGGTGTGTGTGATGGCGGGGT  2939

Qy  2943  GAGAAGGCCACCACCATCCGACTGGTCTCCAAGATGTGCGCAAGAGGGGCTACCTGTTT  3002
          | ||||||||||||| |||||||||||| ||||||||||| |  ||||||||||| |
Db  2940  GAGAAGGGCCACCAACCGTCCGGCTGGTCTCCAAGATGTGTCGCCGAGAGGAGCTTATTTGTTC  2999

Qy  3003  GACCACATGGGCTCTTTCTCGCGGCTCTTGTTGCGACGAGCGCGGCGGCC  3062
          ||||||||| |||| |||||||||||| |||||  ||||||||||||||
Db  3000  GATCATATGGGCTCTTTTCGCGTCGTGTCAAGGAGCGCGGCGGACCAGCT  3059

Qy  3063  TTGGAGCCCCTTGTCATTCATTACTAGGACGACTGTCGCATCATCAGAGATGCCGCGAGGACC  3122
          | ||||| |||||||||||||||||||||||||||||| |||| ||||||||||||||||||
Db  3060  CTTGAACCTGTCGTTCATTCATTACTAGGACGACTGTCTTCGCCCATCATCAGGGATGCCGCGAGGACT  3119

Qy  3123  CTGTCCTGCGGACAGTGCGTCATGGGGTTTACCCGTGCCCACGCCGGCGTGATGAGGTT  3182
          ||||||||| |||  || || |||||||||||| ||||||||||||| ||||||||||
Db  3120  TTGTCCTGCGGGATGTGCGTCATCGGGTTTCATTGGTCCCGCCGTGGTTGATGAGGGT  3179

Qy  3183  CTCATCGGCGTCTTTCAGGATGTGAATCATTTGCCTCCCGGTTTCTCCCACTGCACCA  3242
          ||||||||||||||||||||||||||||||||||| |||||||||  ||||||||||
Db  3180  CTCATCGGCGTCTTTCAAGATGTGAATCATTTTATGGGCATGGAATACCCCTGCGAGCT  3239

Qy  3243  GTTGTCATCCGTGCGGTGCGGAAAGGGCTTCTCGGGGTTCACGAAGGCAGCCTTGACAGGT  3302
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||  ||||
Db  3240  GTTGTCATCCGTGCGGTGCGGAAAGGGCTTCTCAGGGTTCACGAAGGCAGCCTGCCACC  3299

Qy  3303  AGGGATCCTGACTTACATCCAGGGAACGTGTTGGGGACGGTGTTGGGGACGGCTACGTCACGGAAGC  3362
          ||| ||||||||||||||| ||| ||||||| |||||||||||  |||||||||||||||||
Db  3300  CGGGGATCCTTACATCCAGGGAACGTGTTGGGGACGGCTACGTCGCCGAAGC  3359

Qy  3363  ATGGGCACATCTCGAATGGCCTGCTTGTTCACAACTTTCACATCCCGAACC  3422
          |||||| |||||||||||| | || |  |||||||||||||||||||||||
Db  ...                                                  ...
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Db  3360  ATGGGAACATGTCGGGGGCCCTTAATCCCAGGCTGGTCAGCCAGTGATGACGTCACG  3419
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3423  ATCGCCACGCCCGTGGGGCCCTTAATCCCAGGCTGGTCAGCCAGTGATGATGTCACG  3482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3420  ATCGCCACACCCGTGGGGCCCTTAATCCCAGGCTGGTCAGCCAGTGATGATGTCACG  3479

Qy  3483  GTGTACCCGCTTCCAGATGGGCAACTTCGTTGACCCCTGCACTTGCCAGCGGAGTCC  3542
          ||||||||||||||||||||||||||||||||||| | |||||||||||||| |||
Db  3480  GTGTATCCACTTCCCGATGGGCTACTTCGTTAACACCTGTACTTGCCAGCGGAGTCC  3539

Qy  3543  TGTTGGGTTATTAGATCCGACGGGGTTTGTGCCATGGCTTGAGCAAGGGGACAAGGTT  3602
          ||| |||| ||||| ||||||||||| |||||||||||| |||||||||||||||||
Db  3540  TGTTGGGTCATCAGATCCGACGGGGTCTGTGCCATGGCCTGAGCAAGGGGACAAGGTC  3599

Qy  3603  GAGCTGGATGTGGCCATGGAGCTCTGACTTCCGTGTTCGTGTCTGTCCACTCCTCTT  3662
          |||||||||||||||||||||||||| ||||||||||||||||||||||||| ||||
Db  3600  GAGCTGGATGTGGCCATGGAGCTCTCCGTGTTCTCCGTGTCTGTCTCCGGTTCCTA  3659

Qy  3663  TGCGACAAAGGGCACCGCAGTAAGAATGCTCGTCGTCAGTCGTCCACCTGGGCGCAGGGTT  3722
          ||||| || ||||||||||| |||||||||||| ||||||| |||||| |||||||||||
Db  3660  TGTGACCAAGGGCACCGCAGTAGGAATGCTCGTCGTCTGTCGTCTCCGTGTGGTAGGGTC  3719

Qy  3723  ACTGCGCGCGATTCACTAGGCCGTGACTCAAGTACCAACAGATGCCAAGACTACCACCA  3782
          |||||||||||||||||||||||||||||||||||||  |||| ||||||||||||||
Db  3720  ACCGCGCGCCACGTTCACTGGCCGTGACCCAAGTGCCAACAGATGCCAAACCACCACTACT  3779

Qy  3783  GAACCCCCTCCGGTGCCGGCAAAAGAGTTTTCAAGGAGGCCCGTTTATGCCTACG  3842
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  3780  GAACCCCCTCCGGTGCCGGCCAAGGAGTTTTCAAAGAGGCCCGTGTTTATGCCTACG  3839

Qy  3843  GGGCGGGAAAGAGCACCCGGTACCGGTCAACGATGGGCCAACATGGGCCACAAGGTCTTG  3902
          ||||||||||||||||||||||||||| ||  ||||||||||||||| ||||||||||
Db  3840  GGAGCGGGAAAGAGCACTCGCGTCCCGTGGAGTACGGCACGATAACATGGGCACAAGGTCTTA  3899

Qy  3903  ATCTTGAACCCCGGTAGCTCCGGTGTGAGGGCCCATACATGGAGCGGCTGGCGG  3962
          |||||||| ||||| ||||||| | | |||||||| ||||| |||||||||||
Db  3900  ATCTTGAACCCCTCAGTCGGCCCACTGTGCGGCCCATGGGCCCGTACATGGAGCGGCTGCGGCG  3959

Qy  3963  GGGAAACACCCCAGTATTTACTGTGGCCATGACGACCACTGCTTTCACAAGGATCACTGAC  4022
          |  ||||||  ||||||| | ||||||||||||| | | | ||||||||||||||||||||
Db  3960  GGGTAAACATCCAAGTATATACTGTGGCCATGACGATACAACTGCTTTCACAAGGATCACTGAC  4019

Qy  4023  TCGCCCCTTACGTATTCCACTTACGGAGGTTTTTGGCCAACCCTAGGCAGATGCCTGAGG  4082
          |  ||| ||||| ||||||||||||||| ||| | |||||||||||||||||||||||||
Db  4020  TCCCCCCTGACGTATTCAACCTATGGGTTGGGTGGTCCAACCCTAGGCGAGATGCTACGG  4079

Qy  4083  GGTGTGCGGTGGTCATTTGTGACGAGTGCCAGTCATGACGTCAACTGTGTTGTTGGGC  4142
          || ||| ||| ||||| | ||||| ||||||||||||| ||||||||  ||||||||
Db  4080  GGCGTTTCGGTGGTCATTTTGTGATGAGTGCCACAGTCATGGGCTGTGTCGTGTAGGC  4139

Qy  4143  ATTGGGCGTGTCAGGGAGCTGGCCGGAGGATGTGAGTGCCAATTGGTGCTCTCACGCCACT  4202
          |||||||||||||| ||||| | ||| |  || |||||||| |||||||| || ||||||
Db  4140  ATTGGGGAGTCCCAAGGTACTCAAGGTCGCGGTCCGAGGCGTGGGTGCCACTAGTTGCTCTACGCCACC  4199

Qy  4203  GCCACCCCGATCCCCGGATCCCCAGACCAGCCATCAATCATTGAGACAAAACTGGAC  4262
          ||||||||||||||||||||| ||||||||| |||||| || ||||| ||||||||
Db  4200  GCTACACCCCGGATCCCCAGATCCCCATAATTCCATAATTGAGACAAAATTGGAC  4259

Qy  4263  GTGGGAGAGATCCCCTCTATGGCAGATGGCATGGAACGGAGGCGGACCGGAAGG  4322
          ||||| || |||||||  |||  |  |  |||||| |||||||||||||||||||
Db  4260  GTGGGCGAGATTCCCTTTTATGGGCATGGCATGGAATACCCCGAGCGGACCGGAAGG  4319

Qy  4323  CATCTCTATTCTGCCCACTCCAAGGCTACCTTGACCAGGGTTTCCGGCT  4382
          |||| ||||| ||||||||||||| ||  | | ||||||||||||||||
Db  4320  CACCTCGTGTTCCAAGTCCAAGGCTCGAGCCCTTGTCTGCTCTCCGGCT  4379

Qy  4383  AGGGGGTAAATGCCATCGCCTATTACAGGGGGAAAGACAGTTCTATTCATCAAAGATGGA  4442
          |||||||||| || |||| |||| ||||| |||||| |||||||||||||||||||||||
Db  4380  AGGGGGGTCAATGCCATTGCCTATTATAGGGGTAAAGACAGTTCTATTCATCAAGGATGGG  4439

Qy  4443  GACCTGGTGTGTGTCTACAGACGACCTCCACTGGGTACACCTCCACTGGAACTTCGATTCT  4502
          ||||||||||||||||||||||||| |||||||||||||| |||||||||||||||| ||
Db  ...                                                          ...
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Db  4440 GACCTGGTGGTCTGTGCTACAGACGCGCCTTTCCACTCGGTACACTGGAATTTCGACTCC 4499

Qy  4503 GTCACCGGATTGTGGGTTAGTGGTGGAGGAGGTCGTCGAGGTGACCGTTGATCCCACCATT 4562
         ||||||||    ||||||||| |||||||||||||||| || |||||||| ||||||||||
Db  4500 GTCACCGACTGTGGATTAGTGTGGCGGAGGAGGTCGTTGAGGTGACCGTTGATCCCACCATT 4559

Qy  4563 ACCATCTCCCTGCCACGGTGCCCGCTGCGGCTGAACTGTCGATGCGGCGAGGACGGC 4622
         |||||||||||| ||||||||||||||||||||||||||| |  ||||||||||||||
Db  4560 ACCATCTCCCTGCGCTGCCCGCTGCGGCTGAACTGTCGATGCGGCGAGGACGGC 4619

Qy  4623 ACGGGTAGGGCAGGTCTGGGCGCGCTACTACTACCGCGGGGGTCGGCAAGGCCCCTGCTGGT 4682
         ||||||||||||||||||||||||||||||||||||| |||||||||||||||||| |  | |
Db  4620 ACGGGTAGGGCAGGTCTGGACGCGCTACTACTACCGCGGGGTCGGCAAAGACCCCTGCCGGT 4679

Qy  4683 GTGGTGCCGCTCAGGTCCTGCTGTCGGCGGTGGAAGCCGGTGTGACCTGTACGGGAATG 4742
         |||||||||||||||||  |||||||| ||||||||||||||||||||||||||||||||
Db  4680 GTGGTCGCGCTCAGGTCCTGCTGTCGGCGTGGAAGCTGGTGTGACCTGTACGGGAATG 4739

Qy  4743 GAACCTGACCTGACAGCAAAACTACTGAGACTTTACCACAACTGCCCTTACACCGCAGCC 4802
         |||||||||||||||||||||| ||| |||||||||||||||||||||||||||||||||
Db  4740 GAACCTGACCTGACAGCTAACCTACTGAGACTTTGACCACGACTGCCCTTACACCGCAGCC 4799

Qy  4803 GTCGCAGCTGACATTGGGGAAGCCGCGGCGGTGTTCTTTTCGGGGCTTGCCCCGTTGAGGATG 4862
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4800 GTCGCGGCTGATATCGGGGAAGCCGCGGCGGTGTTCTTTTCGGGGCTGCCCCGTTGAGGATG 4859

Qy  4863 CATCCCGATGTTAGCTGGCAAAAGTTCGCGGCGTCAACTGGCACACTGGTTACACCGCAGCTG 4922
         ||  || ||||||| ||||||||||||||||||| ||||||||||||||||||||||||||||
Db  4860 CACCCTGATGTTCAGCTGGCAAAAGTTCGCGGCGTCAACTGCACACTGGTTACACCGCAGCTG 4919

Qy  4923 CAGCGGACCACTGTGCCGGAAAACACTGTCCGGCCATCGGATGACCCCCAGTGGGCA 4982
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4920 CAGCGGACCACTGTGCCGGAAAACACTGTCTCGGCCATCGGATGACCCCCAATGGGCA 4979

Qy  4983 GGTCTGAAGGGCCCGAATCCTGTCCCACTCGCTGAGGTGGGCAATGATTTACCATCT 5042
         ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  4980 GGTCTGAAGGGCCCAAATCCTGTCCCACTCGCTGAGGTGGGCAATGATTTACCATCT 5039

Qy  5043 AAAAGTGCCGGCCATCACATCGTGGAACGACCTGGACCACGTGGTCGGGGGGCATG 5102
         |||||||||||||||| ||||||||||||||||||||| ||||||||||||||||||
Db  5040 AAAGTGCCGGCCACCATAGTGGACGACCTGGACCACGTGGTCGGGGGGGGGGT 5099

Qy  5103 TACGTCCGCTGCGATGCGGACCATCTTGATGGTGGGCCTCGCGTATTGCGGGGGCATG 5162
         |||||||||||||||  |||||||||||||||  |||||| ||||||||||||||||
Db  5100 TACGTCCGCTGCGACCATCGGGCCGATCTTGATGATCCGGTCTATCGGGGGGGAATG 5159

Qy  5163 ATCTATGCGTCATACACCGGGTCTCTCGTGGTGTTACAGACTGGGATGTGAAGGGGGGT 5222
         |||||| |||||||||||||||||||||| |||||| |||||||| |||||||||||||
Db  5160 ATCTACCGGTCATACACCGGGTCGCTCGTGGTGTGACTATCATGACTCGTCGATCGGGAGA 5219

Qy  5223 GGCAGCGCCCCTTATCGGCCATGGAGACCCACCAGCGCCACCGCGTGTCGCAGGTCCCC 5282
         || ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  5220 GCGCCCCTTTATCGGCCATGGAGACCCACCAGCGCCACCGCGTGTCGCAGGTTCCT 5279

Qy  5283 CCGGTAGACACCATCGGCCGCGGGGAGAGTCTGCGCCATCGGATGCCAACACAGTGACAGAT 5342
         |||||||||||||||||||||||||||| | |||||||||||||||||||||||||||||
Db  5280 CCGGTAGACACCATCGGCCGCGGGGTGAATCAGCACACAGTCGGAATCGGCCAAGACGACAGAT 5339

Qy  5343 GGGGTGCGGCAATCCAGGTGCGATTGCGATTGGTCAGTGATCATGACCCTGTCGATCGGGGAA 5402
         |||||||||||||||||||||||| |  || ||||||||| |||||||||||||||||||||
Db  5340 GGGGTGCGGCAATCCAGGTGCGATTGGACTGGTCATCATGACTCGTCGATCGGGAGAA 5399

Qy  5403 GTGGTCGTCCTTGGCCTGAGGCGTAGGCACCGCTACCGGCCTACCACCAAGTGGCTT 5462
         |||||| ||||||||||||||| |||||||||||||||||| ||||||||||||||
Db  5400 GTGTTGTCCTTGGCCTCAGGGCTAAGACGGCGGGGCCCGAGCCTACCACAGCAACCGCCAAGTGCTC 5459

Qy  5463 GCTGGCTGCTACACGGGACGCGGGGCCGTCCCCACTGTTTCAATTGTTGACAAGCTCTTC 5522
         ||||| ||||||||||||| ||||| |||||||||| |||||||||||||||||||||
Db  5460 GCTGGCTGCTATCACGGGGGACGCGGGGACCGGGGCCGGGGCCCCTTCCAATTGTTGACAAGCTCTTC 5519

Qy  5523 GCCGGGGGCTGGGCGGTTGGGCGGGCGTGTGTGTAGGCCATTGCCACAGTGTTATAGTCGGGTGGCG 5582
         ||| || ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5520 GCCGGAGGGCTGGGCGGTTGGGCGGGCGTGTGGCCGGCCATTGCGGCCATTGGTGGGCCGGGTGGGCG 5579
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Db       GCCTATGGGGCTTCTAGGAGCGCCCTCCATTGGCTGCTGCGCGCTTCCTACCTCATGGGGTTG 5642

Qy  5583 GCCTATGGGGCTTCTAGGAGCGCCCTCCATTGGCTGCTGCGCGCTTCCTACCTCATGGGGTTG 5639
         |||||||||||  ||||||||||||||||||||||||||||  |||||||||||||||||||
Db  5580 GCCTACGGGGCTTCAAGGAGCCTTCAAGGAGGTTGGCAGCCCGTGGCAGCGGCTCGGCTTCCTACCTGATGGGGTTG 5639

Qy  5643 GGGGTCGGAGGCAACGGCAAACCCGGTCAAACCCGCGTTAGCCTCCGCGTCTCCGCCGCTGGG 5702
         ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  5640 GGGCGTTGGAGGCAACGGCTCAGACGGCGCTCAGACGCGCCTGGCGTCTGGCCGCTGCGGGGGTGCTGA 5699

Qy  5703 ACCGGCTCTGGGCACGCCGTGTGGGTGTTAACCATGGCGGCGCCGTTCATGGGAAGTGCT 5762
         ||||  |||||||||||||||||||| |||||||||||||||||||||  ||||||||||
Db  5700 ACCGGCCTGGGCCACTCCGTGTCGTGGGCTTGACCATGGCGGCGTGCTGGCTCATGGGGGGGGCC 5759

Qy  5763 AGCGGCTCTCCCCTCTCCTTGGTCACCATTTTACTGGGGGGCCGTGGGGGGGCGTG 5822
         ||||||||||||||  ||| |||||||||| |||||||||||||||||||||||||
Db  5760 AGTGTCTCCCCCTCCTTTGGTCACCATTTTATTGGGGCGGTCGGAGGGTTGGGAGGGTGTT 5819

Qy  5823 GTGAATGGCGCTAGCCTTGTCTTCGACTTTTATGGGGGGGGAAAACTATCATCAGAAGATCTG 5882
         |   ||||||| |||| |||  || ||||| || |||  ||||||||||||||||||||||||
Db  5820 GTCAACCGCGGAGCCAGTCTTTGACTTCATGGCCACTTTCATCAGAAGATCTG 5879

Qy  5883 TGGTATGCCATCCCAGTGCTAACCAGTCCGGGGCTTCGGGGGCACGGACTTGCGGGGACCCTCGG 5942
         ||||||||||||  |||| |||||||||||||  ||||||||||||||  ||||||||||||||
Db  5880 TGGTATGCCATCCCGGGTACTGACCAGCCCGGGCTTGCGGGGATCGCTCTCGG 5939

Qy  5943 TTGGTGTTGTACTCAGTGACTAACAACTCTGGCACTAACAACTCTGGTGCTGCTGCTGCTGACT 6002
         |||||| ||||||||||||||||||||||||||||||| ||  |||||||||||||||||||
Db  5940 TTGTTTTGTATTCAGCTGACTAACAACTCTGGCACTAACAACTCTGGTTGGACCGTTCTCTGACT 5999

Qy  6003 ACATTGCCAAGTCCTCAGTCCTGCATCCGCATGGATCGATCTTCAGCAGGCCGATTACTGTGAC 6062
         |||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db  6000 ACGTTACCAAGGTCTTCATGTATCCCGGACAGTTCAGCAAGTTGACTTGACGAC 6059

Qy  6063 AAGGTCTCAGCTGTCTGTCCCACTCGTGAGCCTGACGTTGCCCTGGTCAAC 6122
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6060 AAGGTCTCAGCTGTCTGTCCCACCTCGTGAGCCTGCACAGTGGTTGCCCTGGTCAAC 6119

Qy  6123 AGGGAGCCTAAGGTGGATGAGGTTCAGGTGGGGTACGTCTGGGGACTTGTGGGGAGTGGATC 6182
         |||||||| |||||||| ||||||||||||| ||||||||||||||||||||||||||||
Db  6120 AGGGAGCCTAAGGTGGATGAGGTGTAGGTGGGATGTGTGGGGAGTGGATC 6179

Qy  6183 ATGCGTCAAGTGCGCATGGTGATGGCAGACTGTGCCCGTCGGCCCCTCGTCCCCGGGTCATTA 6242
         ||||||| |  ||||||| |||||||||||||||||||||||||  |||||||||||| |||
Db  6180 ATGCGCCAAGTGCGCTGCGTGTCATGGCCAGACTGTCATCATTGGAACAGTGCCCGTGTCCACTA 6239

Qy  6243 CCCTTATGGCACTGCGGGGAGGGGTGGTCCGGAGAATGTGTTGTTGGACGGCCATGTTGAG 6302
         ||||  |||||| |  ||||||||  ||||||||||||| || |||||||||||||||||
Db  6240 CCCTTGTGGCATTGCGGGGAGGGGTGGTCCGGAGAATGTGTTGCTTGACGGTCATGTTGAG 6299

Qy  6303 AGTCGTTGTCTTTTGTGGTTGCGTGATCACCGGGTGATGTTTTGAATGGCAACTCAAAGAT 6362
         |||||||||||||||||||  ||||||||||||||||||||  ||||||||||||||||
Db  6300 AGTCGCTGCGTGTCGGCGTCGGGGCGTGATCACTGGGTGACGTTCTGAATGGCAACTCAAAGAA 6359

Qy  6363 CCAGTTACTCTACCAAGCTGTGCAGAACATGTGCGCCAGCAAATCCTGTCGCGGCCCTTATTAC 6422
         |||||| ||||||||||||| ||||||||||||||||||  |||||||||||||||  |||
Db  6360 CCAGTTACTCTACCAAGCTGCTGCGGGCCAGCAAATCCTATTCGCGGGGACTGTCCTATATTAC 6419

Qy  6423 CTGGGCTATGGCCAGCTGATTGCGATTGGTCAGTCATGACCTGTCGATCGGGGAA 6482
         ||||||| ||||| |||  |||||  || |||||||||||||||||||||||||
Db  6420 CTGGGTTACGGTGAAACGTCGGGCTGCGGCCCGACACCCCGAAGGTGTCCCTTC 6479

Qy  6483 GGGACGTCTGGGTGGGCTGAGGTGTGGTGATCACCGGGTGATGTTTTGATGATCAGGCGAACA 6542
         |||||||||||||||||||||||||  |||||||||||||||||||||||| |||||||||
Db  6480 GGGACGTCTGGGTGGGCTGAGGTCGTGGGATCACCACGGGTGAATCGGGTAATCAGGAGGACC 6539

Qy  6543 TCCGCCTACAAACTGCTGCGGCCCACTGTTTCAATTGTTGACAAGCTCTTC 6602
         |||||| |||||| |||||  | || ||||||||||||||||||||||||
Db  6540 TCCGCCTATAAGCTGCTGCGGCCCAGCAAATCCTATTCGGGCTGCTGTAGCTGTGAGCCCTATTAC 6599

Qy  6603 GTCGACGGCATACCGGTCTCATGGGACGCGCCGAGCGCCTGCTATGGC 6662
         |||||||||||| ||||||||||||||||||||||||||||||||||
Db  6600 GTCGACGGCATTCCGGTCTTCATGGGACGCGCCGAGCGCCCGCCATGGTCTATGGC 6659
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Qy  6663 CCTGGGCAAAGTGTCACCATTGACGGGGAACCTACACCCTTCCGCATCAACTGCGGCTT 6722
         |||||||||| |||||||||||||||||| |||| || |||| |||||| || ||||||
Db  6660 CCTGGGCAAAGTGTACCATTGACGGGGAGCCGGAGCGGCGCCTCCACCTTGCCTCAGGCCTC 6719

Qy  6723 AGGAATGTGGCGCCCTCTGAGTGTCATCCGAGGTGTCATTGACATTGGGACGGAGACT 6782
         |||||||| |||||||||||||||||||||| ||||||||||||||||| ||||||||
Db  6720 AGGAATGTCGCCACCCTCTGAGTTCATCCGAGGTGTCATTGACATTGGGACGGAGACT 6779

Qy  6783 GAAGACTCAGAACTGACTGAGGCGACCTGCCGCGGCGCTGCGCCCTTCAGGCTATC 6842
         |||||||||||||||||||||||||||| || ||||||||| |||| || |||
Db  6780 GAAGACTCAGAACTGACTGAGGCCGATCCGCCCGCGGCGCTGCCTGCTCTCCAAGCGATC 6839

Qy  6843 GAGAATGCTGCGAGAATTCTTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTACA 6902
         ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  6840 GAGAATGCTGCGAGAATTCTTGAACCGACACATTGATGTCATCATGGGACGACTGCAGTACA 6899

Qy  6903 CCCTCTCTTTGTGGGAGTAGCCGAGAGATGCCTGTGTGGGAGAAGAGCATACCCCGCACT 6962
         |||||||||||||||||||||||||||||||||||||||||||| ||||||| |||| ||
Db  6900 CCCTCTCTTTGTGTAGTAGCCGAGAGATGCCTGTGTGGGAGAAGAGCATACCCCGTACT 6959

Qy  6963 CCATCCGCCAGCACTTATCTCGGTTACTGAGAGCAGCCCAGATGAGAAGACCCCCTCGGTG 7022
         |||||||||||||||||||||||||||||| |||||||||||||||||||||||| ||||
Db  6960 CCATCCGCCAGCACTTATCTCGGTTACTGAGAGCAGCTCAGATGAGAAGACCCCCGTGGTG 7019

Qy  7023 TCTTCCTCCGAGGAGATACCCCGTCTTCAACGTGCTCTTTCCGTACTAAAAGCCTTGTT 7082
         || ||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  7020 TCCTCCTCCGAGGAGATACCCCGTCCTCAACGTGCTCTTTCCGTATTAAAAGCCTTATT 7079

Qy  7083 ACAGCCGAAGGGAGGGAGGAAAGCGTCTTCAACGTGTCTTTCCGTACTAAAAGCCTTGTT 7142
         |||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||
Db  7080 ACAGCCGAAGGGAGGGAGGAAAGTGTCTTCAACGTGTCTTTCAACGTGTATTAAAAGCCTTATT 7139

Qy  7143 CCACAGAGCGATGCCACAGAAAGCTTACCGTTAAGATGTCATGCTGTGTTGAGAAGAGC 7202
         ||||||||| |  || ||||||||||||||||||| ||||||||| |||||||| |||||
Db  7140 CCAGAGAGCGACGCGACCACAGGAGCTTCAAGATGTCGTGCTGCTTGAAAAGAGC 7199

Qy  7203 GTAACACGCTCTTTTCATTGGATTGACGGTCGCTGACCTGTCGCAAGCCTGTGTGAGATG 7262
         ||  ||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  7200 GTCACCGCGCTTTTTCATTGGGGTGACGGTCGCTGATGTTGCTAGCCTGTGTGAGATG 7259

Qy  7263 GAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCGCACTCCGCTTGAATTGCAGGTT 7322
         ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  7260 GAAATCCAGAACCATACAGCCTATTGTGACCAGGTGCGCACTCCGCTTGAATTGCAGGTT 7319

Qy  7323 GGGTGCTGTGGGCAATGAACCTTTGAAGTGTCAAAGTGTGAGGCTAGGCAGAG 7382
         ||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db  7320 GGGTGCTGTGGGCAATGAACCTTTGAAGTGTGACAAGTGTGAGGCTAGGCAGAA 7379

Qy  7383 ACCTTGGCTTCCTTCTACATTTGGTCTGGGTGCCACTGACGAGGGCCACTCCGGC 7442
         ||||||||||||||||| ||||||||||||||||||||||| ||||||||||
Db  7380 ACCTTGGCTTCCTTCTACATTTGGTCTGGGTGCCACTGACTAGGGCCGCACGGC 7439

Qy  7443 AAGCCCCTGTGGTGAGGCCGGTTGGCTCCTTGCTGTGGCCGACACCACCAAGGTGTAT 7502
         ||||||||||||||||||||||||||||| ||||||||||||| |||||||||||||||
Db  7440 AAGCCCTGTGGTGAGGCCGGTTGGCTCCTTGTTGTGGCCGACACTACTAAGGTGTAT 7499

Qy  7503 GTCACCAACCGGACGAATGTGGGAGAAGAGTTGACAAGGTACCTTCTGGCGTGCCCCT 7562
         |||||||| |||||| ||||||||||||||||||| | |||||||||||| |||||||
Db  7500 GTTACCAATCCAGACAATGTGGGACGAGGGTGACAAGTTTGACCTTCTGGCCGTGCTCCT 7559

Qy  7563 AGGGTTCATGACAAATTCCTCGTGGACTCCATAGAGGGCGGCTAAGAGGGCGCTCAAGCC 7622
         |||||||||||||||||||||||||||| |||||| |||||| ||||| |||||||||||
Db  7560 AGGGTTCATGATGATAAGTACCTCGTGGACTCTATTGAGAGGGCGGCTAAGAGGGGCGCTCAAGCC 7619

Qy  7623 TGCCTTAAGCATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCC 7682
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7620 TGCCTTAAGCATGGGTTACACTTATGAGGAAGCAATAAGGACTGTAAGGCCACATGCTGCC 7679

Qy  7683 ATGGCTGGGGATCTAAGGTGTCGGTCAAGGACCTTGCGCCACCCCTCGCGGGGAGATGGCT 7742
         |||||||||||||||||||| |||||||||||  |||||||||||| ||||||||||| |
Db  7680 ATGGCTGGGGATCTTAAGGTGTCACTTAGGACTTAGCCACCCCGGGGGAAGATGGCC 7739

Qy  7743 GTCCATGACCGGCTCCAGGAGATACTTGAAGGGACGGCCAGTCCCTTTACTCTTTACTGTG 7802
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Db  7740 GTCCATGACCGGCTTCAGGAGATACTTGAAGGGACTTCCGGTCCCCGTTTACTCTTTACTGTG 7799

Qy  7803 AAAAGGAGTGTCTTCAAAGACCGAAAGACGAGAAGGAGCAAGGCCCCCGCCCCCCATTGTTC 7862
         |||||| |||||||||||||||||||||||||||||||||||| |||||| |||| |||||
Db  7800 AAAAGGAGTGTCTTCAAAGACCGGAGCGGAGGAGGAGGAAGGCCCCCGCCCCCCATTGTTC 7859

Qy  7863 CCCCCTTGGACTTCCGGATAGCTGAAAAGCTTATTCTGGAGACCCCTGACGCGGGTAGCC 7922
         |||||||||||||||||||||||||||| ||||||||||||||||||||| ||||||||
Db  7860 CCCCCTTGGACTTCCGGATAGCTGAAAAGCTCATCTTGGGAGACCATCAGGCCGGGTAGCC 7919

Qy  7923 AAGGCGGTGTTGGGGGGGCCTACCCTTCCAGTACACCCCAAATCAGCGAATTAGGGAG 7982
         |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  7920 AAGGCGGTGTTGGGGGGGCCTACCCTTCCAGTACACCCCAAATCAGCGAGTTAAGGGAG 7979

Qy  7983 ATGCTCAAACTGTGGGAATCAAAGAAGACACCATGCGCCATCTGTGTGGACGCCACATGC 8042
         |||||||||||||||||||||| |||||||||||||| |||||||||||| ||||||||
Db  7980 ATGCTCAAGCTATGGGAGTCTAAGGAGACCCTTGCGCCATCTGTGTGGACGCGCCACCTGC 8039

Qy  8043 TTCGACTAGTAGTACTGAAGAGGACTGGCGTGCCCTGGAGACAGAGCTTTATGCCCTGGCT 8102
         ||||||||||||||||||||||||| |||||||||||||||||| |||||||||| |||
Db  8040 TTCGACTAGTAGTACTGAAGAGGACTGGCGTGCCCGTCCCATCTGTGGACGCACCTATGCCC 8099

Qy  8103 TCAGACCATCCAGATGGGTGCGTCCCTGGGTGAGGGTATTGTAGATCCTCGGCACAATGGTA 8162
         || |||||||||||||||||||||||| |||||||| |||||||||||| |||||| ||||
Db  8100 TCTGACCATCCAGATGGGTGCCGTGGTCCGGTGAGGGTATTGCAGATCCTCGGGTGTCCTAACAACT 8159

Qy  8163 ACCCCCGAGGGGTGCCAGTGGGTGAGAGGTATTGTGAGATCCTCTGGCACCACC 8222
         |||||||||||| |||| |||||||| ||||||||||| ||||||||||| |||||||
Db  8160 ACCCCCGAGGGGGTGCCCGTGGGTGAGAGGTATTGCAGATCCTCGGGTGTCCTAACAACT 8219

Qy  8223 AGTGCGAGCAACTGCTTGACTTGCTGTATATCAAGGTGAAAGCCGCCTGTGAGAGGTGGGG 8282
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  8220 AGCGCGAGCAACTGCTTGACCTGCTGTACAATCAAGGTGAAAGCTGCCTGTGAGAGTGGGG 8279

Qy  8283 CTGAAAATGTCTCGCTCCTCATCGCGGATGATGCTGTTTGATCATATGCGAACGGCCT 8342
         |||||||||||| |||||||||||| |||||||||||||||||||||||| |||||||
Db  8280 CTGAAAATGTCTCTTCCTTCCTCATAGCCGGCATGATGCTTGATCATATGTGAGCGGCCA 8339

Qy  8343 GTGTGCGATCCTAGCGACGACCGTTTGGCGAGCAGAGCCCTGGCGAGCTACGCCATGCGAG 8402
         || ||| |||| ||||||| ||||||||||||||||||||||||||||||||||| ||||||
Db  8340 GTGTGCGACCCCAAGCGACGCGCTTGGGCAGCCCCTTAGCGAGCTATGGCGTACGCGGTCGAG 8399

Qy  8403 CCTTCGTATCATGCATCACTGACAATCGATCACTCCACTTGGCCTTGGCTTAGCTGTGTGCTGT 8462
         |||||||||||||||||| |||||||| ||| ||||||||||| ||||||| |||||| ||||
Db  8400 CCCTCATCATGCATCACTCGAACGCCGATCACTCCACTTGGCGTGGCGTGCTGCTAGTCAGTGC 8459

Qy  8463 AATGCAGATGGGAAACGCCATTCTTCGTGTGTGGGTCCGGGCCACTCCGGCCCCTCCGCGC 8522
         ||| |||||||||||| ||||||||| |||||||| |||||||||||| || |||||||||
Db  8460 AATGCAGATGGGAAAGCGCCATTTCTTCCTGACCAAGGCGAGGAGGGCCGGCGCGCTCGC 8519

Qy  8523 ATGTCGAGCAGTACAGTGACCCAATGGCTTCGGCCAATCCTGGTTACATCCTTCCTATACCCT 8582
         ||||||||||||||||||||| |||||||||||| |||||||||||||| |||||||||||
Db  8520 ATGTCGAGTAGTAGTGATGTACCCGATGGCTTCGGCATCGGCTGTTACATCCTTCTCTTTTATCCT 8579

Qy  8583 TGGCATCCATCACACGGTGGGTGCATCATCCGTGTGCATCCTCACGTGCTCACCGGCGTTAGGGGT 8642
         |||| |||| |||||||||||||||||||||||| |||||||||||||||| |||||| ||||||
Db  8580 TGGCACCCCATCACACGGTGGGTGCATCATCCGTGTCATCCTCATGTGCGCATTACAGGGGT 8639

Qy  8643 GGTGGCACACCGTCGATCCTCGTGTGTGTGGCCAGTGTACATGGTAATTACTACAAGTTTCCA 8702
         |||||| |||||||||| |||| |||||||||||||||||||||||| |||||||||||||||
Db  8640 GGAGGCACACCGTCCTGATCCTGATCCGGTTGGTGTGTGTAACTACTACAAGTTTCCA 8699

Qy  8703 CTGGACAAACTGCCTAACATCATCATCGGACCCAGCCTCCACGGACCAGCAGCAGTTGAGGGTTACC 8762
         |||||||||||||||||| |||||||||| ||||| |||| |||||||||||||||| ||||||||
Db  8700 CTGGACAAACTGCCTAACATCATCATCGTGGCCCTCACGTCGGCCACGACCAGCAGCAGTTGAGGGTTACC 8759

Qy  8763 GCAGACAACAACTAAGACAAAAATGAGGGCGTGAGCGACCGTTCGGCGACCTCAAGCTCCCCT 8822
         ||||| || ||||||||||||  |||||||||||||||||||| ||||||||||||||||||
Db  8760 GCAGACAACAACTAAAACAAAGATGAGGGCTGGTAAGGTTCGAGCGAAGATGGCC 8819

Qy  8823 GGCCTAGCTGCAGTGGGGCTCCAGGACACGCCGAGTCCCTTTACTCTTTACTGTG 8882
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Db  8820  GGCTTAGCAGTCCACCGAAAGAAGGCCGGGGCGCTTGCAACACGCATGCTCCGCTCCGCGC  8879

Qy  8883  GGTTGGGCTGAGTTGGCTAGGGGGCGTGTTGTGGCGTCCAGGCGCTTCAGGCGCTTCCCCCTTCCG  8942
          ||||||||||| ||||||||      |||||| || |||||||||||| || ||
Db  8880  GGTTGGGCTGAGTTGGCTAGGGGCTTGTTGTGGCATCCAGGCCTACGGCTTCCTCCCCCT  8939

Qy  8943  GAGATTGCTGGTATCCCGGGGGTTTCCCCCTTCCCCCCCTATATGGGGGTGGTTCAT  9002
          |||||||||||||||||||||| || |||||||||||
Db  8940  GAGATTGCTGGTATCCCGGGGGTTCCCTCTCCCCCCCTATATGGGGTGGTACAT  8999

Qy  9003  CAATTGATTTCACAAGCCAGAGAGAGTCGCTGGCGTGGTTGGGGTTCTTAGCCCTGCTC  9062
          |||||||| ||||||||||||||||||||| ||||||||||||||||||||||||||
Db  9000  CAATTGGATTTCACAAGCCAGAGAGTGCGCGGTTGTTGGGGTTCTTAGCCCTGCTC  9059

Qy  9063  ATCGTAGCCCTTCTTCGGGTGAACTAAATTCATCTGTTGCGGCAAGGTCCGGTGACTGATC  9122
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9060  ATCGTAGCCCTTCTTCGGGTGAACTAAATTCATCTGTTGCGGCAAGGTCGGTGACTGATC  9119

Qy  9123  ATCACTGAGAGGAGTTCCCGCCCCCCAGGGGTCTCCCCGCTGGGTAAAAAGGG  9182
          |||| |||||||||||||||||||||||||||||||||||||||||||||||
Db  9120  ATCACCGGAGAGGAGTTCCCGCCCCCCAGGGGTCTCCCCGCTGGGTAAAAAGGG  9179

Qy  9183  CCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCTGGCAGGGTCAAAGCCTGATGGTGC  9242
          |||||||||||||||||||||||||||||||| ||||||||||||||
Db  9180  CCCGGCCCTGGGAGGCATGGTGGTTACTAACCCCTGCAGGGTCAAAGCCTGATGGTGC  9239

Qy  9243  TAATGCACTGCCACTTCGGTCGTGGTCGGCTCGCTACCTTATAGCGTAATCCGTGACTACGGGC  9302
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  9240  TAATGCACTGCCACTTCGGTCGTGGTCGGCTCGCTACCTTATAGCGTAATCCGTGACTACGGGC  9299

Qy  9303  TGCTCGCAGAGCCCTCCCCGGATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCC  9362
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  9300  TGCTCGCAGAGCCCTCCCCGGATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC  9359

Qy  9363  GGTAAGAGCTCGGCCCAAAGGGCCGGGT  9389
          | |||||||||||||||||||||||||
Db  9360  GGGAAGAGCTCGGCCCCGAAGGCCGGTT  9386
```

RESULT 8
US-08-466-033-234
; Sequence 234, Application US/08466033
; Patent No. 5766840
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, LaVonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dehlinger & Associates
;   STREET: 350 Cambridge Ave., Suite 250
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/466,033
;   FILING DATE:
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/389,886
;   FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/357,509
;   FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/329,729
;   FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/344,271
;   FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,558
;   FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,543
;   FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/246,985
;   FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Fabian, Gary R.
;   REGISTRATION NUMBER: 33,875
;   REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 324-0880
;   TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 234:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9327 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
;   INDIVIDUAL ISOLATE: 3ZHGV-6, HGV FROM PNF2161
US-08-466-033-234

Query Match   83.9%;   Score 7885.6;   DB 1;   Length 9327;
Best Local Similarity 90.4%;   Pred. No. 0;
Matches 8433;   Conservative 0; Mismatches 894; Indels 1; Gaps 1;

```
Qy  40  GCAAGCCCCATAAACCGACGCCTATCTAAGTAGTAGACGCAATGACTCGGCGCCGACTCGGCG  99
        |||||||   |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  GCAAGCCCCAGAAACCGACGCCTATCTAAGTAGTAGACGCAATGACTCGGCGCCGACTCGGCG  60

Qy  100  ACCGGCCAAAAGTGGTGGATGGGTGGTTGACAGGTTGGTCGTAAATCCCGGTCAT  159
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  ACCGGCCAAAAGTGGTGGATGGGTGGTTGACAGGTTGGTCGTAAATCCCGGTCAC  120

Qy  160  CCTGGTAGCCACTATAGGTGGTCTTAAGAGAAGTCAAGACTCCTCTTGTGCCGCGGC  219
         | ||||||||||||||||||||||| |||  |||||||||||||||||||||||||
Db  121  CTTGGTAGCCACTATAGGTGGTCTTAAGAGAAGTTAAGAATCCTCTTGTGCCGCGGC  180

Qy  220  GAGACCGGCGCACGGTCCACAGGTGCTGGCCCTACGGTGTGAATAAGGGCCGACGTCAG  279
         |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  181  GAGACCGGCGCACGGTCCACAGGTGTTGGCCCTACGGTGTGGAATAAGGGCCGACGTCAG  240

Qy  280  GCTCGTCGTTAAACCGAGCCCGTTACCCACCTGGGCAAACGACGCCCACGTACGGTCCAC  339
         |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  241  GCTCGTCGTTAAACCGAGCCCGTTAACCCACCTGGGCAAACGACGCCCACGTACGGTCCAC  300

Qy  340  GTCGCCCTTCAATGTCTCTTCTTGACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAGT  399
         ||||||||||||||||||||||||||| || |||||||||||||||||||||||||||||
Db  301  GTCGCCCTTCAATGTCTCTTCTTGACCAATAGGCTGCCGGCGAGTTGACAAGGACCAGT  360

Qy  400  GGGGGCCGGGGGTTATGGGAAGGAGACCCCAAAACCTGCCCTTCCGGTGGCCGGGGAAAT  459
         || ||||||||||||||| ||  || | ||||||||||||| |||||||||||||||||
Db  361  GGGGGCCGGGGGCT-TGGAGAGGAGGACTCCAAGTCCCGCCCTTCCGGTGGCCGGGGAAAT  419

Qy  460  GCATGGGGCGCACCCAGCTCCGGCGGCCTGCCAGCCGGGGTAGCCCAAGAATCCTTCGGG  519
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  420  GCATGGGGCGCACCCAGCTCCGCGGCCTGCCAGCCGGGGTAGCCCAAGAATCCTTCGGG  479

Qy  520  TGAGGGCGGTGGCATTCTCTTTTTCTATACCATCATGGCAGTCCTTCTGCTCTCCTTCTCG  579
```

A DNA sequence alignment listing is shown, consisting of paired rows labeled "Qy" (query) and "Db" (database) with consensus match bars ("|") between them and flanking position numbers.

Right-hand alignment block (selected position numbers):

```
Db                                                                                     1619
                                                                                      1719
                                                                                      1679
Qy                                                                                    1779
Db                                                                                    1739
Qy                                                                                    1839
Db                                                                                    1799
Qy                                                                                    1899
Db                                                                                    1859
Qy                                                                                    1959
Db                                                                                    1919
Qy                                                                                    2019
Db                                                                                    1979
Qy                                                                                    2079
Db                                                                                    2039
Qy                                                                                    2139
Db                                                                                    2099
Qy                                                                                    2199
Db                                                                                    2159
Qy                                                                                    2259
Db                                                                                    2219
Qy                                                                                    2319
Db                                                                                    2279
Qy                                                                                    2379
Db                                                                                    2339
Qy                                                                                    2439
Db                                                                                    2399
Qy                                                                                    2499
Db                                                                                    2459
Qy                                                                                    2559
Db                                                                                    2519
Qy                                                                                    2619
Db                                                                                    2579
Qy                                                                                    2679
Db                                                                                    2639
Qy                                                                                    2739
Db                                                                                    2699
```

Left-hand alignment block (selected labels and position numbers):

```
Db                                                                                     539
Qy                                                                                     639
Db                                                                                     599
Qy                                                                                     699
Db                                                                                     659
Qy                                                                                     759
Db                                                                                     719
Qy                                                                                     819
Db                                                                                     779
Qy                                                                                     879
Db                                                                                     839
Qy                                                                                     939
Db                                                                                     899
Qy                                                                                     999
Db                                                                                     959
Qy                                                                                    1059
Db                                                                                    1019
Qy                                                                                    1119
Db                                                                                    1079
Qy                                                                                    1179
Db                                                                                    1139
Qy                                                                                    1239
Db                                                                                    1199
Qy                                                                                    1299
Db                                                                                    1259
Qy                                                                                    1359
Db                                                                                    1319
Qy                                                                                    1419
Db                                                                                    1379
Qy                                                                                    1479
Db                                                                                    1439
Qy                                                                                    1539
Db                                                                                    1499
Qy                                                                                    1599
Db                                                                                    1559
Qy                                                                                    1659
```

```
Qy  2740 AGGGGGTCTCCACCAAGCTTCTGACGTTCGCCTGCTGGTGCTTCGCCTGCTGGCCTCATACATCTGCCGG 2799
         |||||| |  ||  ||  ||  ||  ||||||||||||| |    ||||
Db  2700 AGGGGGCGGCCTGCCAAACCCTGGCCTTGGCCTTGGCCTTGGCCTTCGCCTCGTACACTGCCCAG      2759

Qy  2800 ATGCTGTGATGATGGTTGGTGTTGCCTTGGTTCCTCTTCCGGCCCTGTTCGGACGCGCACTGG        2859
         |||||||||||||||||||||||||||||||| ||| || | ||||| ||||| |||| |||
Db  2760 ATTGCTGTGATGATGGTTGGTGTTGCCTTGGTTCTTCTCTTTGGCCTTGGCGTTTCGGACGCGGTTGG  2819

Qy  2860 ACTGGGCCCTGAGGAGACTCCTGGTCTCCGGCCCTCGTTACGGCGACTGGCACGGGTGG           2919
         | |||||||||||||||||  ||||  ||  | ||| ||||| ||||  |||||  |||
Db  2820 ATTGGGCCTTGGAGGAGATCTTGGTGTCCGGCCCTCGCGTTGGCTGCGCGTTGGCGTCGGGTGG      2879

Qy  2920 TTGAGTGCTGTGTGATGGCGGGCGAGAAGGCCACCACCATCCGACTGGTCTCCAAGATGT         2979
         |||||||||||||||||||||||  ||||  ||||||||  |||||  ||| ||||||||
Db  2880 TTGAGTGCTGTGTGATGGCGGGCGGTGAGATGCCCACCAACCGTCCGCTGGTCTCCAAGATGT    2939

Qy  2980 GCGCAAGAGGGGCCTACCCGTTGACCACATGGCCTCTTCTCCGCGGCCGTCGTGTCAAGGAGC       3039
         || || ||||||||| | ||||| | |  |  ||  ||  |  ||||| ||| |||||||||
Db  2940 GTGCGCAGGAGGAGCCTTATTTGTTCGATCATATGGCTCATTTGTCGCGTCGTGCTGTCAAGGAGC  2999

Qy  3040 GCTTGTTGGAATGGGACGCGGCTTGGAGCCCTTGTCATTCACTAGGACGGACTGTCGCCA         3099
         ||||||||||||||||| |||| ||  | | ||||| |||  ||||| ||||||||||||
Db  3000 GCTTGTTGTTCCGACCGCGCCTCTTGAACCTGTCATTCACTAGGACGGACTGTCGCA         3059

Qy  3100 TCATCAGAGATGCCGCGAGGACCCTGTCCTGCGGACAGTGCCTCATGGGTTTACCCGTGG        3159
         |||| | | || || | ||| ||  ||||| ||| ||| | | | |||  |||||||||
Db  3060 TCATACGGGATGCCGCGAGGACTTGTGCTGCGGCAGTGCAATGCGTCATGGGTTTACCCGTGG  3119

Qy  3160 TAGCACGGCGGCGTGATGAGGTTCTCATCATGGCCTCTTCAGGATGTGAATCATTGGCTC        3219
         | || || |||| ||| |||||  | |||| ||||  ||||||||||||| || |||||
Db  3120 TTGCGGCCCGTCGTGATGAGGTTCTCATCGGCGTCTTCAGGATGTGAATCATTGCCCTC      3179

Qy  3220 CCGGGTTTGTCCCGACTGTCATCCGTCGGTGCGGAAGGGCTTCCTGGGG                   3279
         ||||| |||  || | ||| || || ||||| ||||||| |||| |||||
Db  3180 CCGGGTTGTTGTTCCGACCGTCATCCACGACGTGCGGAAGGGCTTCTTGGGGG              3239

Qy  3280 TCATCAGAAGGCAGCCTGACAGGTAGGGATCCTGACTTACCAGGGAACGTCATGGTGT         3339
         |||| || |||||||| |||||||||| ||| ||| ||||||||||||| |||||||
Db  3240 TCATACGGGATGCTGCCAGTGATGATGATGATGCGGCGGATCCTGACTTACCAGGGAACGTCATGGTGT  3299

Qy  3340 TGGGGACGGCTACGTCACGAAGCAATGGCACATGTCGAATGCTGTCGTTCACAACTT         3399
         ||||||| |  ||||  | ||||||||||||||  |||| ||||  | | ||||||
Db  3300 TGGGGACGGCTACGTCGAGTCCTGAGTCTGGGTCATCAGAATGGCTTGAACGGCCTGCTGTTCACGACCT  3359

Qy  3400 TCCATGGGGCTTCATCCCGACCCACCGCCGACAATCGCCACCGCCACACCCGGGGGCCTTAATCCCAGGTGGT 3459
         ||| | |||||||| |  |  | |  | || |||| ||||  | ||  ||  ||||||||||  |||||||||
Db  3360 TCCAATGGGCTTCATCCCGACCCACCGCCGACAATCGCCACCGCCACACCCGGGGGCCTTAAATCCCAGGTGGT  3419

Qy  3460 GGTCAGCCAGTGATGACGTCACGGTTACCCGCTTCCGGGCAACTTCGTTGACGC             3519
         ||||||||||||||||||| ||  |  ||| || ||||||| || ||  | ||
Db  3420 GGTCAGCCAGTGATGATGATGATGCGGCGGATCCTGATCCCAGCGGGATGGGCTACTTCGTTTAACGC  3479

Qy  3520 CCTGCACTCTGCGGCCAGGGGGAGTTGATTCCGACGGGCTTTGTGCCATG                   3579
         ||| |||| || | | ||||| |    ||  | ||  |||| ||  |||
Db  3480 CTTGTACTTGCCAGGTGTCAGTCGTGATTCGGGTTATTAGATCCGACGGGCCCTATGCCATG         3539

Qy  3580 GCTTGAGCAAGGGGACAAGGTTGAGCTGGCATGGCAAAGGGCGAGTTCTCGTTCCGTG            3639
         ||||||||| || ||||||||||| ||| |||| |  |||||| || || || ||||||
Db  3540 GCTTGAGCAAGGGGACAAGGTGGAGCTGGCATGGCAAAGGGCTAGGAGTCTCCCTGATTTCCGTG      3599

Qy  3640 GTTCGTCTGGTTCACCGGTCTCACGGGTCCGGACAAAGGGCACGCAGTAAGAATGCTCGTGTCTCAG     3699
         |||||| ||  | ||| | |  |  |  ||| ||| |||||||| | ||| || || |  |||  |
Db  3600 GCTCGTCTGGCTCACCGGTCGTGATGTGACGCGGCAAAGGGCACGCAGTAGGAATGCGTCGTGTCTG    3659

Qy  3700 TGCTCCACTCTGCGGCCAGGGTTACTGCCGCGGCCGATTCACTAGGCCGTGGACTCAAGTAC         3759
         || || ||||| ||  ||||| ||||  |  ||| || ||||| | | || ||  | ||
Db  3660 TGCTTCACTCCGGTGTACGGCCTAGGCGCGCGGCCACGCGATATCCGGCCTAGGCCCAAGTGC        3719

Qy  3760 CAACGATGCCAAGACTACCACAGACACCCCCTTCCCGGTGCGGCCAAAAGTTTTCAAGG            3819
         |||| |||||||  | || || | ||||||  |||||||| || ||||| |||||| |||
Db  3720 CAACAGATGCCAAAACCACCACTGAACCCCCTTCGCCGGTGCGGCCAAAAGGAGTTTCAAAG        3779
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Qy  3820 AGGCCCGTTGTTGTTTATGCCTACGGGGGCGGGAAAGAGCACCCGGTACCGTTGGAGTACG 3879
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3780 AGGCCCGTTGTTGTTTATGCCTACGGGGGCGGGAAAGAGCACTCGCGTCCGTTGGAGTACG 3839

Qy  3880 GCAACATGGCCACAAGGTCTTGATCTTGAACCCGTCGGTAGCTTGACGAGGCCCATGG     3939
         |||||||||| || |  |   |  || | ||   | |  | || ||||| |||| |||||
Db  3840 GCAACATGGGCACAAGGTCTTAGTCTTGAACCCCTCAGTGGCCGTTGCGGCGCCATG       3899

Qy  3940 GCCCATACATGGAGCGGCTTGGCGGCGAAACACCCCAGTATTACTTGTGCCATGACACCA  3999
         |||||||  |||||||| | ||| |||||| | |    |   |   | |||||  | |
Db  3900 GCCCGTACATGGAGCGGCTGGGCGGCGTAAACATCCAAGTATATACTGTGGGCATGATGATACAA  3959

Qy  4000 CTGCTTTCACAAGGATCACTGACTTCGCCCCTTACGTATTCCACTTACGGAAGGTTTTGG      4059
         || |||||| || | |  || | |  | ||||  | | ||| |  | | ||  |||| ||
Db  3960 CTGCTTTCACAAGGATCACTGACTTCAACCCTTACGTCGTCTTCAACCTATGGGAGGTTTTTGG  4019

Qy  4060 CCAACCCTAGGCAGATGCTGAGGGTGTGTCGGTGGTCATTTGTGACGAGTGCCACAGTC   4119
         ||||||||||||||||||  | |  |||| || | |  | | | || ||||| ||||  |
Db  4020 CCAACCCTAGGCAGATGCTACGGGCGTTTCGGTGGTGTCATTTGTGATGAGTGCCACAGTT  4079

Qy  4120 ATGACTCAACTGTGTTGTTGGGCATTGGGGAGCTCGCCGCCAGGATGTGGAG               4179
         ||| | |||| ||| | |  ||  |||||||||||| | || || || ||
Db  4080 ATGACTCAACCGTGCTCGTTAGGCATTGGGGAGCTCGGCGGCGCTGGTGCGAG             4139

Qy  4180 TGCAATTGGTGCTCTACGGCCACTGCCACCCCTCCCACCCGATGCCCAGCACCCAT      4239
         ||||||| || |  |  || ||||  |  | ||| |||| ||| ||||| ||||| |
Db  4140 TGCAACTAGTGCTCTACGGCCATTGGCCTTCCCGGATCCCCTATGGGCCATGGCCAGCACCCTT  4199

Qy  4240 CAATCATTGAGACAAAACTGGACGTGGAGAGAGATCCCTTCTATGGGCATCCGACTC     4299
         || | |||||| |||| || | | ||||||  || ||  ||| | | | | | || |
Db  4200 CCATAATTGAGACAAAATGGACGTGGGCGAGATTCCCTTTTATGGGCACGGAATACCCC  4259

Qy  4300 TTGAGCGGATGGCGACCTTCGATTCGTATTCGCCACTCCAAGGCTGAGTCGCGAGC      4359
         | || | | |||| ||  | ||  | |||||||||||| ||||||| |||||| |||
Db  4260 TCGAGCGGATGGCGAACTCGTGGATTCTGTGTCCGTGTCCGTGTCCATTCTAAGGCTGAGTCGAGC  4319

Qy  4360 GCCTGGCGGCACGTTTCGGCTAGGGGTAAATGCCATTACGGGGAAAG                    4419
         |  |||||| ||||| |||| || |||  |||| || ||  |||| |
Db  4320 GCCTTGCTGGGCCAGTTCTCCGGCCAGTGGTCAATGCCATTATAGGGGTAAAG              4379

Qy  4420 ACAGTTCTATCATCAAAGATGGAGACCGTGGTGGTGCTACAGCGCACTATCCACTG            4479
         ||||||| | ||  |||  | |    | ||||| |||  |||||| ||| | ||||
Db  4380 ACAGTTCTATCATCTATCAAGGATGGGGACCGTGGTGGTGCTGCCACAGCGCGCTATCCACTG    4439

Qy  4480 GGTACACTGGGAACTTCGATTCGTCACCATTCCCTGCGCCATTGTAGTCGTCG              4539
         ||| ||||| ||  | |||  |  ||||    |  | | | | ||||  ||||
Db  4440 GGTACACTGGAAATTTCGAAATTTCGACTCCGTCACGACTGTGGTGATTAGTGGTGAGGAGTCGTTG  4499

Qy  4540 AGGTGACCCTTGATCCCACCATTACCATCTCCCTGCGCACGGTGCCCGCTCGGCTGAAC         4599
         |||||||| |||| |||| | ||||||  |||| |||||||||| |  ||||||||||
Db  4500 AGTGACCCTTGATCCCATCATTACCATCTCCCTGCCGCACGTGGTCGCGCTGCGCTGAAC        4559

Qy  4600 TGTCGATGCAGCGGCGAGGACGGCCAGTCGGCGTCGGGCGCTACTACGCG                  4659
         || |||  ||| |||||  |  || ||||||||||||||| |||||| ||
Db  4560 TGTCGATGCAAAGACGAGGACGGCCAGTCGGCGTCGGGCGGTTACTACTACGCG             4619

Qy  4660 GGGTCGGCAAGGCCCCCTGGTCGTCGTCGGTGGAAG                               4719
         ||||| |||||||||  ||| |||| || ||||||
Db  4620 GGGTGGGCAAAGCCCCTGCGGGGTGTCGTCGTCGTCGTCCAGGTCCCTGGAAG             4679

Qy  4720 CCGGTGACCTGTACGGAATGAACAACTACTGAGACTTTACG                          4779
         ||   | |||  ||||  | | |||||  |  |||| |||
Db  4680 CTGGAGTGACCTGTACGGAATGAACAACTGAACCTGACAGCTAACCTACTGAGACTTTACG       4739

Qy  4780 ACAACTGCCCTTACCACCCGGAAGCCGGGTGTTCTTTT                              4839
         | |||| || |||||||| || ||| ||| ||| | |
Db  4740 ACGACTGCCCTTACCACCCCGACGAGACCCGCGTGATATCGGAGAAGACCCGGTGTTCTTTCT    4799

Qy  4840 CGGGGCTTGCCCCGTTGAGGATCGCCGATGGTTAGCTGGGCAAAAGTTCGGCGCGTCA          4899
         |||||||||||   | || | ||| |||| ||| | ||| ||||||| |||||| | |
Db  4800 CTGGGCTCGCCCCCATTGAGGATGCGGCTTGATGTCAGTCGGGCAAAAGTTCGGCGCGGTCA     4859

Qy  4900 ACTGGCCCTTCCTGGTGTTCAGCGGGACCATGTGCCGGAAACACTGTCTCCCGGCC           4959
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Qy  7120  TTTCCGTACTAAAAGCCTTGCTTGTTTCCACAGAGCGATGCCACAAGAGAAAGCTTACCGTTAAGA  7179
          ||||||||  ||  ||||  ||  |||||||||||||       |||||||||||||||  ||||
Db  7080  TTTCCGTATTAGAAGCCTCATTTCCACAGAGCGACGCGACCAGGAAGCTTACCGTTCAAGA       7139

Qy  7180  TGTCATGCTGTGTTGAGAGAGCGTTAACACGCTTCTTTTCATTGCTTGACGGTCGCTG          7239
          ||||  |||||  ||||||||||||  |  ||||| |||||||||||   ||||  ||||
Db  7140  TGTCTGCTGCGTTGAAAAGAGCCTCACCGCGCTTTCATTGGGTTGACGGTGGCTG            7199

Qy  7240  ACGTGGCAAGCCTGTGTGAGATGGAAATCAGAACCATACAGCCTATTGTGACAAGGTGC         7299
          ||  || ||||||||||||||| ||| |||||||||||||||||||||||||||||||||
Db  7200  ATGTTGCTAGCCCTGTGTGAGATGGAAATGCAGAACCATACAGCCTATTGTGACAAGGTGC      7259

Qy  7300  GCACTCCGCTTGAATTGCAGGTTGGTGCTTGGTTGGTGGCAATGAACTTACCTTTGAATGTG     7359
          |||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db  7260  GCACTCCGCTTGAATTGCAGGTTGGTGCTTGGTTGGTGGCAATGAACTTACCTTTGAATGTG     7319

Qy  7360  ACAAGTGTGAGGCTAGGCAAGAGACCTTGGCTTCCTTCTTTACATTGGTTGTCTGGGGTGC      7419
          ||||||||||||||||||||||||||| ||||||| ||  ||||||||||| ||||||||||
Db  7320  ACAAGTGTGAGGCTAGGCAAGAAACCTTGCCTTCCTTCTTTACATTGGTTGTCTGGGGTGC      7379

Qy  7420  CACTGACGAGGGCCACTCCGCCCAAGCCCCGCCGAGGGCCTGTGAGGCCGGTTGGCTCCTTGCTGG  7479
          |  ||||||||||||||||||||||||| || |||||||||||||||||||||||| ||| ||  |
Db  7380  CGCTGACTAGGGCCACGCCGCGCCCAAGCCTCGTGGGCCTGTGAGGCCGGTTGGCTCTTGGCTCTT  7439

Qy  7480  TGGCCGACACCACCAAGGTGTATGTCACCACCCGGACAAATGTTGGGAGAAGAGTTGACA       7539
          |||||||||||||| ||||||| |||||| |||||||||||||||||||||||||||||||
Db  7440  TGGCCGACACTACTAAGGTGTATGTTACCATCCAGACAATGTGGGACGGAGGGGTGGACA       7499

Qy  7540  AGGTTACCTTCTGGCGTTGCGCCCTAGGGGTTCATGATGACAAAATTCCTCGGACTCCATAGAGC  7599
          |||||| |||||||||||| | ||||||||| |  ||||| ||| |||||||||||||||||||||
Db  7500  AGGTTACCTTCTGGCGTTGCGCCCTAGGGGTTCATGATGACAAAATTCCTCGGACTCTATTGAGC  7559

Qy  7600  GCGCTAAGAGGGCAGCTCAAGCCTGCCTAGCAGCTGGGGATCGGGGATCTAAGGTGTCGGTCAAGG 7659
          ||||||||||||||||||||||||||| ||||||| ||||||||||| |  |||||||| ||||||
Db  7560  GCGCTAAGAGGGCCGCTCAAGCCTGCCTAGCAGCTGGGGATCGGGGATCTAAGGTGTCGGTCAAGG  7619

Qy  7660  GGACTGTAAGGCCACATGGCCATGGGCTGCCATGGGCTGGGGATCTAAGGTGTCGGGTTAAGGACCTCG  7719
          |||||| |||||||||||||||||||| |||||||||||||||||||||||||||   |||||||||
Db  7620  GGACTGTAAGGCCACATGCCCATGGGCTGCCATGGGCTGGGGATCTAAGGTGTCGGTTAAGGACTTAG   7679

Qy  7720  CCACCCCTGCGGGGAAGATGGCTGTCCATGCAGCCGGCTCCAGGAGTACTTGAAGGGACGC       7779
          ||||||    |||| |||||||||  |||||||||||||||||||||||||||||||| || |
Db  7680  CCACCCCCGCGGGGAAGATGGCGTTCCATGCAGCCGGCTCCAGGAGTACTTGAAGGGACTC       7739

Qy  7780  CAGTCCCCTTTACTCTTACTGTGAAAAAGGAAGTCTTCTTCAAAGACCGAAAGGAAGAGA       7839
          ||||||   ||||| ||| |||||||||| |||| |||||||||||||||||||||||||
Db  7740  CGGTCCCCTTTACTCTTACTGTGAAAAAGGAAGTGTTCTTCAAAGACCGAAAGGAAGAGGAGG     7799

Qy  7840  AGGCCCCGCGCCTCATTGTGTTCCCCCCTGGACTTCCGGATAGCTGAAAAAGTTATTC        7899
          |||||| || | |||||| ||||||||||||||||||||||||||||||||||||||
Db  7800  AGGCCCCCGCCCCGCCATTGTGTTCCCCCCTGGACTTCCGGATAGCTGAAAAAGCTCATCT       7859

Qy  7900  TGGGAGACCTGGACGGGCGTAGGCAGCCGGCCGTGTGTGGGGGGCCTTACGGCTTCCAGTACA     7959
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7860  TGGGAGACCCGGACGGGCGTAAGGCAGCCGGCCGTGTGTGGGGGGCCTTACGGCTTCCAGTACA     7919

Qy  7960  CCCCAAATAGCGAATTAGGGAGATGCTCAAACTGTGGAATCTGGAATCTGGGATCAAAGCACCATGCGG  8019
          ||||||||||||  ||||||  || ||||| |||||||| |||||||||||||||||| ||||||||
Db  7920  CCCCAAATCAGCGAGTTAAGGAGATGCTCAAGCTGTGGAATCTGGAATATGGGATCAAAGCTCATGCG    7979

Qy  8020  TGGGAGACCCTGGACGCGGTAGCCAAGGCCGGCCGTGTGTGGGGGGGCCTTACGGCTTTTGG       8079
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  7980  TGGGAGACCCTGGACGCGGTAGCCAAGGCCGGCCGTGTGTGGGGGGGCCTTACGGCTTTTGG       8039

Qy  8080  AGACAGAGCCTCTGGCACAATGGTAACCCCCGAGGGGGTCGCCCTGCCTCCTGGGAAAT       8139
          |||||||||||||| || ||| || ||| |||||||| || || |||||||||||||||
Db  8040  AGACAGAGCTGTACGCGTCACCATGGTGCGGGGACTTGTCGGGCCGTGTGCGGGAAAT        8099

Qy  8140  ACTATGCCTTCTGACAAATGGTAACCCCCAGGGGGTGCCAGTGCCCAGTGGGTATTGTA       8199
          ||||||||||||| ||||  ||||||||| ||  |||||| |||||| |||||||||||
Db  8100  ACTATGCCTTCAGGACGTCACCATGGTACGCCACTTCGTGCCGTGTGCGGGAGGTATTGCA       8159
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Qy  8200  GATCCTCAGGGTCTTGACCACCAGTGCGAGCAACTGCTTGACTGTTGCTATATCAAGGTGA      8259
          |||||| || ||  |  |  ||||| ||||||||||||||||| ||  ||| ||||||||||
Db  8160  GATCCCTCGGGTGTCCTAACAACTAGCGGCAACTGCTTGACCTGCACACTGGCTATATCAAGGTGA   8219

Qy  8260  AAGCCGGCCTGTGAGAGGGCTGGGGCTGAAAAAATGTCTCGCTCCTCATCGCTGGCGATGACT    8319
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  8220  AAGCCGGCCTGTGAGAGGGCTGGGGCTGAAGAATGTCTCTCTTCCATAGCCGGCGATGACT      8279

Qy  8320  GTTTGATCATATGCGAACGGCCGTGTGCGATCGTGCGATCCTTAGCTGACGCCTTTGGGCAGAGCCCTGG  8379
          |    |||||| |||||  || |||||||||||||| |||||||||||||||||||||||||||||||||
Db  8280  GCTTGATCATATGTGAGGGCTGCGGCCAGCGCTTTGGGCAGCGCCCTAG                  8339

Qy  8380  CGAGCTACGGGTACGCATGCGAGCCTTCGTATCATGCATCGCCTCCTCACG               8439
          |||||||||||||||||||||||  |  |||| |  |||| ||| ||||| ||
Db  8340  CGAGCTATGGGTACGCGTGCGAGCCCTCATATCATGCATCATCCCTCATG                 8399

Qy  8440  GCTCCACTTGCTAGCTGAGTGCAATGCAGATGGAAACGCCATTCTTCCTGACCACGG          8499
          |||||||||||||||  ||||||||| | ||| || |||||||||||  |||||||||
Db  8400  GCTCCACTTGCTTGCTGAGTCAATGCAATGCAGATGGGAGGCGCCATTTCTTCCTGACCACGG       8459

Qy  8500  ACTTTCGGAGGCCCCTCGCTCGGCCCCAATGCGCTTCGACCCAGTACAGTGACTTCGGCCA       8559
          ||||  ||||||||| | || || |||||||| |  ||||| ||||||||  |  ||||||
Db  8460  ACTTCCGGAGGCCGCTCGCTCGGCCCCCAATGTGCGATGTGAGTAGTGACCGGATAGGTTCGGCGA   8519

Qy  8560  TCGGTTACATCCTCCTATACCCTTGGCATCCTATCACACGGTGGGTCATCATCCTCACG       8619
          |||||||||| |||||| ||  |  | ||  | ||| |||||||||||||||||||||||
Db  8520  TCGGTTACATCCTCCTTTATCCTTGGCACCCCATCACACGGTGGGTCATCATCCTCATG       8579

Qy  8620  TGCTCACCTGGCGCGTTTAGGGTGGTGGCCACACCGTCTGATCCTGTGGTGCCAGGTAC       8679
          |||||| |||  | ||   ||||||||| ||||||||||||||||| || ||||||||||
Db  8580  TGCTAACGTGGCGACCTTCAGGGTGGTGGCCACACCGTCTGATCCGGTGGTGCCAGGTAC       8639

Qy  8680  ATGGTAATTACTACAAGTTCCACTGACAAACTGCCTAACATCATCGTGGCCCTCACG          8739
          ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db  8640  ATGGTAACTACTACAAGTTCCACTGACAAACTGCCTAACATCATCGTGGCCCTCCACG         8699

Qy  8740  GACCAGCAGCGTTGAGGGTTACCGCAGCACAACTAAGACACAACAAAAATGAGGCTGGCAAGG    8799
          |||||||||||| ||||||||||||||||||||||||||| ||||  |||||| |||||||||
Db  8700  GACCAGCAGCGTTGAGGGTTACCGCAGCACAACTAAAACAAACTAAAAATGAGGCTGGTAAGG    8759

Qy  8800  TGCTGAGCGACCTCAAGCTCCTGGCTCCTAGCAGTCCACCGGAAGAAGAGGCCGGGCATTGC     8859
          |||  ||||||||||| |||||| |  |||||||||||| ||||||||||||||||||||||
Db  8760  TTCTGAGCGACCTCAAGCTCCCGGCTCCTAGCAGTCCACCGGAAGAAGAGGCCGGGCGTTGC     8819

Qy  8860  GAACGGCTATGCTCCGGCGCGGTGAGTTGGGCTTAGTTGTGGGTCGTGTGGTCGTC          8919
          ||||| |||  | |  ||||| ||||||||| | |||||||||| || ||||||||||
Db  8820  GAACACGCATGCTCCGGCGCGGTGAGTTGGGCTGGTTGGGTATCCCGGGTTGTTGTGGCATC      8879

Qy  8920  CAGGCCTGCGCGGTTCCCCCTCCGGGGTTGTGTATCCCCGGGTTTCCC         8979
          |||||||||| |||  |   ||||||||||| |||  |  |||||||||
Db  8880  CAGGCCTACGGCCGTTCCGGATTGCTGGTATCCCGGAGATTGCTGTCTCTCCCC             8939

Qy  8980  CCCCTATATGGGGTTCTTAGCCCTGTTCATCAATTGGATTTCACAAGCCTCGGGTGAACTTCATCTGTT  9039
          |||| |||||||||||||||||| || || ||||| |||| |  |||||||||||||||||||||||||
Db  8940  CCCCCTATATGGGGTTCTTAGCCCTGTTCATCATCAATTGGATTTTACAAGCCTCGGGTGAACTTCATCTGTT  8999

Qy  9040  GCGGCAAGGTCCGGTGGGATGCTCAAACTGTCTAAACTGTGGAATCTGGAAGAAGACACCATGCGG     9099
          |||| || ||||| ||||||||| ||||||||| |||||||||||  || |||||| |||||||||
Db  9000  GCGGCGAGGTCTGGGACTGTGGGACTGTGGGACTGTGGGACTTGGGAGGTTCCCGGAGGAGAGGACGTTCCCG  9059

Qy  9100  GCGGCAAGGTCCGGTGGGTAAAAGGGGCCCTGGGAGGCCATGGTGTGGTTACTAACCCCCTG    9159
          ||||| |||||||| ||||||||| |||||||||||||||||| || |||| ||||||  ||
Db  9060  GCGGCGAGGTCGGTGGGTAAAAGGGGCCCGCCGTCTGGGAGGCCATGGTGTGGTTACTAACCCCCTG   9119

Qy  9160  GCGCGGAGTCCCGTGGCTAATGGTGGCTAATGCACTGCTGCTAATGCAGTGGTCGGCGGTCTACCTTA     9219
          ||||||| ||| ||||||||| |  | ||  |  ||| ||||||||||||||||| ||||||||||||
Db  9120  GTCTCCCCCGTGGGTAAAAGGGACTGGTGGTGGTTACTAACCCCCTG                       9179

Qy  9220  GCAGGGTCAAAGCCTGATGGTGCTAATGCACTGCTGCTAATGCAGTGGTCGGCGGTCGCTACCTTA     9279
          |||||| ||||| ||||| | |||| ||||  ||||||||||||||||||||| ||| |||||||||
Db  9180  GCAGGGTTAAAGCCTGGTTAAATGGTTGCTAATGCACTGCTGCTAATGCAGTGGTCGGCGGTATTGCA     9239

Qy  9280  TAGCGTAATCCTGACTACGGCGCTGCTCGCAGAGCCTGTGCGCAGAGCCCTCTCCCCGGATGGGCACGCAC   9339
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Db  9240 TAGCGTAATCCGTGACTACGGCGCTGCTCGCAGAGCCCTCCCCGGATGGGGCACAGTGCAC 9299
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  9340 TGTGATCTGAAGGGGTGCACCCCGGTAA 9367
          || ||||||||||||||||||||| ||
Db  9300 TGAGATCTGAAGGGGTGCACCCCGGGAA 9327
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;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   INDIVIDUAL ISOLATE: 3ZHGV-6, HGV FROM PNF2161
US-08-444-733-234

Query Match   83.9%; Score 7885.6; DB 1; Length 9327;
Best Local Similarity   90.4%; Pred. No. 0;
Matches 8443; Conservative 0; Mismatches 894; Indels 1; Gaps 1;

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Qy    40 GCAAGCCCCATAAACCGACGCCTATCTAAGTAGACGCAATGACTCGGCGCCGCCGACTCGGCG 99
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Db     1 GCAAGCCCCAGAAACCGACGCCTATCTAAGTAGACGCAATGACTCGGCGCCGCCGACTCGGCG 60

Qy   100 ACCGGCCAAAAGGTGGTGATGGTGTGGTGACAGGGTTGGTAGTCGTAAATCCGGTCAT 159
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    61 ACCGGCCAAAAGGTGGTGATGGTGATGACAGGGTTGGTAGTCGTAAATCCGGTCAC 120

Qy   160 CCTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTCAAGACTCCTCTTGTCCTCGCGC 219
          | |||||||||||||||||||||||||||||||||||| |||| |||||||||||| ||
Db   121 CTTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTTAAGATTCCTCTTGTCCTCGGC 180

Qy   220 GAGACCGCACGGTCCACAGGTGCTGCCCTACCGGTCGTGAATAAGGCCCGACGTCAG 279
          |||||||||||||||||||||| |||||||||||||||| |||||||||||||||||
Db   181 GAGACCGCACGGTCCACAGGTGTTGCCCTACCGGTCGTGGGAATAAGGCCCGACGTCAG 240

Qy   280 GCTCGTCGTTAAACCGACCCGTCACCCACCTGGGCAAACGACGCCCACGTACGGTCCAC 339
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   241 GCTCGTCGTTAAACCGACCCGTTACCCACCTGGGCAAACGACGCCCACGTACGGTCCAC 300

Qy   340 GTCGCCCTTCAATGTCTCTCTTGACCAATAGGTTTATCCGGCAGTTGACAAGGACCAGT 399
          |||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||
Db   301 GTCGCCCTTCAATGTCTCTCTTGACCAATAGGCTAGCCGGCAGTTGACAAGGACCAGT 360

Qy   400 GGGGGCCGGGGTTATGGGAAGACCCCAAACCCTGCCCCTTCCCGGTGGGCCGGGAAAT 459
          |||||||||||| ||  ||| || |||||||||||||||||||||||||||||||||
Db   361 GGGGGCCGGGGGCT-TGGAGAGGGACTCCAAGTCCCGGCCCTTCCCGGTGGGCCGGGAAAT 419

Qy   460 GCATGGGGCCACCCAGCTCCGCGGCCGGCCTGCAGCCGGGGTAGCCCAAGAATCCTTCGGG 519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 GCATGGGGCCACCCAGCTCCGCGGCCGGCCTGCAGCCGGGGTAGCCCAAGAATCCTTCGGG 479

Qy   520 TGAGGGCGGGTGCATTTCTCTTTCTATACCATCATGGCAGTCCTTCTCGCTCCTTCTCG 579
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   480 TGAGGGCGGGTGCATTTCTTTTCTATACCATCATGGCAGTCCTTCTCGCTCCTTCTCG 539

Qy   580 TGGTTGAGGCGGGCCATTCTGGCCCCCGGAAGAATGGCCAAT 639
          ||||||||||||||||||||||||||||||||||||||||||
Db   540 TGGTTGAGGCGGGCCATTCTGGCCCCCGGAAGAATGGCCAAT 599

Qy   640 ATTTCCTCACAAATTGCTGTGCCCCGGAAGACATCGGTTCTGCCTGGAAGGCGGATGCC 699
          |||||||||||||||| ||||||||||| ||||||||||||| |||| |||||||||||
Db   600 ATTTCCTCACAAATTGTTGTGCCCCGGGACATCGGTTCTCCCTGAGGGTGGATGCC 659

Qy   700 TGGTGCCCTGGGGTGCACGGTTGCACCGACGCCGGGATCCTGGTCTATCAGGCGGGTT 759
          |||||||||||||||||||  ||||||| ||||||||| ||||||||||||||||||
Db   660 TGGTGCCCTGGGGTGCACGATTTGCACTGACCAATGCTGGCCACTGTATCAGGCGGGTT 719

Qy   760 TGGCTGTGCGGCCTGGCAAGTCCGCGGCCCAGCTCGTTGGGGAGCCTGTACG 819
          ||||||||||||||||||||||||| | |||| |||| |||||||| ||||||
Db   720 TGGCTGTGCGGCCTGGCAAGTCCGCCCAACTGGTGGGGGGAGCTGGTAGCCCTATACG 779

Qy   820 GGCCCTTGTCGGTCTCCGGCTTACGTAGCCGGGATCCTTGGGTCTTGGGCCGAGGTTTACTTCCG 879
          |||||| |||||||||||||||| ||| ||  ||| ||||||||||||| |||| ||| ||||||
Db   780 GGCCCCTTGTCGGTCTCCGGCTTATGTGGCTGGGGCCTGGGTCTTGGGTGAGGTGTACTTCCG 839

Qy   880 GGGTCCTTGACAGTTGGTTGTCGGTTGAGGCGGGCCTACCTGATGCCCAACCTGAAGT 939
          | |||| |||  ||| || |||||||| ||| |||| ||| |||||| ||||||| |||
Db   840 GTGTCCTTAACGGTGGGAGTGCGGTTGACGCGCCGGATCTACCCCGGTGCCTAACCTGACGT 899

Qy   940 GTGCAGTAGAATGTGACGTTAAGTGGGGAAGTGAGTTTTGGAGATGGGACTGAGCAGTTGG 999
          |||||||  | ||||| |||| ||||| ||||||||||||||| ||||| |||| |||||
Db   900 GTGCAGTGCGCGTGTGAGTTAAAGTGGGAAAGTGAGTTTTGGAGATGGGAAAGTGAGTTTTGGAGAGTGAACAGCTGG 959
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RESULT 9
US-08-444-733-234
; Sequence 234, Application US/08444733
; Patent No. 5824507
; GENERAL INFORMATION:
;   APPLICANT: Kim, Jungsuh P.
;   APPLICANT: Wages, John
;   APPLICANT: Young, LaVonne M.
;   APPLICANT: Fry, Kirk E.
;   APPLICANT: Linnen, Jeffrey M.
;   TITLE OF INVENTION: Hepatitis G Virus and Molecular
;   TITLE OF INVENTION: Cloning Thereof
;   NUMBER OF SEQUENCES: 277
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dehlinger & Associates
;   STREET: 350 Cambridge Ave., Suite 250
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/444,733
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/389,886
;   FILING DATE: 15-FEB-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/357,509
;   FILING DATE: 16-DEC-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/329,729
;   FILING DATE: 26-OCT-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/344,271
;   FILING DATE: 23-NOV-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,558
;   FILING DATE: 03-AUG-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,543
;   FILING DATE: 03-AUG-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/246,985
;   FILING DATE: 20-MAY-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Fabian, Gary R.
;   REGISTRATION NUMBER: 33,875
;   REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 324-0880
;   TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 234:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 9327 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: unknown
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO

Left column:

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Qy  1000  CCTCCAATTACTGGAATACCTTTGGAAAGTCCCATTTGAATTTGGAGAGGAG  1059
          |||||||||||||||||||||| || |||||| ||  ||||||| |
Db   960  CCTCCAACTACTGGAATTCTGGAAGTCCCATTTGATTTCTGGAGAGGCG     1019

Qy  1060  TGATGAGCCTGACCCCTCGTTGGTTTGGTTTGCGGTGGCCGCAATTGCT     1119
          |||||||| ||||| ||||||||||||||||  ||||||| | ||||||
Db  1020  TGATAAGCCTGACCCCCTTGTTGGTTTGGTTTGCGGTGGCCGCAGCAACGGG  1079

Qy  1120  TTGTCATGGTTTCCTGCTGGTGACGATGGCGGGGATGGTGTCAAGGCGCCCCCGCTCCG  1179
          |||||||| || ||||| |||||| ||  |||||||||||||
Db  1080  TTGTCATGGTCTTCCTGTTGGTGACGATGGCGGGGATGGTGTCGCAAGGCGCCCCTGCTCCG  1139

Qy  1180  TTTTGGGGTCCGCGCCCTTTGACTACGGGTGAAGTGGCAGTCATGCTCCTGCAGGGCTA  1239
          |||||||| ||||||||||||||||||||||| |||||
Db  1140  TTTTGGGGTCACGGGCCCCTTTGACTACGGGTGACCTTGGCAGACCTGGGTATGCCTCCG  1199

Qy  1240  ACGGGTCGCGTATTCCCACTGGGGAGAGGTGTGGGATCGAGGGAATGTCACGGCTCTTGT  1299
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Db  1200  ACGGTTCGCGTTTTTCGACTGGGAGAAGGTGTGGACCGGTGGGAACGTTACGGCTTCAGT  1259

Qy  1300  GTGACTGCGCCCAACGGCCCCCTGGGTTTGGGTCCCGGCTTTGCCAGGCGGTGGGTGGGG  1359
          ||||||||||||||  || ||||||||||  ||| |||||
Db  1260  GTGACTGCCTAACGGCCCCCTGGGTGTGGTTGCCGGTGGGTGTGAGTGGGTTGCCGGGTGGG  1319

Qy  1360  GCGACCCCATCACCCCATTGGAGCCACGGACAAAACCAGTGCCCCTATCATGCCCCCAAT  1419
          | |||||||||||| ||||||||||||||||||
Db  1320  GTGACCCCATCACTCAGTTATTGGAGCCAAATCAGTGCGCCCTTTCATGCCCCCAGT  1379

Qy  1420  ATGTCTATGGGTCTGTGTCCGTGGGTTCCGTGTTGTTGGCTGCGTGCTCGA  1479
          | |||||||||| ||  ||||||||| || |||||||  |
Db  1380  ATGTCTATGGGTCTGCTGCTACAGTCACTGCGTGGGGTTCCGTGTTCCATGGGTATGCCTCCA  1439

Qy  1480  CCGGCGGTGATTCGAAGATCGATGTGGTTTGGTGCCGGTTGGTGGATCTGCCAGCT  1539
          |  | ||||  |||||||||| |||| ||||
Db  1440  CCAGTTGCTGCGACTCGAAGATAGATGTGGAGTTTAGTGCCAGTTGGCTCTGCCACCT  1499

Qy  1540  GCACCATAGCCGTCTAGGGTCATCGGATCCGACACGGTTGAGCTCTCCGAGTGGG  1599
          | |||||||||  ||||||||||| ||||||||||||||||
Db  1500  GCACCATAGCCGCCACTTGGATCATCGGATCCGACACGGTGTTTGCCTGTCCGAGTGGG  1559

Qy  1600  GAGTCCCGTCGTAACGTGTATTCTGGACCGTGTTCATGTGGCACCTGTGTGC  1659
          |||||||| || |||  ||||||||||||||  || ||||||||||||
Db  1560  GAATCCCGTGACGTGTTCTGTTCTCGGACCGTGTTCATGCGGCACCTGTGTGA  1619

Qy  1660  GGGACTGCTGCGCCCGAAAACCGTCGGTTAGATTCCCTTCCCGGTGCGGCACGGGGGC  1719
          || ||||||||||||||||||||||||||| |||  |||| |||||||  ||||
Db  1620  GGGACTGCTGCGCCCGAGAACCCGGGTCGTTCGGTTTAGGTTCCCATTCCGGTGCGGCACCAG  1679

Qy  1720  CTCGGCTGACAAAGGACTTGGAAGCTGTGCCCTTCGTCAACAGGACAACTCCTTCACCA  1779
          |||||||||||||||||| | ||||  ||||||||  |||||| |||||||
Db  1680  CTCGGCTGACAAAGGACTTGGAAGCTGTGCCCTTCGTCAATAGGACAACTCCCTTCACCA  1739

Qy  1780  TAAGGGCCCCCTGGGCAACCAGGGGAGAGGCCAACCCGGTGCGGTCGCCCCTGGGTTTTG  1839
          |||  |||||||||||||||  |||||||||||||||||||
Db  1740  TTAGGGGCCCCTGGGCAACCAGGGCCGAGGCCAACCCGGTGCGGTCGCCCCTGGGTTTTG  1799

Qy  1840  GGTCCTACACCATGACCATGAAGATACCGGGATTCCCTGCATTTGTGAAAATGTCCACCACAG  1899
          ||||||| ||||||||||||| ||||||||  |||||||||||||||
Db  1800  GGTCCTACGCCATGACCATGAAGATACCGGGATCCCGAGATGTGTCCCACCACCAG  1859

Qy  1900  CCATAGAGCCTTCGACTGGAACGTTCGGGTTCTGCCCTTCGTCCCCGGAGTCCCATTAACAACT  1959
          |||| |||  |||||||||||||| | ||||||  ||||||||||
Db  1860  CCATGCAGCCTTCCCACCCGGGACTTGGAAGCTGTGCCCTTCGTCAACAACT  1919

Qy  1960  GCATGCGCGTAGGCACGGAAGTGTCTGAGGCATTGGGTCGGAGCTCGACGGGGGGGT  2019
          |||  |||| || |||||||||||||||||||||||||||||||||||
Db  1920  GCATGCGCGTCTCTCGGCACGGAAGTGTCTGAGGCACTGGGTCGGAGCTCCGACGGGGGGGT  1979

Qy  2020  TCTACGAGCCTCCTGGTTGCGTTGGAGCTGTTGGCAACCCGGTTGCC  2079
          || ||||||||||||||| ||||||||||||||||||||||||
Db  1980  TCTATGAACCCGTTGCGGCAGGTGTTCGGAGCTGTTGGCAACCCGGTTGTC  2039

Qy  2080  CGGGGTACGCGCATGGCTGTCCTCGTAGACCTGACGGTTCATACACGTCCAGGGGCACC  2139
          | | || || | |||||| ||||||||||||||||||||||||||
Db  2040  TAGCACGCGCCGCGTGATCGAGCGTCTCATCGGGTTTCATCGGGTGGCACC
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Right column:

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                                                             2099
          ||||||  ||| ||||||| |||||||||| |||||||||
Db  2040  CGGGGTTTGCATGGCTCTCTTCGGCAGGCCTGATGGGTTTATACATGTCCAGGTCACT

Qy        TGCAGGAGTGGATGCGGGCAACTTCATCCTCCTCCCCAGCCTGGTTCTGTCTTGGATTTTG  2199
          ||||||||||||||||||||||||||||  || || |   ||||| ||
Db  2100  TGCAGGAGTGGATGGGATGCCAGCAACTTCATCCCGCGCCTGTGTTGCTCTTGGACTTTG  2159

Qy        TATTTGTCCTGCTATCTGATGAAGCTGGCTGCTGAGAAGCGGTTGGTCCCGTTGATCTTGC  2259
          |||| || |||||||| |||||| || || ||||||||||||||||||||||||
Db  2160  TATTTGTCGTGTTATACCGTATGAAGCTGGCTGAGAAGCTGTCCCGTGATCTTGC  2219

Qy        TTCTGCTGTGGTGGTGAACCAGTTGGCGGTTGGCGGTTCTAGGACTGGCCGCCGGCTGTGTGGACGCGTG  2319
          |   | ||||||| ||||||||||||||||||||| |||||||||||||
Db  2220  TGCTGCTGATGGTGGGTGAACCAGCTGGCAGTCCAGGCTGCCGGCTGTGTGGAAGCCG  2279

Qy        CCGTGGCGGGTGAAGTTTTGCGGGCCCCTGCCTTGTCATGGTGTTTGGGCCTTCCCCACTG  2379
          |||||||||||||||| ||||||||||| ||||||||||||   ||  || ||
Db  2280  CCGTGGCAGGTGAGGTCTTCGCGGGCCCCTGCCCCGTCCGTGTCTGGGACTCCCGGTCG  2339

Qy        TCAGTATGATACTAGGTCTAGAAAACCTGGTGTTGTACTTTCGGTGGATGGGCCCTCAGC  2439
          |||||||||||   |||||||  ||||||||| || ||||||||| ||
Db  2340  TCAGTATGATATTGGGTTTGGCAAACCTGGTGTTGTACTTTAGATGGTTGGGACCCCAAC  2399

Qy        GCCTCATGTCCTCGTGTTGTGGAAGCTCGCCGGGGGAGCTCGCTCGGGGCCACTTTGA  2499
          |||| |||| ||||||||| | |||| |||||||||||| ||||||||||||||||
Db  2400  GCCTGATGTCCTCGTGTTGTGGAAGCTTGCTCGGGGGAGCTTCCCGCCTGGCCCTCTTGA  2459

Qy        TGGGGATTTCGGGCGACCCGCGGGGGCCACTCTGTCTCGGGGGGCCGAGTTCTGCTTCGATG  2559
          |||||||| |||||||||||||||||| ||||||||||||| |||||||||||||||||
Db  2460  TGGGGATTTCGGGCGACCCGCGGGGGCCACTCAGTGCTCTCCAGTGTCTGCTTCGATG  2519

Qy        TCACATTCGAGGTGGACACTTCGGTGTTGGTGGTGCCAGCGTGTGGTGCTTGGG  2619
          ||||||| ||||||||||||| || ||||| |||||||||||||
Db  2520  CTACATTCGAGGTGGACACTTCGGTGTTGGGTGTGGCCAATGTGGTAGCTTGGG  2579

Qy        CCATAGCCGTCCTCGAGCTCAATGAGCGGAAGCACAAGGCCGTGGAAGATCTATA  2679
          ||||| ||| ||||||||| || ||||||||||||||||||||  ||||||||||
Db  2580  CCATTGCCGTCTCGAGCTCGATGAGCGCAGGGGTGGAGGCCACAAAGCCGTGATCTCTATA  2639

Qy        GGACGTGGTGTAAAGGTACCAGGCTGTGCGCCAGAGGGTGGTCGGGGAGCCCCCTCGGGG  2739
          ||||||||||| ||| |||||||| ||||| |||||||||||||||||||| || ||||||
Db  2640  GGACGTGGTGTAAGGGTACCAGGCGTCAGCAATCCGTCAAAGAGGTGGTGAGGAGCCCCTCGGGG  2699

Qy        AGGGGCCGTCCTACCAAGCTTCTGACGTTCGCCGGTTGGCCTCATACATCTGGCCCGG  2799
          ||||||||||||||| ||||| |||| |||||||||||| |||||| |||||||||
Db  2700  AGGGGCGGTCGTCCTACCAAACCCTGACCCTGCCTTGGCCTGGCGTACATCGGGCCCAG  2759

Qy        ATGCTGTGATGATGGTGGTGGTGGAAGCGGGTGAAGAGCACCACTCG  2859
          |||||||||||||||||||||||| ||| |||  |||| |||||||
Db  2760  ATGCTGTGATGATGGTGGTGGTGGTTGCCTGTTGCCTGTGGCCGTGGTCAAGGAGC  2819

Qy        ACTGGGCCCTGGAGGAGCTCCTGGTTACGGCGACTGGCACGGGTGG  2919
          ||| ||||||||||| |||| |||||| |||||| || ||||||||||||||
Db  2820  ATTGGGCCCTTGGAGGAGATCTTGGGTCTCCTGCGCCGGTTTGGCTGGTCACGGTGG  2879

Qy        TTGAGTGCTGTGTGATGCGGGCCAGAAGTGCTCCAAGATGT  2979
          ||||| ||| ||||| ||  |||||||||| |||| |||||||
Db  2880  TTGAGTGCTGTGTGATGGCGGGGGTGAGAAGGCCAACCGCCGGCTGTGTCCAAGATGT  2939

Qy        GCCAAGAGGGGCCTACCTGTTTGACCACATGGCTGCTCTTCCGCGCTGTCAAGGAGC  3039
          | ||||||||||||||||  || || |||||||||||| ||||||||||||||||||
Db  2940  GTGCAGAGGAGCTTATTGTCGCATCATATGGCTCATTTTGCGTGCTGTCAAGGAGC  2999

Qy        GCTTGTTGGAATGGACGCGGCCTTTGGAGCCCTTTGCATTCACTAGGACGACTCGCA  3099
          || |||||||||||||| ||||| |||||||| ||||||||||||||||||||||||||
Db  3000  GCCTGTTGGAATGGACGCGGCCTTGAACCTGCTCTTCATTCACTAGGACGACGTCGCA  3059

Qy        TCATCAGAGATGCCGGGGCAACATGGGCTGGTATGCTGCTCATGGCGTCATGGGTGG  3159
          || |||| |||||| |||||||||||| |  ||| ||||||| ||||| |||||||||||
Db  3060  TCATACGGGATGCCGGAGGGACTTGTCTCTGGGGCAATGCCGGGGTTTACCCGTGTG  3119

Qy        TAGCACGCGCCGCGTGATCGAGCGTTCTCATCGGGTTTCATCGGGTGAATCATTTGCCTC  3219
          | || || || || ||  ||| ||||||||||||||||||||||||||||
Db  3160
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Left column:

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Db 3120 TTGCGCGCCGTGGTGATGAGGTTCTCATCGGCGTCTTCCAGGATGTGAATCATTTGCCTC 3179
        ||||||| |||| |||||||||  ||| ||||||||
Qy 3220 CCGGGTTGTCCCACTGACCAGTTGTCATCCGTCGGTGCGGAAAGGCTTCCTGGGGG      3279
        |||||||||  ||  |||||| |||||||||| ||||||||  || |||||
Db 3180 CCGGGTTTGTCGACACCGCGCCTCGTTGTCATCCGACGGTGCGGAAAGGCTTCTTGGGGG  3239

Qy 3280 TCACGAAGGCAGCTTGACAGGTAGGATCCTGACTTACATCCAGGGAACGTCATGGTGT    3339
        |||| ||||| |||||||||  ||||||||||||||||||||||||||||||||||||
Db 3240 TCACAAAGGCGCCTTGACAGTCGGGATCCTGACTTACATCCAGGGAACGTCATGGTGT    3299

Qy 3340 TGGGGACGGCTACGGTCACGAAGCATGGGCATGGCCACATGTCCTGCTGTTCACAACTT   3399
        ||||||||||||||  | |||||||||| ||||||||  ||  ||| |||||||||||
Db 3300 TGGGGACGGCTACGTCGCGGAGCATGGGACATGGCCATGTCGTGCACAGAGCGCCTTCACAACTT 3359

Qy 3400 TCCATGGGGCTTCATCCGAACCATCGCCACGCCACCCGTGGGGCGCCCTTAATCCCAGGTGT   3459
        ||||||||||||||||||  | || |||  |||||||  ||||||||||||||||||||||
Db 3360 TCCATGGGGCTTCATCCCGAACCATCGCCACGCCACCCGTGGGGCGCCCTTAATCCCAGGATGT  3419

Qy 3460 GGTCAGCCAGTGATGACGTCACGGTGTACCGCTTCCAGATGGGCAACTTCGTTGACGC    3519
        |||||||||||||||||||  || |||||||||||||||||  |||||  || ||| ||||
Db 3420 GGTCAGCCAGTGATGAATGTCACGGTGTATCCCCGGATGGGCTACTTCGTTCGTTAACGC   3479

Qy 3520 CCTGCACTTGCCAGGCGGAGTCCTGTTGGGTTATTAGATCCGACGGGCTTTGTGCCATG   3579
        |  ||||||||||||||||  ||  ||||||||  || ||| |||||||| ||||||||
Db 3480 CTTGTACTTGCCAGGCTGCGTCCTGTTCGGTTCATCAGATCCGACGGGCCCTATGCCATG  3539

Qy 3580 GCTTGAGCAAGGGGACAAGGTTGAGCTGGATGTGGCCATGAAGTCTCGACTTCCCGTG   3639
        |||||| |||||||||||||||| ||||||| | ||||||  |||||| |||  |||||
Db 3540 GCTTGAGCAAGGGGACAAGGTGGAGCTGGATGTGGCCATGAAGTCCCTGATTTCCGTG    3599

Qy 3640 GTTCGTCTGGTTCACCGGTCCTTTGGACAAAGGGCACCGCAGTTAAGAATGCTCCGTCAG 3699
        |  |||||||||||||||  || |||||| |||||||||||||||  || |||||||||
Db 3600 GCTCGTCCTGGTTCACCGGTCCTATGTGACGAGGGGCACCGCAGTAGGATCCTCCGTGTCTG 3659

Qy 3700 TGCTTCCACTCTGGCGCGGGCAGGGTTACTGCCGCGATTCACTAGGCCGTTGGACTTCAAGTAC 3759
        ||||||||||||| |||| | |  |||||| |||||| |||| |||||||||||||| ||||
Db 3660 TGCTTCCACTCCCGGTAGGCTGGCGTCACCGCGCCGCGCACCTAGGGCCGTTGGACCCCAAGTGC 3719

Qy 3760 CAACAGATGGCCAAGACTACCACAGAACCCCCCGTCCCGTGCCGGCAAAAGAGAGTTTTCAAGG  3819
        |||| ||  | |  || ||| ||||||| |||||||  |||| ||||||| | |||||||||
Db 3720 CAACAGATGCCAAAACCACCACTGAACCCCTCGGTGCCGGCTAAACATCCAAGTATAACTGTGGCATGATACAA 3779

Qy 3820 AGGCCCGTGTTTATGCCTACGGGGCCGGAAAGAGCACCCGTACCGTTGGAGTACG       3879
        |||||||||||||||||||| ||||||||||||||||| |||| |||||||||||
Db 3780 AGGCCCGTGTTTATGCCTACGGGGCCGGAAAGAGCACCTCGCGTCCCGTTGGAGTACG    3839

Qy 3880 GCAACATGGGCCACAAGTCTTGAGGGTGTCGGTAGCTACCGTCGAGGGCCATGG        3939
        |||||||||||||| |||| |||||| |  ||| |||||| |||| |||||||||
Db 3840 GCAACATGGGGCACAAGTCTTAGTCTTGAACCCTGTTGTGAACCCTCAGTGGGCCACTGGCCATGG 3899

Qy 3940 GCCCATACATGAGAGCGGCTGGCGGGGAAACACCCCAGTATTTACTGTGCCATGACACCA  3999
        |||| |  ||||| | ||||||||||  ||||  |  ||  || || |||||| ||| ||
Db 3900 GCCCGTACATGGAGCGGCTGGCGGGGTAAACATCCAAGTATAACTGTGGCATGATACAA   3959

Qy 4000 CTGCTTTCACAAGGATCACTGACTCGCCCCTTACGTATTCCACTTACGGAAGGTTTTGG   4059
        |||| |||| ||||||||||||||  || | ||||  || || |||  |  ||| ||||
Db 3960 CTGTCTTCACAAGGATCACTGACTCCCCTCCCCTGACGTATTCAACCCTATGGGAGGTTTTTGG 4019

Qy 4060 CCAAACCCTAGGCAGATGTCGAGGGTGTGTCAGTTGTCGTGGTCATTTGACGAGTGCCACAGTC 4119
        |||||||||||||||||||||||| |||| ||| || ||| ||||||||| ||||||||||||
Db 4020 CCAAACCCTAGGCAGATGTCCTGAGGGTGTGTCAGTTGTCGTGGTCATTTGTGATGAGTGCCACAGTT 4079

Qy 4120 ATGACTCAACTGTGTTGTTGGGCATTGGGCGTGTCAGGGAGCTGGCCGCGAGGATGTGGAG   4179
        |||| ||||| ||| ||| |||||| ||   || ||||||||| | ||| || | ||||||
Db 4080 ATGACTCAACCGTGCTTGCTAGGCATTGGGAGGGTTCGGGAGCTGGCGGTCCCGCTGCGCGAG 4139

Qy 4180 TGCAATTGGTGCTCTACGGCCACTGCCCACCCTTCCCGGATCCCCAGCACCCCAT        4239
        ||||| |  ||||| |||||  ||||||||||| || |||||||||||||||||||
Db 4140 TGCAACTAGTGCTCTACGGCCACCACCGGATCCCCATGACGACGCAGCACCCTT      4199

Qy 4240 CAATCATTGAGACAAAAATTGGACTGGGCGAGATCCCTTCTATGGCATGGCCATACCTC   4299
        ||||||||||||| |  ||||  |||||||||||||| |||  || ||  |||||||||
Db 4200 CCATAATTGAGACAAAATTGGACTGGGCGAGATTCCCTTTTTATGGCACGGAATACCCC  4259
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Right column:

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Qy 4300 TTGAGCGGATGGCGGAAGGCATCTCGTATTCTGCCACTCGTAGTGCCGAGC          4359
        |||||||||||  | |  |||||||||||||| | || || ||||||||||
Db 4260 TCGAGCGGATGCGGAACCGGAAGGCACCTCGTTGTTCTGCCATTCTAAGGCTGAGTGCCGAGC 4319

Qy 4360 GCCTGCGCGGGCCAGTTTTCGGCTAGGGGGTAAATGCCATCGCCTATTACAGGGGAAAG   4419
        |||| ||   |||||| ||| || ||||||| |||||||  ||  || || |||| ||||
Db 4320 GCCTTGCTGCCCAGTTCTCCCGCTAGGGGGTCAATGCCATTTATTATAGGGGTAAAG    4379

Qy 4420 ACAGTTCTATCATCAAAGATGGAGACCTGGTGGTGTGTCTACAGACGCACTATCCACTG   4479
        |||||||||||||||| |||||  |||||| ||||| ||  || |||||  ||||||||
Db 4380 ACAGTTCTATCATCAAGGATGGGGGACCTGGTCGTGTGTCTGTGCCACAGACGCGCTTTCCACTG 4439

Qy 4480 GGTACACTGGGAACTTCGATTCTGTCACCGATTGTGGTTAGTGGTTGGAGAGGTCGTCG    4539
        |||||||||||||||  |  ||| ||||  |||  |  |||  |||||||||||||||
Db 4440 GGTACACTGGAAATTTCGACTTCACCACCGCTGTGGATAGTGGTTGGAGAGGTCGTTG    4499

Qy 4540 AGGTGACCCTGATCCCACCATTACCATCTCCCTGCCGCACGTGCCCGCGTCGGCGTGAAC 4599
        |||||||||| ||||  |||  ||| |  |  ||| || || ||||| |||||| ||||
Db 4500 AGGTGACCCTTGATCCTACCATTACCATCTCCCTGGCAGTGCTGCCTGCGTCGGCTGAAC 4559

Qy 4600 TGTCGATGCAGCGGCGAGGACGCGCAGGACGCCTAGGGCAGGTCTGGGCCGTAGTACGCGG 4659
        ||||||||||||||||  || | ||  || ||||| |||  ||| |||||||  ||||||
Db 4560 TGTCGATGCAAAGACGAGGAAAGCGCCCGTGTCGGTAGGGCAGGTCTGGACGCTGGACTACTACGCGG 4619

Qy 4660 GGGTCGGCAAGGCCCCTGCTGGTGGTGCGCTCAGGTCTCTGTCTGGTCGCGGTGGAAG   4719
        |||||||||| | || | | |||| ||||| |||||| | |||| ||||| ||||| |||
Db 4620 GGGTGGGCAAAGCCCTCGTGCGCGTGTGTGCCCTCAGGTCTCCCAGGTCCCTCAGGTCGGTCGTGGTGAAG 4679

Qy 4720 CCGGTGTGACCTGGTACGGAATGAGAACCTGACCTGCGCAGAGCAAACCTACTTGGAGACTTTACG 4779
        | |||| || |||||||| ||||| |||||||||| | |  ||||||| |||||||||||||||
Db 4680 CTGGAGTGACCTGGGTACGGAATGGAGAACCTGACCTGCGTCGGCGGAGCAGTCTAACACTACTAACTTTACG 4739

Qy 4780 ACAACTGCCTTACACCCGCAGCTGACATTGGGGAAGCGCCGGAAGTTCGCGCGTCTTTT  4839
        | ||||||| ||||||| |||||||  ||||| |||||||| || ||||||| ||||
Db 4740 ACGACTGCCCTTACACCCGCAGCTGACTTTGTGATCGGACCCGCGAAGCAGCCGCGGTGTTCTTCT 4799

Qy 4840 CGGGGCTTCGCCCCGTTGAGGATGCATCCCGATGTGAGCTGCGGCAAAAGTTCGCGGCGTCA 4899
        | |||||||  |||| | || | |  | ||||| | || |||| ||||||| |||||||||
Db 4800 CTGGGCTCGCCCATTGAGGGCTCGCCCAATTGAGCTGCGGCAAAAGTTCGCGGCGTCA    4859

Qy 4900 ACTGGACCCCTTCCTGTTGGTGTTCAGGCACCCCGGACCATGCCCGGACACTGTCCCCGGCC 4959
        ||||||||  || ||||| || ||| || ||||||||||| |||| | |||||| |||||||
Db 4860 ACTGGACCCCTCTTGTGGTGTTCAGGACCACCATGTGCGACCACATGTGTCGGACCACTGTCTCTCCGGCC 4919

Qy 4960 CATCCGATGACCCCCAGTGGGCAGTCTGAAGGGCCGAATCCTGTCCCACTCCTGCTGA    5019
        ||||||| |||||  |||  ||||||||||||||||| | || ||||||||| || |||
Db 4920 CATCCGATGACCCCCAAATGGGCCCAAATCCTGTGAAGGGCCCAAATCCTGTCCCACTCCTGCTGA 4979

Qy 5020 GGTGGGGCAATGATTTACCATCTAAAGTGGCCGGCCATCACATCGTGGACGACCTGGTCC   5079
        ||||||||||||| || |||| ||||||  ||||||||||| |||||| ||||  ||| ||
Db 4980 GGTGGGGCAATGATTTACCATCTAAAGTGGCCGGCCACCATAGTGGACGACCTGGTCC    5039

Qy 5080 GTAGGCTCGGAGGGTGCCGGAGGGTTACGTCCGCGATGGTGATGGTGG            5139
        | | ||| ||| | |||||  |||| |||||| || | |  || || |||
Db 5040 GGAGACTCGGTGTGCGGAGGGTTACGTCCGCGACGCTGCGACGTTGATGATCG       5099

Qy 5140 GCCTCGTATTGCGGGGGCCATGATCTACACCGGGTCTCATCACCTCTGGTGTTA       5199
        ||| || ||||| ||||| |||||||| |||||||||||||||  ||||||| ||
Db 5100 GTCTAGCTATCGCGGGGGCATGATGATCTACACCGGGTCGCGTACGTGGTGGTGA      5159

Qy 5200 CAGACTGGGATGTGAAGGGTGCCAGGAGCTGGCCGCATGTGAGAGACCAGGCCACGC    5259
        ||||||||||| || |||| |||||||||  ||  |||||| |||  ||||||||||||
Db 5160 CAGACTGGGAATGTGAAGGGGCGCGGGCTGGCCGCATGTGGCATGCAGGCCAGCCACGC 5219

Qy 5260 CCCAGCCGTGTGCAGTGCCCCCGGATCCCGATGACCCCAGCACCCCAT          5319
        ||||  || |||| ||||  |   |||| | | |||| |||| || |||
Db 5220 CTCAGCCGTGGTGCAGGTTCCTCCCGGATCCTAGCAGCATCGGCCACCAT         5279

Qy 5320 CGGATGCCAACACAGTGACGATGCGCGGCGCATCCAGGTGCGATTGGCATTCGGTCAG  5379
        ||||||||| ||| ||| ||||| || ||||||||||| |||| |||  || |||| |
Db 5280 CGGATGCCAAGAGACAGAGTGACGATGCGGTGCGGCGACATCCAGGTTCCAGTTGGACTA 5339
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Db   6420 ACACCCCGAAGGTTGTGCCTTGGCGTCTCGGGACGTCTGGCTGGTGTGGTGACCACTA 6479

Qy   6520 CCCACGTTGTGATCAGGCGAACATCCGCTTCGGGACGTCTGGCTGGTGCGGCCAGCAAATCCTGTCGG 6579
Db   6480 CCCACGTGGTAATCAGGAGGACGAACCTCCGCTTCGGGACGTCTGGCTGGTGCGGCCAGCAAATCCTATCGG 6539

Qy   6580 CTGCTGTTGCTGAGCCTATTACGTCGACGGCATACCGGTCTCATGGGACGCGGGACGCGC 6639
Db   6540 CTGCTGTAGCTGAGCCCTACTACGTCGACGCGCATTCGGGTCTCATGGGACGCGGGACGCTC 6599

Qy   6640 GAGCGCCTGCCATGGTCTCATGGGCCTTAGGAGCTCACCAAGTGTCACCATTGACACGACGGGAACGCTACA 6699
Db   6600 GTGCGCCCGCCATGGTCTCATGGGCCCTGGGCAAAGTGTTACCATTGACACGGGAGCGCTACA 6659

Qy   6700 CCCTTCCGCATCAACTGCGGCTTAGGAATGTGGCGCCCTCTGAGGTGTCATCCGAGGTGT 6759
Db   6660 CCCTTCCTCATCAACTGAGGCTCAGGAATGTGGCGCCCTCTGAGGTTTCATCCGAGGTGT 6719

Qy   6760 CCATTGACATTGGGACGGAGACTCAGAACTGATGCTGCAGAATTCTTGAACCTCACATAGATG 6819
Db   6720 CCATTGACATTGGGACGGAGACTGAGAACTGATGCTGCAGAATTCTTGAACCGCACATTGATG 6779

Qy   6820 CGGCTGCAGCCCTTCAGGCTGCATCGCAGCCCTCTCTTGTGGGAGTAGCCGAGAGATGCCTGTGT 6879
Db   6780 CGGCTGCTGCTCTCCAAGCGATCGCAGCCCTCTCTTGTGGTAGTAGCCGAGAGGATGCTGTAT 6839

Qy   6880 TCATCATGGAAGATTGCAGTACACCCCTCTCTTGTGGGAGTAGCCGAGAGATGCCTGTGT 6939
Db   6840 CCATCATGGAGGACTGCAGTGCAGTACACCCCTCTCTTTGTGGTAGTAGCCGAGAGGATGCTGTAT 6899

Qy   6940 GGGGAGAAGAACATACCCCGACTACCCCGGCCAGCACTTATCTCGGCCAGCACTTATCTCGGTTACTGAGAGCAGCC 6999
Db   6900 GGGGAGAAGAACATCCCCGTACTCCCGGCCAGCACTTATCCCGTACTGAGGTTACTGAGAGCAGCT 6959

Qy   7000 CAGATGAGAAGACCCCGTCTCGGTGTCTTCCTCGCAGGAGGATACCCGTCTTCTGACTCAT 7059
Db   6960 CAGATGAGAAGACCCCGTCTCGGTGTCTCTCGCAGGAGGATACCCGTCTTCTGACTCAT 7019

Qy   7060 TCGAGGTCATCCAAGCTCCCAGAGTCCGAGACAGCCGAGGGGAGGAAAGCGTCTTCAACGTGCGCTC 7119
Db   7020 TCGAGGTCATCCAAGTCCCAGAGTCCGAGACAGCCGAGGGGAGGAAAGCGTCTTCAACGTGCGCTC 7079

Qy   7120 TTTCCGTACTAAAAGCCTTGTTTCCACAGAGAGCCATGATGCCAAGAGAAAGCTTACCGTTAAGA 7179
Db   7080 TTTCCCTATTAGAAGCCTCATTTCCACAGAGCGTAACAGCGTAACAGCCTTACCGTTCAAGA 7139

Qy   7180 TGTCATGCGTGTTGAGAAGAGCGTAACAGCTGTAACACGTCTTCTTTCATTGGGATTGACGGTTCGCTG 7239
Db   7140 TGTCGTGCTGCGTTGAGAGTGTCGCTGGTCACGGTTCTTTTTCTCATTTGGTTCTCGGAGTGC 7199

Qy   7240 ACGTGACGAGGGCCACTCCGTGTGTGAGATGGAAATCCAGAACCATACAGCCTATTGTGACAAGGTGC 7299
Db   7200 ATGTTGCTAGCCTGGTCGTGTGTGAGATGGAAATCCAGAACCATACAGCCTATTGTGACAAGGTGC 7259

Qy   7300 GCACTCCGCTTGAATTGCAGGTTGGTGCTTGGTGCTTGGCCTTGTCTTCTCATTGCAATGAACTTTGAATGTG 7359
Db   7260 GCACTCCGCTTGAATTGCAGGTTGGTGCTTGGTGCTTGGCCTTGTCTTCTCTTTACATTGGTTCTCGGGGTGC 7319

Qy   7360 ACAAGTGTGAGGCTAGGCAAGAGACCTTGGCCTTGTCGTGGATCACCGGTGATG 7419
Db   7320 ACAAGTGTGAGGCTAGGCAAGAGAAACCTTGGCCTCTTTACATTTGGTTCTCGGAGTGC 7379

Qy   7420 CACTGACGAGGGCCACTCCGTGTGGTTGGCCGGTTGGCCGTCCTTGCTG 7479
Db   7380 CGGTGACTAGGGCCCACGCCGTGTGGTTGGCCGGTTGGCCGTCTCTTATTAG 7439

Qy   7480 TGGGCCGACACCACCAAGGTGATGTGATGTCACCCAACCCGACACAATGTTGGGAGGAAGAGTTGACA 7539
Db   7440 TGGGCCGACACTACTAAGGTGTATGTTACCAATCCAGACACAATGTGGGACGAGGGTGGACA 7499

Qy   7540 AGGTTACCTTCTGGCGTTCATTGGCACATTCTCGTCGGTGACATAGAGC 7599
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Db   7500 AGGTGACCTTCTGGCCTGCTCCTAGGGTTCATGATGAAGTAGTACCTCGTGGACTCTATTGAGC 7559

Qy   7600 GCGCTAAGAGGCAGCTCAAGCCTGCCTAAGCAATGGGTTACACCTTATGAGGAGGCAATAA 7659
          |||||||| |||| |||||||||||||||||||| || || ||||| |||||| |||||
Db   7560 GCGCTAAGAGGCAGCCCGCTCAAGCCTGCCTAAGCAATGGGTTACACCTTATGAGGAAGCAATAA 7619

Qy   7660 GGACTGTAAGGCCACATGCTGTTCCCCCCTGGGGATCTAAGGTGTCGGTCAAGGACCTCG 7719
          ||||||||||||||||||| |||||||||||| ||||||||||||||| ||||| || ||
Db   7620 GGACTGTAAGGCCACATGCTGTTCCCCCCGCTCATTGGGGATCTAAGGTGTCGGTTAAGGACTTAG 7679

Qy   7720 CCACCCCTGCGGGGAAGATGGCTGTCCATGACCGGCTCCAGGAGATACTTGAAGGGACGC 7779
          | ||| |||||||| ||||||||||| |||||||||||||||||||||||||||||||||
Db   7680 CCACCCCGCGGGGAAGATGCCGTCATGACCGGCTCCAGGAGATACTTGAAGGGACTC 7739

Qy   7780 CAGTCCCCTTTACTCTTACTGTGAAAAAGGAAGTGTTCTTCAAAGACCGAAAGGAAGAGA 7839
          || ||| |||||||||||||||||||||| |||||||||||||||||||| |||||||||
Db   7740 CGGTCCCCTTTACTCTTACTGTGAAAAAGGAGTGTGTTCTTCAAAGACCGGAAGGAGGAGG 7799

Qy   7840 AGGCCCCGCTCATTGTGTTCCCCCCCTGGACTTCCGATAGCTGAAAAGCTTATTC 7899
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   7800 AGGCCCCGCTCATTGTGTTCCCCCCTGGACTTCCGATAGCTGAAAAAGCTCATCT 7859

Qy   7900 TGGGAGACCCTGGACGGGTAGCCAAGGCGGTGTTGGGGGGCCTACGCCTTCCAGTACA 7959
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7860 TGGGAGACCCCGGACCACCGGGTAGCCAAGGCGGTGTTGGGGGGCCTACGCCTTCCAGTACA 7919

Qy   7960 CCCCAAATCAGCGAATTAGGAGAGATGCTCAAACTGTGGAATCAAAGAAGACACCATGCG 8019
          |||||||||||| | ||||| || | |||| |||||||||||||||||||||||||||||
Db   7920 CCCCAAATCAGCGAGTTAAGGAGAGATGCTCAAGCTCGAGAGTCTAAGAAGAGAAGCACCCCTTGCG 7979

Qy   8020 CCATCTGTGTGGACGCGCCACATGCTTCGACAGTAGCATAACTGAAGAGGACGTTGGCGCCTGG 8079
          |||||||||||||||||||||| ||||||||||| |||||||||| ||||||||||||||||
Db   7980 CCATCTGTGTGGACGCGCCACCTGCTTCGACAGTAGCATAACTGAAGAGGACGTGGCTTTGG 8039

Qy   8080 AGACAGAGCTTTATCGCCTGCTTCAGACCATCCAGAATGGTGCGCTGCCCGTGGGAAAT 8139
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   8040 AGACAGAGCTGTACGGCTGCTCTGCCCTCGCCCAGAATGGTGCGCTGCCCGGCACTTGGGAAAT 8099

Qy   8140 ACTATGCCTCTGGCACAATGGTAACCCCGAGGGGGTGCCAGTGGGTGAGAGGTATTGTA 8199
          ||||||||||||| ||||||||| || |||||||||||||||||||||||||||||||
Db   8100 ACTATGCCTCAGGCACCACCATGTCACCCGAAGGGGTGCCAGTGGGTGCGGTCGGTATTGCA 8159

Qy   8200 GATCCTCAGGGGTCTTGACCACCAGTGCGAGCAACTGCTTGACTTCGTATATCAAGGTGA 8259
          ||||| ||||| | || | |||||||||||||||||| |||| |||||||||||||||
Db   8160 GATCCTCCGGGTGTCCTAACAACTAGCGGCGAGCAACTGCTCGACCTGCTCTACACTCAAGGTGA 8219

Qy   8260 AAGCCCCTGTGAGAGGGTGGGGCTGAAAAATGTCTCGCTCCTCATCGTCTGGCGATGACT 8319
          ||||||||||||||||||||||||||||||||||||| ||||||||| ||| ||||||||
Db   8220 AAGCCCCGTGTGAGAGGGTGGGGCTGAAGAATGTCTCTCTCCTCATAGCCGGCGATGACT 8279

Qy   8320 GTTGATCATATGCGAACGGCCTGTGTGCGATCCTAGCGACGCCTTGGGCAGAGCCCTGG 8379
          | ||||||||||| || |||||||| | || |||| ||||||||||||||||||||||
Db   8280 GCTTGATCATATGGTGACGGTACGCCATGCCAGTGCGCCAGTGCGACCGCGCTTGGGCAGAGCCCTAG 8339

Qy   8380 CGAGCTACGGGTACGCATGCAGCCCCTTCGTATCATCACTGACACCGGCCCCCCTTCT 8439
          ||||||||||||||||||| |||||||||| |||| || |||||||||||||||||
Db   8340 CGAGCTATGGGTACGCTGCGAGCCCCTCATCATGCAGCCCCATCACCGGCCCCCCTTCT 8399

Qy   8440 GCTCCACTTGCTAGCTGAGTGCAATGCAGATGCAGAAACGCCATTTCTTCCTGACCACGG 8499
          |||||||||||||| ||||||||||||||||||||| | |||||||||||||||||||||
Db   8400 GCTCCACTTGGCTTGCTGAGTGCAATGCAGATGGGAAGCGCCATTTCTTCCTGACCACGG 8459

Qy   8500 ACTTTCGGAGGCCCCCGGCCGCCTTCGCTTCGCCATGTGACCCCAATGGCTTCGGCCA 8559
          ||||| ||||| | ||| ||||||||||||||||| |||| |||||||||||||||| |
Db   8460 ACTTCCCGGAGGCCGCCCGCTTCGCTCGCCATGTGACCCGATATAGTGACCCGATGCTTCGGCGA 8519

Qy   8560 TCGGTTACATCCTCCTCTATACCCTTGGCATCTCTATACACACGGTGGCTCATCCCTTCACC 8619
          |||||||||||| ||||| || |||||| |||||| ||||||||||||||||||||||||
Db   8520 TCGGTTACATCCTCTTTATCCTTGGCACCCCCATCACACACGGTGGGTGGTCATCATCCCTCATG 8579

Qy   8620 TGCTCACCTGGCCGCGTTTAGGGGTTGGGCATTTCAGGGGCCAGGTAC 8679
          ||||| ||||||||||||||| ||||| || ||||||||||||||||
Db   8580 TGCTAACGTGGCCATTCAGGGGGTGAGGCGACCACGGCGTTTGGTGCCAGGTAC 8639

Qy   8680 ATGGTAATTACTACAAGTTCCACTGACACAAATCGCCTAACAATCATCGTGGCCCTTAACATCA 8739
          ||||||||| ||||||||||||||||| ||||| ||||||||||||||||||||||||||||
Db   8640 ATGGTAACTACTACAAGTTCCACTGGACACAAATCGCCTAACAATCATCGTGGCCCTTAACATC 8699

Qy   8740 GACCAGCAGCGTTGAGGGTTACCGCAGACAACTAAGACAAAAATGGAGGCTGGCAAGG 8799
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Db   8700 GACCAGCAGCGTTGAGGGTTACCGCAGACAACTAAAACAAGATGGAGGCTGGTAAGG 8759

Qy   8800 TGCTGAGCGACCTCAAGCTCCCTGGCCTTCACCGGGAGAAGGCCGGGGCATTGC 8859
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Db   8760 TTCTGAGCGACCTCAAGCTCCCTGGCCTTAGCAGTCCACCGGGAGAAAGAAGCCGGAGTTGC 8819

Qy   8860 GAACGGCTATGCTCCGTCCGGCGCGGGGTTGGGCTGGCTAGGGGGCTGTTGTGGCGTC 8919
          ||| ||||||||| || ||||||||||||||||||||| |||||||| |||||||||||
Db   8820 GAACACGCATGCTCCGTCCGGCGGGGTTGGGCTGTCAGTTGGCGTTGGGCCGTTGTTGGCCATC 8879

Qy   8920 CAGGGCTGCGGCTTCCCCCTCCGGAGATTGCTGGTATCCCGGCGTTTCCCCCTTTCCC 8979
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Db   8880 CAGGCCTACGGCTTCCCCCTCCCGAGATTGCTGGTATCCCGGGGGGTTTCCCTCTCTCCC 8939

Qy   8980 CCCCCTATATGGGGTGTTCATCAATTGGATTTCACAAGCCAGAGGAGTCGCTGGCGGT 9039
          ||||| ||||||||||||||||||||||||| | |||||||||||||||||||||||
Db   8940 CCCCCTATATGGGGTGTGGTACCAATTGGATTTTACAAGCCAGAGGAGTCGCTGGCGGT 8999

Qy   9040 GGTTGGGGTTCTTAGCCCTGCTCATCGTAGCCCTCCTTCGGGTGAACTAAATTCATCTGTT 9099
          ||||||| |||| |||||| ||||| | ||||||||||||||||||||||||||||||||
Db   9000 GGTTGGGGTTCTTAGCCCTGCTCATCGTAGCCCTCCTTCGGGTGAACTAAATTCATCTGTT 9059

Qy   9100 GCGGCAAGGTCCGTGACTGATCATCACTGACGAGGAGTTCCCGCCCCCCAGGG 9159
          |||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   9060 GCGGCAGGTCGTGGTGACTGATCGTCACCGAGGAGTTCCCGCCCTTCCCCCCAGGG 9119

Qy   9160 GTCTCCCCGCCGGTGGTAAAAAGGGCCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCTG 9219
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Db   9120 GTCTCCCGCCGGTGGTAAAAAGGGCCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCTG 9179

Qy   9220 GCAGGGTCAAAGCCTGATGTGCTAATTGCACTTGCCACTTCCGGTTCGGTCGCCGGTCGCTACCTTA 9279
          |||||||| || |||||| ||| | || || ||||||||||| ||||||| |||||||||||||||
Db   9180 GCAGGGTTAAAGCCTGATGTGCTAATCGACTGCCACTTCCGGTTCGGTCGCCGGTCGCTACCTTA 9239

Qy   9280 TAGCGTAATCCTGACTACGGCCGTCGCGAGCCTGCTCGCAGACGCCCTCCCCGATGGGCACAGTGCAC 9339
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9240 TAGCGTAATCCTGACTACGGCCGTCGCGAGCCTGCTCGCAGACGCCCTCCCCGATGGGCACAGTGCAC 9299

Qy   9340 TGTGATCTGAAGGGGTGCACCCCGGTAA 9367
          || ||||||||||||||||||||||||
Db   9300 TGAGATCTGAAGGGGTGCACCCCGGGAA 9327

RESULT 10
; GENERAL INFORMATION:
;   APPLICANT: Kim, Jungsuh P.
;   APPLICANT: Wages, John
;   APPLICANT: Young, LaVonne M.
;   APPLICANT: Fry, Kirk E.
;   APPLICANT: Linnen, Jeffrey M.
;   TITLE OF INVENTION: Hepatitis G Virus and Molecular
;   TITLE OF INVENTION: Cloning Thereof
;   NUMBER OF SEQUENCES: 277
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dehlinger & Associates
;   STREET: 350 Cambridge Ave., Suite 250
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible

us-09-828-498-1.rni

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  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/464,134
  FILING DATE:
  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/389,886
  FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/357,509
  FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/329,729
  FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/344,271
  FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/285,558
  FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/285,543
  FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/246,985
  FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
  NAME: Fabian, Gary R.
  REGISTRATION NUMBER: 33,875
  REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 324-0880
  TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 234:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 9327 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: unknown
  MOLECULE TYPE: cDNA
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
  ORIGINAL SOURCE:
  INDIVIDUAL ISOLATE: 32HGV-6, HGV FROM PNF2161
US-08-464-134-234
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Query Match             83.9%;  Score 7885.6;  DB 2;  Length 9327;
Best Local Similarity   90.4%;  Pred. No. 0;
Matches  8433;  Conservative    0;  Mismatches  894;  Indels   1;  Gaps   1;

Qy     40 GCAAGCCCATAAACCGACGCGCTATCTAAGTAGACGCCAATGACCTCGGCCGCCGACTCGGCCG   99
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAAGCCCCAGAAACCGACGCGCTATCTAAGTAGACGCCAATGACCTCGGCCGCCGACTCGGCCG   60

Qy    100 ACCGGCCAAAAGGTCGTGGATGGGGTTGGTAGGGTGACCAGGGTTGGTAGGTCGTAAATCCCGGTCAT  159
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACCGGCCAAAAGGTGTGGATGGGGTTGGTAGGGTGATGACAGGGTTGGTAGGTCGTAAATCCCGGTCAC  120

Qy    160 CCTGGTAGCCACTATAGGTGGTCTTAAGGAAGTCAAGACTCCTTGTGCCTGCGGC  219
          | ||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    121 CTTGGTAGCCACTATAGGTGGTCTTAAGGAAGTTAAGGAATTCCTTCTTGTGCCTGCGGC  180

Qy    220 GAGACCGGCGACGGTCCACAGTGTCTGGCCCTACCGGTGTGAATAAGGGCCGACGTCAG  279
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    181 GAGACCGGCGACGGTCCACAGTGTTGGGCCCTACCGGTGGAATAAGGGCCGACGTCAG  240

Qy    280 GCTCCGTCGTTAAACCGAGCCCGTCACCCACCTGGGCAAACGACGGCCCACGTACGGTCCAC  339
          | ||| |||||||||||||||||| ||||||||||||||||| |||||||||||||||||||
Db    241 GCTCCGTCGTTAAACCGAGCCCGTTACCCACCTGGGCAAAACGACGCCCCACGTACGGTCCAC  300

Qy    340 GTCGCCCTTCAATGTCTCTCTTGACCAATAGGTTTATCCGGCCGAGTTGACAAGGACCAGT  399
          ||||||||||||||||||||||| || |||||||||||||||||||||||||||||||||||
Db    301 ...
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Db    301 GTCGCCCTTCAATGTCTCTCTTGACCAATAGGCTAGCGGCCGAGTTGACAAGGACCAGT  360

Qy    400 GGGGGCCGGGGTTATGGGAAGGACCCCAAACCTGCCCTTCCCGGTGGGCCGGGGAAAT  459
          |||||||||||  ||||| ||||||||||||||||||||| |||||||||||||||||
Db    361 GGGGGCCGGGGCT-TGGAGAGGGACTTCCAAGTCCCGCCCCTTCCCGGTGGGCCGGGGAAAT  419

Qy    460 GCATGGGGCCACCAGCTCCGCGGCCTGCAGCCGGGGTAGCCAAGAATCCTTCGGG  519
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GCATGGGGCCACCAGCTCCGCGGCCTGCAGCCGGGGTAGCCAAGAATCCTTCGGG  479

Qy    520 TGAGGGCGGGTGCATTCTTTTCTATACCATCATGGCAGTCCTTCTGCTCCTTCTCG  579
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    480 TGAGGGCGGGTGCATTCCTTTTCTATACCATCATGGCAGTCCTTCTGCTCCTTCTCG  539

Qy    580 TGGTTGAGGCCGGGGCCATTCTGCCCCCGGCCACCACGCTTGTCGAGCGAATGGGCAAT  639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 TGGTTGAGGCCGGGGCCATTCTGCCCCCGGCCACCACGCTTGTCGAGCGAATGGGCAAT  599

Qy    640 ATTTCCTCACAAATTGCTGTGCCCGGAAGACATCGGGTTCTCGCTGGAAGGCGGATGCC  699
          ||||||||||||||| |||||||||||| ||||||||||||||||||||| |||||||||
Db    600 ATTTCCTCACAAATTGTGTGCCCGGAGGACATCGGGTTCTCGCTGGAGGGTGGATGCC  659

Qy    700 TGGTGGCCCTGGGTGCACGGTTGCACCGACCGGTGTATCGGGCCACTGTATCAGGCGGGTT  759
          |||||||||||||||||||| |||||| |||| ||  |  |||||||||||||||||||||
Db    660 TGGTGGCCCTGGGTGCACGATTGCACTGACCAATGCTGGCCAATGTGGGCACTGTATCAGGCGGGTT  719

Qy    760 TGGCTGTGCGGCCTGGCAAGTCCGCGGCCCAGTCGTCGGGAACTGGGAACTGGGAGCCTGTACG  819
          |||||||||||||||||||||||||||||||| || |||||| ||||||||| |||| |||||
Db    720 TGGCTGTGCGGCCTGGCAAGTCCGCGGCCCAACTGGTGGGAGCCTGGGTGGGTAGCCTATACG  779

Qy    820 GGGCCTGTCGGTCGCGGCTTACGTAGCGGGATCCTCGGGTCTCGGGGCGCCCAACCTGAAGT  879
          ||||  ||||||||| |||| | ||||||||||| |||||||||| || |||  |||||||||
Db    780 GGCCCCGTTGCGTCCTGTCTCCGGGTCTCTATGTGGCCTATGGGCTGGGTGAGGGTGACTCGG  839

Qy    880 GGGTCCTGACAGTTGGTTGCGTTGCGGCGCCGGGTCTACCTGATGCCCAACCTGACGT  939
          ||||| ||||||||||||| |||| |||||||||| || ||||||||| ||||||||||
Db    840 GTGTCCTAACGGTGGGAGTCGCGGTTGACGCGCGGGATCTACCGGTGCCTAACCTGACGT  899

Qy    940 GTGCAGTAGAATGCAGCGTGTTAAGTAGTGGGAAGTGAGTTTGGAGGACTGAGCAGTGG  999
          |||| |||| ||||| ||||| ||||  ||| |||||||| ||||||||||||||||||||
Db    900 GTGCAGTCGCGTGTGAGTTAAAGTGGGAAGTGAGTTTGATTTGATTTCTGGAGGACGTGG  959

Qy   1000 CCTCCAATTACTGGATTTTGGAATACCTTTGGTTGCCGATTTGTTTGCTGGAGCCAACGGA  1059
          ||||||||||| | |||||||||||||||||  ||||| |||||  ||||| |||||||||
Db    960 CCTCCAACTACTGGATTCTGGAATACCTCTGGAAGTCCCATTGAAGTCCCATTGATTTCTGGAGGAGGCG  1019

Qy   1060 TGATGAGCCTGACCCCTCTGTTGGTTGGTTGGTGGCCGCAATGGTTTGCTGGAGCAACGGA  1119
          || ||| | |||||  || ||||||| ||||| |||||||||||| || |||||||||||||
Db   1020 TGATAAGCCTGACCCCGTTGTTGGTTGGTTGGTGGCCGCAATTGCTGCTGCTGAGCAACGGG  1079

Qy   1120 TTGTCATGGTTTCCTGCTGGTGGACGATGGCCGGGATGTTGCAAGGCGCCCCCGCCTCCG  1179
          |||||||||||||| ||||||| |||||||| |||||||||| ||||||||  |||||||||
Db   1080 TTGTCATGGTCTTCGTGTTGGTGGTGACGATGGCCGGGATGTTGCCAAGGCGCCGAAGGCCGCCCCCTGCCTCCG  1139

Qy   1180 TTTTGGGGTCCCGCCCCTTTGACTACGGGTTGAAGTGGCAGTCATGCTCCTGCAGGGGTA  1239
          || |||||| ||||||  |||||||||| || ||||| |||| ||||||||||||||||||
Db   1140 TTTTGGGGTCACGGCCTTTGACTTGACGGTGGTCGTTGGTAGGTCCAGGGGCA  1199

Qy   1240 ACGGGTGCGTATTCCCACTGGGGAGAGGGTGGGATCGAGGGAAGTCACCGCTCTTGT  1299
          |||| |||| ||| ||||  |||||||||| || ||||| |  ||||||||||  |||
Db   1200 ACGGTTGCGTTTTTCGACTGGGGAGAAGGTGTGGCACCGTGGGACCGTGGGAACCGTTACCGCTTCAGT  1259

Qy   1300 GTGACTGCCCCAACGGCCCCTGGTTGGGTCCCGGCCTTTGCCAGCGGTGGTGGG  1359
          |||||||||||  ||  ||||  |||| || || |||  ||||||||  ||||||
Db   1260 GTGACTGCCCTAACGCCCCTGGTGGTGTTGGTTGCCAGCCTTTTGCCAAGCAATCGGCGTGGG  1319

Qy   1360 GCGACCCCATCACCCATTGGAGCCCACGACAAAACCAGTGGCCCCCCCAAT  1419
          | |||||||| |  |||| |  ||||||| |||| ||||| || |||||||||
Db   1320 GTGACTGCCCATCACTTATTGGAGCCACGGCAAAATACGGGCCCAAAAATACAGTGGCCCCCTTTCATGCCCCCAGT  1379

Qy   1420 ATGTCTATGGGTCGTGTCGCTACAGTCACTTGCGTGTGGGGTTCCGTCTTCGA  1479
          |||||||||||| | ||||  | ||| |||| |||| ||||||| |||  |||||
Db   1380 ATGTCTATGGGTCGTCGTACAGTCACTTGCGTGTGGGGGGTTCCGCGTTCCGCGTTCCTCCA  1439
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Qy  1480  CCGGCGGTCGTGATTCGAAGAGATCGATGGTGTGGAGTTTGGTGCCGGTTGGATCTGCCAGCT  1539
          || |  ||||||| || |||| ||| |||||||||||||||||| |     |||||  ||
Db  1440  CCAGTGGTTGCGCGACTCGAAGATAGATGTGTGGGAGTTTAGTGCTTGGCTCTGCTGCCACCT  1499

Qy  1540  GCACCTAGCAGCGGATCGGATCGCGCACCGTCGGCCGCCTGGGCCTCTCCGAGTGGG  1599
          || ||| |||||||||||||||||||| ||||||| |   | |||||||||||||||
Db  1500  GCACCATAGCCGCACTTGGATCATCGGATCATCGGACCGTCGGCCTCTCGGAGTGGG  1559

Qy  1600  GAGTCCCGTGCGTAAGCGTGTATTCGGACCGTCGGCCTGCTTCATGTGCACCTGTGTGC  1659
          ||  ||||||||||||| || |||||||||||||||||||||||||| |  |||||||
Db  1560  GAATCCCGTGCGTGACGTGTGTTCGGACCGTCGGCCTGCTTCATGCGGCACCTGTGTGA  1619

Qy  1660  GGGACTGCTGGCCCGAAACCGGTCGTTAGATTCCCTTCCATCGGTGCGGCGGCACGGGGC  1719
          |||||||||||| | |   ||||| |||||| |||||||||||||| || |||| ||| |
Db  1620  GGGACTGCTGGCCCGAGACCGGTCGGGTTAGGTTCCCATTCCATCGGTGCGGCGGCGGGGGC  1679

Qy  1720  CTCGGCTGACAAAGGACTTGGAAGCTGCCCTTCGTCAACAGGACAACTCCCTTCACCA  1779
          |||||||||||||||||||||||||||||||||||||| || |||||||||||||||
Db  1680  CTCGGCTGACAAAGGACTTGGAAGCTGTGCCCTTCGTCAATAGGACAACTCCCTTCACCA  1739

Qy  1780  TAAGGGGCCCCCTGGGCAACCAGGGAGAGGCAACCCGGTGCCGTCGCCCTGGGTTTG  1839
          | |  |||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  1740  TTAGGGGCCCCCTGGGCAACCAGGGCCCGAGGCAACCCGGTGCCGTCGCCCTTGGGTTTTG  1799

Qy  1840  GGTTCCTACACCATGACCAAGATCCGGGATTCCCTGCATTTGGTGAAATGTCCACACCAG  1899
          |||||||||||||||||||||||||||||||||| |||||| |||||||||||||||||
Db  1800  GGTTCCTACGCCATGACCAAGATCCGAGATCCGAGATACCTGGTGGAGTGTCCACACCAG  1859

Qy  1900  CCATAGAGCCCTCCGACTTGGAAGCTCGGTCTCTCCCCGGAGTCCCCCATTAAACAACT  1959
          |||||||||||||| | ||||||||||||| |||||||||||||||  ||||| |||||
Db  1860  CCATCGAGCCCTCCACCGGGACGCCGGTCTTTGGGGTTCTTCCCCGGACGCCGCCTCTCAACAACT  1919

Qy  1960  GCATGGCCTAGGCACGGAAGTGTCTGAGGCATTGGGCGGAGCTGGGCTTACGGGGGT  2019
          ||||| ||| ||||||||||| | ||||||||  |||||||||||||||||||||||
Db  1920  GCATGCTCTTGGGCACGGAAGTGTCCGAGGCACTTGGGGGGGCTGGGCTGGCTTCACGGGGGGGT  1979

Qy  2020  TCTACGGAGCCCTCTGGTTCGCAGTGTTCGGAGCTGATGGGACCGCGAAATCCGGTTTGCC  2079
          ||| ||||||| ||||||||||||||||||||||||||||| |||||||||||||||||
Db  1980  TCTATGGAACCCCCTGGTTCGCAGTGTTCGGAGCTGATGGGGAAGCCGAAATCCGGTTTGTC  2039

Qy  2080  CGGGGTACGCATGGCCATGGCCTGTGTGCTAGACCTGCACGGTCATACACGTCCAGGGCACC  2139
          || || ||| | ||||| |||||| |  |  |||  ||||||||||||||||||||||||
Db  2040  CGGGGTTTGCATGGCCATGGCCTCTTCGGCAGCCTCGGCCCGCAGCCTGATGGTCCAGGGTCACT  2099

Qy  2140  TGCAGGAGGTGGATGCGGGCCAACTTCATCCCTCCTCCACGCGTCGTGTTCCGCGTTTTTG  2199
          ||||||||||||||| |||| ||||||||||| | || |  ||||| || |||||||||
Db  2100  TGCAGGAGGTGGATGCGGGCCAACTTCATCCATCCTCCCGCCCCGCGTCCTGTTCTTGGACTTTG  2159

Qy  2200  TATTTGTCCTGCTCTATCTGATGAAGCTGGCTGAGGCACGGTTGGTCCCGTTGATCTTGC  2259
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Db  2160  TATTTGTCCTGTTTATACCTGATGAAGCTGGCTGAGGCACGGTTGGGTCCCGCTGATCTTGC  2219

Qy  2260  TTCTGCTTGGGGTGTGGGTGAACCCAGTTGGCGGGGTTCTAGGAGGCTGCCGTGTGACCGCTG  2319
          |||||||||||||| | || |||||||||||||||| ||||| ||||| ||||| || |
Db  2220  TGCTGCTATGGTGTGGGTGGGTGAACCAGCTGGCGGGGTTCTAGGAGGCTGCCGTGTGGACTTCCCCACTG  2279

Qy  2320  CCGTGGCGGGTGAAGTTTTGCGGGCCTGTGTTTGGGCCTTCCCACTG  2379
          || || || ||||| |  | || || |  || |||| |||||||
Db  2280  CCGTGGCGGGTGAGGTGGGTCGCATGGTGTGTCTGGGACTCCCGGTCG  2339

Qy  2380  TCAGTATGATACTAGGTCTAGCAAACCTGTGTTTTCGGTGATGGGCCCTCAGC  2439
          || |||||| | |||||| |||||||| |||||||||  ||||| ||| |||||
Db  2340  TCACTATGATATTGGGGTTTGGCAAAACCTGTTGTTGTTTTAGATGGTTGGGACCCCTCTTGA  2399

Qy  2440  GCCTCATGTTCCTCGTGTTGTGGGAGCTTCCCCTGGGATGGGACCTTTGA  2499
          ||||| || |||||||||||||||||||||||| ||| ||| ||||||||
Db  2400  GCCTGATGTTCCTCGTGTTGTGTGGGAGCTTCCCCGCTGGCCTGGCCTCTTGA  2459

Qy  2500  TGGGGATTTCGGCCACCCTGCTCTGCGTGCCACCTCTGCGGGGCCGAGTTCTGCTTCGATG  2559
          |||||||||||||||| ||||||||||||| ||||||||||||||||||||||||||||||
Db  2460  TGGGGATTTTCGGCCACCCTGCTCTGCGTGCCACCTCTGCGGGGCCGAGTTCTGCTTCGGATG  2519


Qy  2560  TCACATTCGAGGTGGACACTTCGGTGTTGGCGTGGTGGTGGCCAGCGTGGTGGCTTGGG  2619
          ||||||||||||||||||| |||||||| ||||||||||||||  |||| || ||||||
Db  2520  CTACATTCGAGGTGGACACTTCGGTGTTGGTGGTGGCCAATGTGGTAGCTTGGG  2579

Qy  2620  CCATAGCGCTCCTGAGCTCAATGAGCGCAGGGGGTGGAAGCACAAGGCCGTGATCTATA  2679
          |||||| |||| ||| ||| |||| || ||| ||| ||||| ||||| ||||||||||
Db  2580  CCATTCGCTCCTGAGCTCGATGAGACGCAGGGGTGGAGCGCACAAAGCCGTGATCTATA  2639

Qy  2680  GGACGTGGTGTAAAGGGTACCAGGCTGTCGCCGCAGAGGTGGTGCCGAGCCCCTCGGGGG  2739
          ||||||||||  |||||||||||||||||||||||||||| ||||| |||| ||||||||
Db  2640  GGACGTGGTGTAAGGGGTACCAGGCAATCCGTCAAAGGGTGGTGAGGAGCCCCTCGGGGG  2699

Qy  2740  AGGGGCGTCCTACCAAGCTTCTGACGTTCGCCGGTCCGTGCTTGCCCTCGTGCGGCCGG  2799
          |||||  ||||||||| ||| |||| |||| ||||||| ||| ||||||| | |||||
Db  2700  AGGGGCGGCGCCTGCCAAACCCTGACCTTTGCCTGGCTGCTCGTACATCTGGCCCAG  2759

Qy  2800  ATGCTGTGATGATGGTGTGTGGGGTTGTGGTGGCCCTTGGCCTCTTCTCTCGGCGCTGGTG  2859
          |||||||||||| ||| ||||| ||| ||||||||| |||||||||||| |||||||||||
Db  2760  ATGCTGTGATGATGGTGGTGGTTGCCTTTGGCCTGTTGTTGTCTCTTTGGCCTGTCGGACGCGGTGG  2819

Qy  2860  ACTGGGCCCTGGAGGAGCGTCCTGGTCTCCCGGGCCCTGGTTACGGCGACTGGCACGGGGTGG  2919
          | |  ||||| || |||||| ||  | || |||| || |||||| |||||||||||||||||
Db  2820  ATTGGGCCTTGGAGGAGATGGTGTCCCCGGCCCTGCGTGCGTGGTCGGTCGCGACTGTCGCA  2879

Qy  2920  TTGAGTGCTGTGTGATGGCGGCGGAGAAGGCCGAGGGTCTCCAAGATGT  2979
          |||||||||||||||||||| ||||| ||| |||||||||||||||||
Db  2880  TTGAGTGCTGTGTGATGGCGGCGGAGAAGGCCGAGGGTCTCCAAGATGT  2939

Qy  2980  GCCAAGAGAGGGGCTCACCTGTTTGACCACCATGCGTCTTCTCCGCGCGTGTCAAGGAGC  3039
          || | ||||| ||| |||||||||||||||||||||||||||||||||||||||||||||
Db  2940  GTGCCGAGAGGAGCTTGGTCTCATTGTTCGATCATATGGGCCTCTGTCATTTCGCGTCGTGTCAAGGAGC  2999

Qy  3040  GCTTGTTGGAATGGGACGCGGCTTTGGACGCTTTCATTCACTAGGACGGACTGTCGCA  3099
          ||||||||||||||||||| ||||| |||||||||||||||||||||||||| ||||
Db  3000  GCCTGTTGGAATGGGACGCGGCTCTTGAACCTCGTCATTCACTAGGACGGACTGTCGCA  3059

Qy  3100  TCATCAGAGATGCGCGGACCCTGCGGACAGTGCGTCATGGTTACCCGTGG  3159
          ||||  ||| ||||||||||| || |||||| |||||||||||||||||
Db  3060  TCATACGGGATGCGCGGACACTTTGTCCTGGCAATGCGCAATGCGTCATGGGTTTACCCGTGG  3119

Qy  3160  TAGCACGGCGCGGTGATGAGGTTCTCATCGCGCTCTTTCAGGATGGTGAATCATTTGCCTC  3219
          |||||| |  | || ||||||| |||| ||||||| |||||| |||| |||| |||||||
Db  3120  TTGCGCGCCGTGGTGATGAGTTCTCATCGGCGTCTTCATCGGCGTCATTTGCCTC  3179

Qy  3220  CCGGGTTGTCCCGACTGACCAGTTGCATCCGTCGCGGTGCGGAAAGGGCTTCCTGGGGG  3279
          |||||| | ||| |||||| ||||||||||||||||| |||||||||||| |||| ||||
Db  3180  CCGGGTTGTTGTTCCGACCCGCCCTGTGTTGTCATCCGGTATCCACGCCGGTGGTCGCGGAAAGGGGCTTCTTGGGGG  3239

Qy  3280  TCACGAAGGCAGCCTTGCACGAGGTAGGGACGATCCTGACTTACATCCAGGGAACGTCATGGTGT  3339
          ||||  |||||||||||||| |||| ||| | |||||| |||||||||||| ||| |||||||
Db  3240  TCACAAAGGCTGCCTTGCACGAGTCGGATGCCCTGACTTACATCCAGGGAACGTCATGGTGT  3299

Qy  3340  TGGGGACGGCTACGTCACGGAAGCATGGGCACATCGCCACCCTGGGGGCCCCTGTCGTTCACAACTT  3399
          ||||||| || ||| || ||| |||||| ||||||| |||||||||||||| ||| |||||||||
Db  3300  TGGGGACGGCTACGTCGCCGATGATGGGCACATCGCCACCCTGGGGGCCCTTAATCCCAGATGGT  3359

Qy  3400  TCCATGGGCTTCATCCCGAACCATCGCCAGCCGGGGCCCTTAATCCCAGGTGGT  3459
          |||||||||||||||||||||||||||| ||||||||| |||| |||||||||
Db  3360  TCCATGGGCTTCATCCCGAACCATCGCCACACCCCGTGGGGGCCCTTAATCCCAGATGGT  3419

Qy  3460  GGTCAGCCAGTGATGACGTCACGGTGTACCCGCCTTCGTTGACGCC  3519
          |||||||| |||| |||||| || |||| ||| |||||| ||||
Db  3420  GGTCAGCCAGTGATGATGTCACCAGCTCCACTTCGTTAACGC  3479

Qy  3520  CCTGCACTTGCCTCGTTGTTGAGCTGGATGTGGCCATGGGGCGTTTGTGCCATG  3579
          | || ||||  || |  |||||| || ||| ||| |||||||| ||||| |||||
Db  3480  CTTGTACTTGCCAAACCTCTGTATCCACGTGTGGGTCATCAGATCCGTAGGGACTTCGTTAACGC  3539

Qy  3580  GCTTGAGCAAGGGGGACAAGGTTGAGCTGGATGTGGCCATGGACGGGGTCTGACTTCCGTG  3639
          |||||||||||||| |||||||||||||||||||||| |||| ||| || ||||| |||||
Db  3540  GCTTGAGCAAGGGGGACAAGGTTGAGCTGGATGGCCATGGGCCCCTATGCCATGGAGTTCCGTG  3599

Qy  3640  GTTCCTCTGGTTCACGGTCCTTTGCGACAAGGCAGTAGAATGCTCGTGTCAG  3699
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Db  3600  |||||||| |||||| |||||  || ||||||  |||||||||||||||
          GCTCGTCTGCCTCACCGGTCCTATGTGACGAGGGCACCGCAGTAGGAATGCTCGTGTCTG  3659

Qy  3700  TGTCCACTCTGGCGCAGAGGTTACTGCCGGCGGCGATTCACTGAGGCCGTTGGACTCAAGTAC  3759
          |||| |||||| ||||| ||||  || ||||||||||||||||||  ||||  |||| |||||
Db  3660  TGCTTCACTCCGGCGTGGTAGGGTCACCGGCGGTTCACTGACCCGTTCACTGAGGCCCAAGTGC  3719

Qy  3760  CAACAGATGGCCAAGACTACCACAGAACCCCTCCGGTGCCGGCAAAAGGAGTTTTCAAGG  3819
          |||||||||||||||||||| || ||||| ||| |||||||||||| |||||||||||||
Db  3720  CAACAGATGCCAAAACCACACTCGAACCCCTCCGGTGCCGGCAAAAGGAGTTTTCAAAG  3779

Qy  3820  AGGCCCGGTGTTTATGCCGTGAAAGAGCACCCCGCTACCGTTGGAGTACG  3879
          ||||||| |||||||| ||| |||||| ||||| |||||||||||||||||
Db  3780  AGGCCCGGTTGTTTATGCCGTCTACGGAGCACTCGCGCTCCCGTTGGAGTACG  3839

Qy  3880  GCAACATGGGCCACAAGGTCTTGATCTTGAACCCGTCGGTAGCTACCGTGGAGGGCCATGG  3939
          ||||||||||||||||||| |||||||||| ||||| || |||||  |||||| ||||||||
Db  3840  GCAACATGGGCCACAAGGTCTTAGTCTTGAACCCCTCACTGGCCCACTGTGCGGGCCATGG  3899

Qy  3940  GCCCATAACATGGAGCGGCTGGCCGGGAAAACACCCCAGTATTACTGTGGCCATGACACCA  3999
          ||||||||||||||||| |||||||| ||||||| ||||||| ||||||||||||||||||
Db  3900  GCCCGTACATGGAGCGGCGGCGTGGGGCTAAACATCCAAGTATATACTGTGGGCATGATACAA  3959

Qy  4000  CTGCTTTCACAAGGATCACTGACTCGCCCCCTTACGTATTCCACTTACGAGAGGTTTTTGG  4059
          |||| ||||||||||||||| ||||||||| ||||| |||| ||||||| | ||||||||||
Db  3960  CTGCTTTCACAAGGATCACTGACTCCCCCCCCTGACGTATTCAACCTATGGGAGAGTTTTTTCG  4019

Qy  4060  CCAACCCTAGGCAGATGCTGAGCGGCTGCTACGCGGTCGGGTGTGTCATTGTGACGAGTGCCACAGTC  4119
          |||||| |||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  4020  CCAACCCCTAGGCAGATGCTGAGCGGTTTCGGTGTCATTTGTGTCATTTGTGATGAGTGCCACAGTT  4079

Qy  4120  ATGACTCAACTGTGTTGTGGCGCATCTCGTATTCTGCCACTCCAAGGCTCGAGGATGCGGAG  4179
          ||||||||||||||||||||||||||||  || ||||||||||||  |||  ||||||||||||
Db  4080  ATGACTCAACCGTGTCGGTGCGCATCTCGTCATTCGGCACTCCAAGGCTCCAAGGATGCGGAG  4139

Qy  4180  TGCAATTGGTGCTCTACGGCCACTGCCACCCCGGATCCCCGGATGACCCAGCACCCAT  4239
          |||| ||||||||||||||||||||||  || |||||||||||||||  ||||||||||||
Db  4140  TGCAACTAGTGCTCTACGGCCACCACCGCTAGGCTCCCACCGCCTGCCGGATCCCCGATGACGCAGCACCCCTT  4199

Qy  4240  CAATCATTGAGACAAAACTGACGTGGGAGAGATCCCCTGGGAGAGATCCCCTTCTATGGCATGGCATACCTC  4299
          ||||||||||||||||||||||||||||||||| ||||  ||||||| | |||||||||||||||
Db  4200  CCATAATTGAGACAAAATTGACGGATTGGGCCGAGAATTCCCTTTTTATGGGCACGGAATACCCC  4259

Qy  4300  TTGAGCGATGGCGACCGGAAGGCATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGC  4359
          ||||||||||||||||||||||||||||||| ||||||||| ||||||||||||||||||
Db  4260  TCGAGCGGATGGCGAACCGGAAGGCCACCTCGTCATTCGCCATTCTAAGGCTGAGTGCGAGC  4319

Qy  4360  GCCTGGCGGCCCAGTTTCGCGCTAGGAGGGGTAAATGCCATCGCCTATTACAGGGGAAAG  4419
          |||| || |||||||| ||||||||||||||  |||||||||||||  |||||||||||||
Db  4320  GCCTTGCTGGCCCAGTTTCTCCCGCTAGGGGGTCAATGCCAGTTTATTAGGGTAAAG  4379

Qy  4420  ACAGTTCTATCATCAAAGATGGACGCCCCTGGTGTGTTAGTGTTGGTTAGTTGTGAGGAGCTCGTCG  4479
          |||||||||||||||||| |||||| |||||||||||||| ||||||||||||||||||||||||||
Db  4380  ACAGTTCTATCATCAAAGACGAGGACCCCTGGTGTGTTGGTTAGTTGTGAGGAGTCCGTCG  4439

Qy  4480  GGTACACTGGGAACTTGCTGGTTAGTGTGGTTAGTGGTGGCCCGGCTTCTAGGAGCCCTTCCATTGGCTCGTCTG  4539
          |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db  4440  GGTACACTGGGAAATTTCGACTCCCGTCACCGACTGTGGATTAGTGTGGTTGGGAGGAGTCGTTG  4499

Qy  4540  AGGTGACCCTGATCCCACCATTACCACCATCCCGCGCCACGGTGGGCCCGGCTCGCGCTGAAC  4599
          |||||| ||||||||||||  ||||||||||||  |||||| ||||||||||  ||||||||||
Db  4500  AGGTGAGCCCTTGATCTCGATCCTACCATTACCATCTCCCGCTGCAATGGCACCGCTCGCGCTGAAC  4559

Qy  4600  TGTCGATGCAGCGGCGGAGGAGCGCACGGCGTCGGCGCTGAGGCTCGGCGCTACTACGCGG  4659
          ||||||||||||||||||||||||||||||||||||||||||||  |||||||||||||||
Db  4560  TGTCGATGCAAAGACGAGGACGAGGACGAGGCACGGCGTCGGACGCTACTACTACGCGG  4619

Qy  4660  GGGTCGGCAAGGCCCCTGGTGTGGTCCGTCGTGGTCGGCGTGGGTCGGCGGTGGAAG  4719
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  4620  GGGTGGGCAAAGCCCCTGGTGTGGTCGTTCTGTTCGGTGGCGGTGGTGGCGGTGGAAG  4679

Qy  4720  CCGGTGTGACCTGGTACGGAATGGAATGGAACCTGACTGACAGCAAAACCTACTGAGACTTTACG  4779
          | || ||||||||||||||||| ||||||||||||||| |||||||||||||||||||||
Db  4780  ...
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Db  4680  CTGGAGTGACCTGGTACGGAATGGAACCTGACTTGCAGCAGTCAACCTACTGAGACTTTACG  4739

Qy  4780  ACAACTGCCCTACCACCGCACCACCGCCACCGGTGACATTGGGAGAAGCCGCCGGTGTTCTTTT  4839
          || |||||||||||||||||||||||||  ||||||||||| ||||| ||||| |||||| |
Db  4740  ACGACTGCCCTTACCACCGCACCACCGCCGTGATATCGGCTGTGATATGGGAGAAGCCGGGTGTTCTTCT  4799

Qy  4840  CGGGGCTGCCCGTTGAGGATGCATCCGATGTTAGCTGGCAAAAGTTCGCGGCGTCA  4899
          | |||| ||||| || |||||||| ||||||||||||  ||||||| |||||||||||
Db  4800  CTGGGCTCGCCCCATTGAGGATGTCAGCTGGCAAAAGTTCGCGGGGTCA  4859

Qy  4900  ACTGGCCCTTCTGGTTGGTGTTCAGCGGACCATGTGCCGGCGACCACTGTCTCCCGGCC  4959
          ||||||||||||||| ||||||||||||||||||||||||||| |||||||||||| |||
Db  4860  ACTGGCCCTTCTGGTGTTCAGCGGACCATGTGCCGGGAACACTGTCTCCCCGCCC  4919

Qy  4960  CATCCGGATGACCCCCAGTGGGCACGGGTCGAAGGGCTGAAGGCCGTGAGGGCCATGA  5019
          |||||||||||||||| || ||||||| ||||||||||||||||||||||| ||||||
Db  4920  CATCGGATGACCCCCAAATCCTGTCCCACTCCTGTCTTGAAGGGCTCTGAAGAGGGGTCTGAGGGCCATGA  4979

Qy  5020  GGTGGGCAATGATTTACCATCTAAAGTGCCGGCCATCACATCGTGGACGACCTGGTCC  5079
          ||||||||||||||||||| |||| ||||||||||| || ||||||||||||||||||
Db  4980  GGTGGGCAATGATTTACCATCTAAAGTGCCACCACCATAGTGGACGACCTGGTCC  5039

Qy  5080  GTAGGCTCGGGTGGGCGGAGGTTAGCTGCCGCTGATGCGGGACCCATCTTGATGGTGG  5139
          |||  ||| || || |||||||||||||||| || |||||||||||||||||||||||
Db  5040  GGAGACTCGGTGTGCGGAGGTTCCTCCGTGCAGTTCTCCGTGCAGTTACCCCGTGCGGGGGTGGTTA  5099

Qy  5140  GCCTCGCTATTGCGGGGGGCATGATCTATGCCGCTCATACACCGGTCTCTCGTGGTGGTGTTA  5199
          | |||||||||||||||| |||||||||||||||| ||||||||||| |||||||||||||||
Db  5100  GTCTAGCTATCGCGGGGGGAATGAATGATCTCGTACGGTCTACACCGGTCGCTAGTGTGGTGTGA  5159

Qy  5200  CAGACTGGGATGTGAAGGGGGTGGCAGCCCCCTTTATCGGCGATGGCTGGGATGGCCGAGGCCT  5259
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  5160  CAGACTGGGATGTGAAGGGGGTGGGGCCCCCCTTTATCGGCGATGGCTGGGATGGCCGAGGCCGC  5219

Qy  5260  CCCAGCCGGTGTGCAGGTGTGTCAGGTCCCCGGTAGACCATGGCGGTGGGAGAGTCTGCCGCCAT  5319
          |||||||||||||||||||| |||||| ||| |||| || |||||||||||||||| |||||| |
Db  5220  CTCAGCCGTGTGTGCAGTTCTGGGTCGCGTGCAGTTCGGTGCGGTGGCATCGGCCGGGGTGAATCAGCACCAT  5279

Qy  5320  CGGATGCCAACACAGTGACAGATGCCGGCGGCATCCAGCTGGTGATTGGGATTGTCAG  5379
          | |||||||||||||||| ||||| ||||||||| ||||||||||||||||||| ||||
Db  5280  GTCTAGCTATCGCGGGGGGAATGAATGATCTCGTACGGTCGCAGCGATGCCAGGTGGACTGCGATTGGGACTA  5339

Qy  5380  TCATGACCCTGTCGATCGGGAAGTGCTGTCGATCGGGAAGTGCTGAGTGCGAGGCCT  5439
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  5340  TCATGACTCTGTCGATCGGGAAGTGTTGTCGATCGGGAAGTGCTCAGGCTAAGACGCGGGGCGAGCCT  5399

Qy  5440  ACGCAGCTACCACCAGGTGGCTTGCTGCTCCACGCGGGGACGCGGGGCGTCCCCACTG  5499
          || |||||||||| || |||||||||||||||||||||||||||||||||||||||||
Db  5400  ACACAGCAGCACCACCAGGTGGCTTGGGGAGGGGACGCGGGGCGTTCCCCACTG  5459

Qy  5500  TTTCAATTGTTGACAGACTCTCTCGGCCGGCATGGGGCTCTAGGAGCCCTGTGGTTCCATTGCCACA  5559
          ||||||||| ||||||| ||||| |||||||||||| ||||||||||||||||||||||||||||||
Db  5460  TATCCATTGTTGACAGCTCTTCGCGGCCTTGGGGGCTGTGTGGTTGGGGTGGGCCTTGACCATGG  5519

Qy  5560  GTGTAATAGCTGCGGACCGCAGTGGCGGCGTTCTAGGAGCCCTCCATTGGCTCGTCTG  5619
          ||||| |||||| | |||||||| | |||  ||||||||||||||  |||||||||||
Db  5520  ACGTGATTGCTGCGGACGCGGGTGGGGGTTACGCGGGGTTCAAAGAGCCCGTGGCAGCCG  5579

Qy  5620  CCGGCTTCCTACCTCATTGGGGTTGGGGGCCGTGGAGGCGGGGCAAACCCGCTTAGCCTCCG  5679
          |||||||||||||||| ||||| ||||||||||||||||||||||||||| |||||| |||||
Db  5580  CGGCTTCCTACCTGATCGGGGTTGGGGGCTTGGGGGGACCAGCACCGCTCGGCATCTG  5639

Qy  5680  CTCTCCTACTAGGGCCGGCGTCGGGGCTACTACGCGGTGTCGTGTGGGGTGTTAACCATGG  5739
          |||||||||||| ||||||| |||||| || || || |||||||||||||| ||||||||
Db  5640  CCCTCCTATTGGGGGTGGGGTGTGACTCCTGTGGAACCGGCCGCTCGTGTGGGGTGTTGACCATGG  5699

Qy  5740  CGGGGCCGGTTCATGGGAGTTGCTGGGTCGGTCCTCGGTTCCTGGTTCACCATTTTACTGGGGG  5799
          | |||||| ||||||||| || ||||||| |||| ||||| ||||||| ||||||| |||||||
Db  5700  CAGGTCGGTTCATGGGGCGTCGTTCATTGGGTCTCGTTGGTCTCGTTGGTTCACCATTTTATTGGGGG  5759

Qy  5800  CCGGTGTGACCTGGTACGGAATGGAATGGAAACCTGACCTTACG  5859
          | |||||||||||||| |||||||||  || || |||||||||||
Db  5760  CCGGTCGGAGGTTGGGAGAGGGGTGGTCAACGCGCGGAGCCGGAGCTCTTTTGACTTCTTTGACTTCATGCGCGG  5819
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Qy   5860 GGAAACTATCATCAGAAGATCTGTGGTATGCCATCCCAGTGCTAACCAGTCCGGGGGCAG 5919
            |||||| || | | ||||||||||||||||||| || || ||| | |||||||
Db   5820 GGAAACTTTCATCAGAAGATCGTGGTATGCCATCCCGGGTACTCCCCGGGGGGGG   5879

Qy   5920 GACTTGCCGGGGATCGCCCTCGGGTTGGGTGTTGTTGTTATTCAGCTAACAACTCTGCCACTACCA 5979
            |||||||||||| ||||||||||||||||||||| |||| ||||| ||||||||||||||||||
Db   5880 GCCTTGCCGGGGATCGCTCTCGGGGTTGGTTTTTATTCAGCTAACAACTCTGCCACTACCA 5939

Qy   5980 CTTGGTTGAACCGTCGTCGCTGCTGCTACATTGCCAAGGTCTCATGCATCCTGACAGTTACT 6039
            ||||||||||||||||| |||||||||||| |||| ||||||||||||||||||||||||||
Db   5940 CTTGGTTGAACCGTCGTCGCTGCTACCAAGGTCTTCATGTATCCCGGACAGTTACT 5999

Qy   6040 TTCAGCAGGCCGATTACTGTGACAAGGTCTCAGCTGTCCCACGCTTGAGCCTCACTC 6099
            ||||| || | | ||||| ||||||||||| |||||||||||| ||||||||||
Db   6000 TTCAGCAAGTTGACTATTGCGACAAGGTCTCAGCCGTCCTCAGCCTCACCC 6059

Qy   6100 GCACCGGTCGGTTGCCCTGGTCAACAGGAGCCTAAGGTGGATGAGGTTCAGGTGGGGTACG 6159
            ||| ||| ||||||||||||||||||| || || |||| ||| || |||||||| || ||
Db   6060 GCACAGTGCTTGCCCTGGTCAACAGGAGCCTAAGGTGGATGAGGTTCAGGTGGGGTATG 6119

Qy   6160 TCTGGGACTTGTGGGAGTGGATCATGCCTCAAGTGCGCACTTCGG 6219
            |||||||||||||||||||||||||| |||||| ||||||||||||
Db   6120 TCTGGGACCTGTGGGAGTGGATCATGCGCCAAGTGGTGCACTTCGG 6179

Qy   6220 CCCTCGCCCCGTGGTGTCATTATCCCTTATGGCACTGCGGGGAGGGTGGTCCGGAGAAT 6279
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   6180 CCCTCGCCCCGTGGTGTCATTATCCCTTATGGCACTGCGGGGAGGGTGGTCCGGGGAAT 6239

Qy   6280 GGTTGTTGACGGCCATGTTGAGACGTCGTTGTCTTTGTGGTTGCTGTGATCACCGGTGATG 6339
            |||| ||||||||||||||||||||||||||| || | |||||||||||||| |||||||
Db   6240 GGTTGCTTGACGGTCATGTTGAGAGTCTGTGGCTTGCGCGCGGATCACTGGTGACG 6299

Qy   6340 TTTTGAATGGGCAACTCAAAGATCCAGTTTACTCTACCAAGCTGTCGAGGCATTATTGGA 6399
            || ||||||||||||||||||||| |||||||||||||||||||| ||| |||||||||
Db   6300 TTCTGAATGGGCAACTCAAAGAACCAGTTTACTCTACCAAGCTGTCGCCGGCACTATTGGA 6359

Qy   6400 TGGGGACAGTCCCTGTGTACCATTCGGGACGTGGTACCATGGCGAGACGTCTCGCCTTTGCTCGCCCTCAG 6459
            ||||||||||||||||||||||||| || ||||| |||||||||||||||||||||||||
Db   6360 TGGGGACTGTCCCTGTGTACCATTCGGGGACGTGGTACCATGGGTGAGGACGTCTCGCCTTCCG 6419

Qy   6460 ACACCCCGAAGGTGGTACCATTCGGGGACGTGGTACGCTGGGTGGTGGTGACCCCTA 6519
            |||||||||||||||||||||||||| |||||||| || ||| |||||||| ||
Db   6420 ACACCCCGAAGGTGTGCCGTCTCGGGACGTCGGGTACGGTGGTGGTGGTGACCACTA 6479

Qy   6520 CCCACGTTGTGATCAGGCCGAACATCGCCGCCTACAAACTGTCGCGCCAGCAAATCCTGTCGG 6579
            |||||||||| | | |||||| ||| ||||||||||||| |||| ||||| ||||||||||
Db   6480 CCCACGTGGTAATCAGGAGAACCCTGCCGCCTATAAGCTGCGCCGGCAAATCCTATCGG 6539

Qy   6580 CTGCTGTTGCTCGAGCGTCCGACCGGCATACCGGTCGACTGAGGCCGACCGCGGC 6639
            |||||| ||| || |||||||||||||| |||||||| |||||||||||||||||
Db   6540 CTGCTGCTGCTCGCAGGGTCCGACCGGCATTCCGGTCGACTGAGGCCGATCTGCCCGCCG 6599

Qy   6640 GAGCGCCCTGCCATGGTCTATGGCCCTGGGCAAAGTGTCACCATTGACGGGGAACGCTACA 6699
            |||||||||||||||||||||||||||||| ||||| |||||||||||||||||||||||
Db   6660 GTGCGCCCGCCATGGTCTATGGCCCTGGGCAAAGTGTTACCATTGACGGGGAGCGCTACA 6659

Qy   6700 CCCTTCCGCCATCAACTGCGGGCTTAGGAATGTGGCGCCCTCGAGTGTCATCCGAGGTGT 6759
            |||||||||| | |||| ||| ||| |||||||||||||||| ||| |||| |||||||
Db   6660 CCCTTGCCTGCTGCTCAACTGAGGGTTCAGGAATGTGCGCCCTCTGAGGTTTCATCCGAGGTGT 6719

Qy   6760 CCATTGACATTGGGACGGAGACTGAAGACTGAGCAGACTGTCGGCCCGACCTTGCGGGCCGG 6819
            |||||||||||||| ||||||| || |||||||||||||||| |||||||||||||||||
Db   6720 CCATTGACATTGGGACGGAGACTGAGCAGACTGTCGGCCCGATCTGCCCGCCG 6779

Qy   6820 CGGCTGCAGCCCTCAGGCTATCGACGAATTCTTGAACCTCACATAGATG 6879
            ||||| | |||||| |||||| |||||| || ||||||||| ||||||
Db   6780 GTGCGCTGCTGCTTCCAGCGATCGAGAATGCTCAACCGCACATTGATG 6839

Qy   6880 TCATCATGGAAGATTGCAGTCAGTACCACCCTCTTTGTGGGAGTGCCTGTGT 6939
            | |||||||| ||||| |||||||||||||||||||| |||| |||||||||
Db   6840 CCATCATGGAGGACTGCAGTCAGTAGCCGAGAGATGCCCTGTAT 6899

Qy   6940 GGGGAGGAAGACATACCCGACTTCCATCGCCAGCACTTATCTCGGTTACTGAGACGCAGCC 6999
            |||||||||||||||||||||||||||||||||| |||||| |||||||| ||||||||
Db   6900 GGGGAGGAAGACATCCCGACTTCCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCT 6959

Qy   7000 CAGATGAGAGAGACCCCGTCGGTGTCTTCTCCGCAGGAGGATACCCGTCTTTCTGACTCAT 7059
            |||| |||||||||| ||||||||||| |||||||||||||||||||||||||||||||
Db   6960 CAGATGAGAGAGACCCCGTCGGTGTCTTCTCCGCAGGAGGATACCCGTCTTTCTGACTCAT 7019

Qy   7060 TCGAGGTCATCCAAGAGTCCGAGACAGCAGCAGGGGAGGGAGAAAGCGTCTTCAACGTGGCTC 7119
            |||||||||||||||||| ||||||||||| ||||||||| |||||||||||||||||||
Db   7020 TCGAGGTCATCCAAGAGTCCGAGACAGCAGCAGGGGAGGGAGAAAGCGTCTTCAACGTGGCTC 7079

Qy   7120 TTTCCGTACTAAAAGCCTTGTTTCCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGA 7179
            |||| || | || |||| ||||||||||||||||||||||||||| ||||||||
Db   7080 TTTCCTATTAGAAGCCTCATTTCCACAGAGCGACGCGACCAGGAAGCTTACCGTCAAGA 7139

Qy   7180 TGTCATGCTGTGTTGAGAGAGCGTAACACGCTTCTTTTCATTGGGATTGACGGTCGCTG 7239
            ||||||||||||| |||||||||||||||||||| ||| |||||||| ||||||| ||
Db   7140 TGTCGTGCTGCGTTGAAAAGAGCGTCACGCGCTTTTTCTCATTGGGCTTGACGGTGGGTG 7199

Qy   7240 ACGTGGCAAGCCTGTCGTGTGAGATGAAATCCAGAACCATACAGCCATAGGTGTGACAAGGTGC 7299
            | ||| || |||||||||||||||||||| ||||||||| |||| |||| |||||||||||
Db   7200 ATGTTGCTAGCCTGTCGTGTGAGATGAAATCCAGAACCATACAGCGCTATTGTGACAAGGTGC 7259

Qy   7300 GCACTCCGCTTGAATTGCAGGTTGGGTGCACTGCGGGGAGGGTGGTCCGGAGAAT 7359
            |||||| ||||||||||||||| ||| ||||||||||||||||||||||||||||
Db   7260 GCACTCCCGCTTGAATTGCAGGTTGGGTGCACTGCGGGGAGGGTGGTCCGGGGAAT 7319

Qy   7360 ACAAGTGTGAGGCTAGGCAAGAGACCTTGGCTTCCTTCTTCTTACATTTGGTCTGGGGTGC 7419
            |||||||||| |||||||||| |||| ||| | |||||||||||||||||||||||||
Db   7320 ACAAGTGTGAGGCTAGGCAAGAAACCTTGGCCTTCTTCTTACATTTGGTCTGGAGTGC 7379

Qy   7420 CACTGACGAGGGCCACTCCGGCCAAGCCCCCTGTGGTGAGGCCGGTTGGCCGTTCCTTGCTGG 7479
            || | ||| |||| ||| ||||| ||| | |||||||||||||||||||||||
Db   7380 CGCTGACTAGGGCCCACGGCCCTCCCGTGGTGAGGCCGGTTGGCCGTTCTTCTTTATTAG 7439

Qy   7480 TGGCCGACACCACCAAGGTGTATGTCACCAGGGTTCATGACAAAATTCCTCGTGACTCCATAGAGC 7539
            ||||||||||| || |||| |||||||||||||||| ||| | || | ||| ||||
Db   7440 TGGCCGACACTACTAAGGTGTATGTTACCAATCCAGACAGCGTTCATGATAAGTACACCTCCTGGACTCTATTGAGC 7499

Qy   7540 AGGTTACCTTCTGGCGTGCCCGCTAGGGTTCATGACAAATTCCTCGTGACTCCATTGAGC 7599
            ||||||| ||||||||||| ||||||||| ||||| | ||||||||||||||||||||
Db   7500 AGGTGACCTTCTGGCGTGCTGCCTCGGGTTCATGATAAGTTACACTTATGGGATCTATTGAGC 7559

Qy   7600 GCGCTAAGAGGCAGCTCAAGCCTGCCTAAGCGGTTACACTTATGAGGAGCCAATAA 7659
            ||||||| ||| |||| ||||| |||| ||| |||||| |||||||| ||||||
Db   7560 GCGCTAAGAGGGGCCGTCCAAGCCTGCCTAAGCATGGGTTACACTTATGAGGAAGCAATAA 7619

Qy   7660 GGACTGTAAGGCCACCATGGGGCTTAGGACGTGTGGTCGCGTCAAGGACCTCG 7719
            | | |||||||||| |||||||| |||| |||||||||| ||||||| |||
Db   7620 GGACTGTAAGGCCACCATGGGGCTTAGGACTTGTCGGTTAAGGACTTTAG 7679

Qy   7720 CCACCCCTGCGGGAAGATGGCTGTCCATGACGCCTCCAGGAGACTTGAAGGGACGCC 7779
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Db   7680 CCACCCCGCGGGGGAAGATGGCTGTCCATGACGCCTCCAGGAGATACTTGAAGGGACTC 7739

Qy   7780 CAGTCCCCTTACTCTTCTTACTGTGAAAAAGGAAGTGTTCTTCAAAGACCGAAAAAGAGA 7839
            | |||||||||||||||||||| |||||||| |||||| |||||| ||||||||| ||
Db   7740 CGGTTCCCTTTACTCTTCTTACTGTGAAAAAGGAGGAGGTTGTTCTTCAAAGACCGGAAGGGAGG 7799

Qy   7840 AGGCCCTTGGCTCATTGTGTTCCCCCCCTGATAGCTGAAAAGCTTATTC 7899
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Db   7800 AGGCCCTCGGCTTCCTCATTGTGTTCCCCCCCTGGGTGAATAGTGAAAAGCTTCATCT 7859

Qy   7900 TGGGGAGACCCTGAGCACGGGTAGCCAAGGCGGTTGGGGGGCTACGGCCTTCCAGTACA 7959
            |||||||| ||||||||||| |||||||| |||||| |||| |||||||||| |||||
Db   7860 TGGGAGACCCTGAGCACGCGGTAGCCAAGGCCGTGTTGGGGGGGCCTTACGCCTTCAGTACA 7919

Qy   7960 CCCAAAATCAGCGAATTAGGAGGACGTGGAATCAAAGAGAGAACACCATGCG 8019
            |||||||||||| | ||||| ||||| ||| ||||| || || || || |
Db   7920 CCCAAAATCAGCGATTAAGGAGTCTAAGCAACGTTAAGAGAGGAGACCCCTTGCG 7979

Qy   8020 CCATCTGTGTGGACGCCACATGCTTCGACAGTAGCATAACTGAAGAGGACGTGGCGCTGG 8079

Db   6840 CCATCATGGAGGAGACTGCAGTAGGAGTAGTGTGTAGGAGAGATCTTGACAGTAGCCCTGTAT

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Qy   7980  |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||| |||  8039
           CCATCTGTGTGACGCACCACCTGCTTCGACAGTAGCATAACTGAAGAGGACGTTGGCTTTGG

Db   8080  AGACAGAGCTTATGCCGCTTCGGCTTCAGACCATCCAGAATGGTGCGTGCCCTGGGGAAAT  8139
           ||||||| |||| || ||| ||||||||||||||||||||||||| || ||||||||||||
Qy   8040  AGACAGAGCTGTACGCCTCTGGCCTCTGGACCATCCAGAATGGGTGCGGGCACTTGGGAAAT  8099

Db   8140  ACTATGCCTCTGCACAATGGTAACCCCGAGGGGGTGCCAGTGGGTGAGAGGTATTGTA    8199
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Qy   8100  ACTATGCCTCAGGCACCATGTCACCCCGGAGAGGGTGCCCGTCGGTGAGAGGTATTGCA  8159

Db   8200  GATCCTCAGGGGGTGCTTGACCACCAGTGCGAGCAACTGCTTGACTTGCTCTATATCAAGGTGA  8259
           |||||| ||| ||||||||||||||||||||||||||||||||| || ||| ||||||||||
Qy   8160  GATCCTCGGGTGTCCTAACAACTAGCCGCAGCAACTGCTTGACCTGCTCTACATCAAGGTGA  8219

Qy   8260  AAGCCGCCTGTGAGAGGGTGGGGCTGAAAAATGTCTCCCTCCTCATCCTGGCGATGACT  8319
           ||||||||||||||||||||||||||| |||||| || ||||||||||| ||||||||||
Db   8220  AAGCCGCCTGTGAGAGGGTGGGGCTGAAGAATGTCTCTTCTCCTCCATTCCATCCTGGCGATGACT  8279

Qy   8320  GTTTGATCATATGCGAACGGCCTGTGTGCGATCCTAGCGACGCTTTGGCAGAGCCCTGG  8379
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Db   8280  GCTTGATCATATGTGAGCGGCCAGCGGCGGCCCAAGCGACGCTTTGGGCAGAGCCCCTAG  8339

Qy   8380  CGAGCTACGGGTACGCATGCGGAGCCTTCGTATCATGCATCACTGGACACGGCCCCCTTCT  8439
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Db   8340  CGAGCTATGGGTACGCGTGCGGAGCCCTTCATATCATGCATCACTGGACACGGCCCCCCTTCT  8399

Qy   8440  GCTCCACTTGGCTAGCTGAGTGCAATGCAGATGGAAACGCCATTTCTTCCTGACCACGG  8499
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Qy   8500  ACTTTCCGAGGCCCCTCCCGCTCGCCATGTGAGCGAGTACAGTGACCCCAATGGCTTCGGCCA  8559
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Db   8460  ACTTTCCGAGGCCGCCGCTCGCCATGTGAGCGAGTATAGTGACCCCGATGGCTTCGGCGA  8519

Qy   8560  TCGGTTACATCCTCCTATACCCTGGCATCCTATCACACGGTGGGTCATCATCCCTCACG  8619
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Db   8520  TCGGTTACATCCTCCTTTATTCCTTGGCACCCCATCACACGGTGGGTCATCATCCCTCATG  8579

Qy   8620  TGCTCACCTGCGCGTTTAGGGGTGGTGGCACACCGTCGATCCTGTGTGGTGCCAGGTAC  8679
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Qy   8680  ATGGTAATTACTACAAGTTCCACTGACAAAACTGCCTAACATCATCGTGGCCCTCCACG  8739
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Qy   8740  GACCAGCAGCGTTGAGGGTTACCGCAGACAGCAAACTAAGCACAAAATGAGAGGCTGGCAAGG  8799
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Db   8700  GACCAGCAGCGTTGAGGGTTACCGCAGACAGCAACAACTAAAAAACAAAGAGGAGGCTGGTAAGG  8759

Qy   8800  TGCTGAGCGACCTCAAGCTCCCTGGCCTAGCAGTCCACCGGGAAGAGGCCGGGGCATTGC  8859
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Db   8760  TTCTGAGCGACCTCAAGCTCCCTGGCCTGGCTAGCAGTCCACCGGGAAGAAGCCGGGCGTTGC  8819

Qy   8860  GAACGGCGTATGCTCCGGTCGCGCGGTTGGCTGAGTTGGCTGAGGGCTGGCCTC  8919
           |||||| |||| |||||||||||||||||||||||||||||||||||| ||||||
Db   8820  GAACACGCATGCTCCGGTCGCGCGGTTGGCTGAGTTGGGCTGAGGGCTTGTGTTGGCATC  8879

Qy   8920  CAGGGCCTGCGCGGTTCCCCGGGGTTCCCCGGGGTTCTCCCGGGGTTCCCCTTTCCC  8979
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Db   8880  CAGGGCCTACGGGCTTCCCGGTTCTCCCCTGAGATTGCTCCGGGGGTTCCCCTCTCCC  8939

Qy   8980  CCCCCTATATGGGGGTGGTTCATCAATTGGATTTCACAAGCCCAGAGAGTCGCTGGCCGT  9039
           |||||| || |||| |||||||||||||||| | ||||||||||| |||||||||||||||
Db   8940  CCCCCTATATGGGGGTGGTACACCAATTGGATTTTACAAGCCCAGAGAGTCGCTGGCCGGT  8999

Qy   9040  GGTTGGGGTTCTTAGCCCTGCTCATCGTAGCCCCTCTTCGGGGTGAACTAAATTCATCTGTT  9099
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Db   9000  GGTTGGGGTTCTTAGCCCTGCTCATCGTCAGCCCCTTCTCGGGTGAACTAAATTCATCTGTT  9059

Qy   9100  GCGGCAAGGTTCGGTGACTGATCATCACTGGAGGAGGTTCCCGCCTCCCGCCCCCAGGG  9159
           ||||| ||||||||| ||||||||||||||||| |||||||||||||||||||||||||||
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Db   9060  GCGGCGGAGGTCTGGTGACTGATCGTCACCGGAGGAGGTTCCGCCCTCCCGCCCCCAGGG  9119

Qy   9160  GTCTCCCCGCTGGGTGGTAAAAAGGGCCGGCCTTGGAGGCCATGGTGGTGTGTTACTACTG  9219
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Db   9120  GTCTCCCCGCTGGGTAAAAAGGGCGGCCTTGGAGGCCATGGTGGTGTTACTACCCCTG  9179

Qy   9220  GCAGGTCAAAGCCTGATGGTGCTAATGCACTGCCACTTCGTGGGGTCGCTACCTTA  9279
           |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9180  GCAGGTGTAAAGCCTGATGGTGCTAATGCACTGCCACTTCGTGGGGTCGCTACCTTA  9239

Qy   9280  TAGGTAATCCGTGACTACGGGCTGCTCCGCAGAGCCCTCCCCGGATGGGGCCACAGTGCAC  9339
           |||||||||||| ||||||||||||| ||||||||||| ||||||||||||||||||||| |
Db   9240  TAGGCTAATCCGTGACTACGGGCTGCTCCGCAGAGCCCTCCCCGGATGGGGGCCACAGTGCAC  9299

Qy   9340  TGTGATCTGAAGGGGTGCACCCCGGTAA  9367
           || ||||||||||||| |||||||||| ||
Db   9300  TGAGATCTGAAGGGGTGCACCCCGGGAA  9327
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RESULT 11
US-08-461-361-234
; Sequence 234, Application US/08461361
; Patent No. 5856134
; GENERAL INFORMATION:
;   APPLICANT: Kim, Jungsuh P.
;   APPLICANT: Wages, John
;   APPLICANT: Young, LaVonne M.
;   APPLICANT: Fry, Kirk E.
;   APPLICANT: Linnen, Jeffrey M.
;   TITLE OF INVENTION: Hepatitis G Virus and Molecular
;   TITLE OF INVENTION: Cloning Thereof
;   NUMBER OF SEQUENCES: 277
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dehlinger & Associates
;   STREET: 350 Cambridge Ave., Suite 250
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/461,361
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/389,886
;   FILING DATE: 15-FEB-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/357,509
;   FILING DATE: 16-DEC-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/329,729
;   FILING DATE: 26-OCT-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/344,271
;   FILING DATE: 23-NOV-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,558
;   FILING DATE: 03-AUG-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,543
;   FILING DATE: 03-AUG-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/246,985
;   FILING DATE: 20-MAY-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Fabian, Gary R.
;   REGISTRATION NUMBER: 33,875
;   REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11

Wed Oct 9 08:59:37 2002

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;
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (415) 324-0880
;    TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 234:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 9327 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: double
;    TOPOLOGY: unknown
;    MOLECULE TYPE: cDNA
;  HYPOTHETICAL: NO
;  ANTI-SENSE: NO
;  ORIGINAL SOURCE:
;    INDIVIDUAL ISOLATE: 32HGV-6, HGV FROM PNF2161
US-08-461-361-234

Query Match            83.9%;  Score 7885.6;  DB 2;   Length 9327;
Best Local Similarity  90.4%;  Pred. No. 0;
Matches 8433;  Conservative  0;  Mismatches 894;  Indels 1;  Gaps 1;
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Qy      40 GCAAGCCCCATAAACCGACGCCTATCTAAGTAGACGCCAATGACTCGGCCGCCGACTCGGCCG  99
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Db       1 GCAAGCCCCAGAAACCGACGCCTATCTAAGTAGACGCCAATGACTCGGCCGCCGACTCGGCCG  60

Qy     100 ACCGGCCAAAAGGTGGTGGATGGGTGGTTGGTAGGTCGTAAATCCCGGTCAT  159
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Db      61 ACCGGCCAAAAGGTGGTGGATGGGTGGTTGGTAGGTCGTAAATCCCGGTCAC  120

Qy     160 CCTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTGCGGC  219
           ||||||||||||||||||| ||||||||||||||  |||||||||||||| ||||||||
Db     121 CTTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTTAAGATTCCTCTTGTGCCTGCGGGC  180

Qy     220 GAGACCGGCCGCACGGTCCAGAGGTGCTGGCCCTACCGGTGTGAATAAGGGCCCGACGTCAG  279
           |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db     181 GAGACCGGCCGCACGGTCCAGAGGTGTTGGCCCTACCGGTGGGAATAAGGGCCCGACGTCAG  240

Qy     280 GCTCGTCGTTAAACCGAGCCCGTCACCCACGGGCAAACGACGCCACGTACGGTCCAC  339
           ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     241 GCTCGTCGTTAAACCGAGCCCGTTACCCACGGGCAAACGACGCCACGTACGGTCCAC  300

Qy     340 GTCGCCCTTCAATGTCTCTCTTTTCTATACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAGT  399
           |||||||||||||||| | |||||| |||||||||||||||||||||||||||||||||||||||
Db     301 GTCGCCCTTCAATGTCTCTCTTGACCAATAGGCGTAGCGGCGAGTTGACAAGGACCAGT  360

Qy     400 GGGGCCGGGGTTATGGGAAGGACACCCCAAACCCTGCCCTTCCCGGTGGGCCCGGGAAAT  459
           |||||||||| |  ||| ||  | ||||| ||||| || ||||||||||||||||||||
Db     361 GGGGCCGGGGCT-TGGAGAGGAGGACTCCAAGTCCCGGCGCCCTTCCCGGTGGGCCGGGGAAAT  419

Qy     460 GCATGGGGCCACCCAGCTCCCGGGAAGACATCGGTTGCTGCCACTGTATCAGGCGGATGCC  519
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Db     420 GCATGGGGCCACCCAGCTCCCGGGTAGCCGGGGTAGCCCAGTCCAGCCAAGAATCCTTCGGG  479

Qy     520 TGAGGGCGGGGTGGCATTTCTCTTTTCTATACCATCATGGCAGTCCTTGCTCCTCTCTCG  579
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Db     480 TGAGGGCGGGGTGGCATTTCCTTTTCTATACCATCATGGCAGTCCTTGCTCCTCTCTCG  539

Qy     580 TGGTTGAGGCGGGGCCATTCTGGCCCGGCCACCCAGCTTGTGCTGAGCGAATGGGCAAT  639
           |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db     540 TGGTTGAGGCGGGGCCATTCTGGCCCGGCCACCCAGCTTGTGCTGAGCGAATGGGCAAT  599

Qy     640 ATTTCCTCACAAATTGCTGTCCCCGGAAGACATCGGTTGCTGCCACTGTATCAGGCGGGTT  699
           ||||||||||||| || ||||||||||||| || |||||||||||||||||||||||||
Db     600 ATTTCCTCACAAATTGTTGTGCCCCGGAGGAGCGGTTGCTGCCACTGTATCAGGCGGGGTT  659

Qy     700 TGGTGCCCTGGGGTGCACGGTTGCACCGACCACTGACCAATGCCTGCCACTGTATCAGGCGGGGTT  759
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Db     660 TGGTGCCCTGGGGTGCACGATTGCACTGACCAATGCCTGCCACTGTATCAGGCGGGGTT  719

Qy     760 TGGCTGCCCTGCCAAGTCCCGGCCCAACTGGTGGGGAGCCTGGGTAGCCTATACG  819
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Db     720 TGGCTGCCCTGCCAAGTCCCGGCCCAACTGGTGGGGAGCCTGGGTAGCCTATACG  779

Qy     820 GGCCCTTGTCGTCCGTCTCGGCTTACGTAGCCCGGGATCCTCGGGGTCGGGGCGAGTTCCG  879
           ||| ||||||||||||||| || |||| |||  | |||||||||||||||||||
Db     780 GGCCCCTGTCGTCCGTCTCGGCCTATGTGCCGTCGGGATCCTCGGGGTGAGTTCCG  839
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Qy     880 GGGTCCTGACAGTTGGTGTTGCCGTTGAGGCGCGGGGATCCTCGGGGTGAGTTACTCGG  939
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Db     840 GTGTCCTCAACGGTGGAGTGGGTCGCGTTGACGCGCCGGATCTACCCGGTGCCTAACCTGACGT  899

Qy     940 GTGCAGTAGAATGTGACGTTAAGTGGGAAGTGAGTTTGGAGATGACTGAGCAGTTGG  999
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Db     900 GTGCAGTCGCGTGTGAGTTAAGTGGGAAAGTGAGTTTGGAGATGGACTGAACAGCTGG  959

Qy    1000 CCTCCAATTACTGGATTTTGGAATACCTTTGAAAGTCCCATTGATTTTGGAGAGGAG  1059
           ||| |||||| || |||||||||| ||||| |||||||||||||| | ||||||||
Db     960 CCTCCAACTACTGGATTCTGGAATACCTCTGGAAGGTCCCATTGATTTCTGGAGAGGCG  1019

Qy    1060 TGATGAGCCTGACACCCCTCTGTTGGTTTGGGTGGCCCGCATTGCTTTCTGCTGGAGCAACGGA  1119
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Db    1020 TGATAAGCCTGACCCCCTGTTGGTTTGGGTGGCCCATTGCTTCTGCTGCTGGAGCAACGGG  1079

Qy    1120 TTGTCATGGTTTCCTGCTGGTGACATGGCGGGGATGTTCAAGGCGCCCCCGCCTCCG  1179
           |||||||||| ||||| |||||||| ||| ||||||||||||||||||| ||||||||
Db    1080 TTGTCATGGTCTTCCTGTGGTGACGATGGCGGGGATGTTCAAGGCGCCCCCGCCTCCG  1139

Qy    1180 TTTTGGGGTCCCGCCCTTTGACTACACGGTTGAAGTGGCAGTCATCGTCCTGCAGGGCTA  1239
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Db    1140 TTTTGGGGTCCCGCCCTTTGACTACACGGTTGACTTGGCAGACCTGGCCAGCCTGCAGGGCCA  1199

Qy    1240 ACGGGGTCGCGTATTCCCACTGGGAGAGGGTGGGGAATGTCACGCTCTTGT  1299
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Db    1200 ACGGTTCGCGTTTTCGACTGGGAGAGGGTGGGGAACGTTGGGAACGTTACGCTTCAGT  1259

Qy    1300 GTGACTGCCCAACGGCCCCTGGGTTTGGGTCCCAGCCTTTGCCAGGCGGTTGGGTGGG  1359
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Db    1260 GTGACTGCCCTTACGGCCCCTGGGTGTGGTTGGCCCAGCCTTTGCCAAGCAATCGGCTCGGG  1319

Qy    1360 GCGACCCCATCACCACCCCCATTGGAGAGCAACGACCAAAAACCAGTGGCCCCATCATGCCCCCAAT  1419
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Db    1320 GTGACCCCATCATTATTGGAGCAGGTCAAAATCAGTGGCCCCTTCAATCAGTCCCCAGT  1379

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Db    1440 CCAGTGTGCGCACTCCAAGATAGATGTGTGAGTTTAGTGGAGTTTAGTGCCAGTTCGGCTCTGCCACCT  1499

Qy    1540 GCACCATAGCCGCTCAGGGTCATCGGAGTCGGCACACGTGTTGAGCGCTTCCGAGTGGG  1599
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Db    1500 GCACCATAGCCACTTGGATCATCGGATCATCGGATCGGCACACGGTTGAGCTGCCTCTCCGAGTGGG  1559

Qy    1600 GAGTCCCGTGCCTAACGTGTATTCTGACCGTGTCATGTGGTTGCCACCTGTGTGC  1659
           || ||||||||||||||| | |||||||||||| ||||||| ||||||||||| ||
Db    1560 GAATCCCGTGCCTGACGTGTTCTTGACCGTGTTCTCATGCGGTTCATGCGGCACCACCGTGTGA  1619

Qy    1660 GGGGACTGCTGGCCCGAAACCGGGTCGTTAGATTCCTTTCCATCCGTCGCGCACGGGGC  1719
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Db    1620 GGGGACTGCTGGCCCGGGACCGGGCCGGGTTAGGTTCCATTCCATCCGTCGCGTGGGGGC  1679

Qy    1720 CTCGGCTGACAAAAGGACTTGGAAGCTGTGCCCTTCGTCAAACAGGACAACTCCCTTCACCA  1779
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Db    1680 CTCGGCTGACAAAAGGACTTGGAAGCTGTGCCCTTCGTCAATAGGACAACTCCTTCACCA  1739

Qy    1780 TAAGGGCCCCCTGGGCAACCAGGGAGAGGCAACCCGGTGCGGTCGCCGGGTTTG  1839
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Db    1740 TTAGGGGCCCCTGGGCAACCAGGGAGGCAACCCGGTGCGGTCGCCCCTTGGGTTTTG  1799

Qy    1840 GGTCCTACACCATGACCAAGATCCGGAGATTCCTGGTGAAATGTCCACCACCAG  1899
           |||||| ||||| |||||||||||||| ||||||| || | |||||||||||||
Db    1800 GGTCCTACGCCATGACCATGACCAGGATCCGAGATACCGAGAGTCGGTAGTGTCCCACCACCAG  1859

Qy    1900 CCATAGAGCCCTCCGACTGGAACGTTCGGTTCTCCCGGAGTCCGGGCGAGGTTTACTCCG  1959
           |||| ||||| |||||||| || ||  |  ||||||||||||||||||
Db    1860 ...
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Db 1860 CCATCGAGCCTCCACCGGACGTTGGGTTCTTCCCGGGACGCCGCCTCTCAACAACT 1919
        |||||  | ||||||||||||||||||||||||||||||||
Qy 1960 GCATGCCGCTAGGCACGGAAGCGAAGTGTCTGAGGCATTGGGCGAGCTGGGCTTACGGGGGGT 2019
        |||||   | |||||||||||||||||||  ||||||  ||||||  ||| |||||||||||||
Db 1920 GCATGCTTCTTGGGCACGGAAGCGAAGTGTCCGAGGCACTTGGGGGGCTGGCCTCACGGGGGGGT 1979

Qy 2020 TCTACCAGAGCCTTCGGTGTCGGAGTGTTCGAGTGTTCGAGGACGCCGAAATCCGGTTTGCC 2079
        |||| | |||||||||| ||| | ||||| ||||||||| |||||||  |||||||||||||
Db 1980 TCTATGAACCCTGGTGCGGAGTGTCGGCAGGTGTCGGAGCTGATGGGAAGCCCGAAATCCGGTTTGTC 2039

Qy 2080 CGGGGTACGCATGGCGTGTCCTCTGTAGAACCTGACCGGGTTCATCACGTCCAGGGGCACC 2139
        |||||   |||  | ||| |||||||||||||||||  |||||  |||| |||||| ||||
Db 2040 CGGGGTTGCATGGCGTCTTCGGCAGGCCTGATGGGTTTATACATGTCCAGGGGTCACT 2099

Qy 2140 TGCAGGAGGTGGATGCGGGCAACTTCATCATCCTCCTCACGCGGTTGCTCTTGGATTTTG 2199
        ||||||||||||||||||||||||||||||||||||   |||| ||||||||||||||| |
Db 2100 TGCAGGAGGTGGATGCAGGCAACTTCATCCGGCTCATCCCGCGCTGGTTCTCTTGGACTTTG 2159

Qy 2200 TATTTGTCCTCTCTATCTGATGAAGCTGGCTGAGGCACGGTTGGTCCCGTTGATCTTGC 2259
        |||||||||||| | | ||||||||||||||||||||||||||||||||||| ||||||
Db 2160 TATTTGTCCTGTTATACCTGATGAAGCTGGCTGAGGCACGGTTGGTCCCGCTGATCTTGC 2219

Qy 2260 TTCTGCTGTGGTGGTGGTGAACCAGTTGCCGGTTCGGGACTGCCGGCTGTGGACGCTG 2319
        ||||||||||||||||||||||||||||  ||||||||||| |||||||||||||| 
Db 2220 TGCTGCTATGGGTGGGTGAACCAGCTGCCAGCTGGTCCTAGAGGCTGCCGGCTGTGGGAAGCCG 2279

Qy 2320 CCGTGCGGGTGAAGTTTTTGCGGGGCCCTTGTCATGGTGTTTGGGGCCTTCCCACTG 2379
        ||||||||||||||||||||||||||||||  |||||||||||||||||||||||
Db 2280 CCGTTGCAGGTGAAGTTTTTCGCGGGACTCTGCATGGTGTCTGGGGCTCCCCGGTCG 2339

Qy 2380 TCAGTATGATACTAGGTCTAGCAAACCTGGTTGTGTACTTTCGGTGGATGGGCCCTCAGC 2439
        ||||||||||||||  | | | |||||||||| |||||||||||||||||||||| |||
Db 2340 TCAGTATGATGATGATGTCTCACGGTGTATCCCCGGATGGGCTGCCAGTTGGACCCCCAAC 2399

Qy 2440 GCCTCATGTTCCTCGTCTGTTGTGGAAGCTCGCTCGGGGGAGCTTTCCCGCTGCCACTTTGA 2499
        |||||||  | |||||||||||||||||||||||||  |||||||||||||||||||| ||
Db 2400 GCCTGATGTTCCTCGGTGTTGCTCGGGGAGCTTGCTCGGGGAGCTTTCCCGCTGCCCTCTTGA 2459

Qy 2500 TGGGGATTTCCGGCCACCCGGCGGTACCAGGCTGTGCCCAGAGCCGAGTAGTTCTGCTTCGGA 2559
        |||||  ||||||||||| | ||  |||||||||||||||| || ||  ||||||||||||||
Db 2460 TGGGACGTGGTCGGGCCACCTGGCGGTACCAGGCTGTGCCCAGAGTGCCTCGGGCCGAGTAGTTCGCTTCGGTG 2519

Qy 2560 TCACATTCGAGGTGGCACTTCGGTGTTGGGCTGTGGCCAGCGTGGTGGCTGGG 2619
        |||||||||||||||||||||||||||||||||||||||||||||| | ||||
Db 2520 CTACATTCGAGGTGGCACTTCGGTGTTGGGCTGTGGCCAATGTGGTGGCTTAGCTTGGGG 2579

Qy 2620 CCATAGCGCTCCTGAGCTCAATGAGCGCAGGGGGTGGAAGCACAAGGCCGTGATCTATA 2679
        ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db 2580 CCATTGCGCTCCTGAGCTCGATGAGCGCAGGGGGTGGAGCGCACAAAGCCGTGATCTATA 2639

Qy 2680 GGACGGTGGTGTAAAGGGTACCAGGCTGTGCCGCAGAGACTACCAGAAACCCCTCGGGG 2739
        |||| ||||||||||||||||||| | ||||||  | |||||||||||||||||||||||
Db 2640 GGACGTGGTGTAAAGGGTACCAGGCAATCCGTCAAAACCGTGAGCGGGGGCCCAAAGGTCTCGGGG 2699

Qy 2740 AGGGGCGTCTACCAAGCTCGACGTTCGCGGTCGAAGGCCACCACCATCCGGTGGCCGTGG 2799
        ||||||  |||||  | |||||||||||||||| | |||| ||||| ||||||||||||||
Db 2700 AGGGGCCTCCTACCAGGCGTCTTGCCTTGCTGCTTCGACCTGCCACACCTGTACATCTGGCCAG 2759

Qy 2800 ATGCTGTGATGATGGTGGTCCGGCCTTGGTCCTCCTCTCTCGGCCGTGTTCACGACGACTGG 2859
        ||||||||||||||||||||||||||||||||| |||| |||||||||||||||||||||||
Db 2760 ATGCTGTGATGATGGTGGTGCCTTGGTTGCCTTGGTTCTTGGCCCTTGGCCTTTCACGCGGCGTTGG 2819

Qy 2860 ACTGGGCGCTTGGAGGAGCTCCTGGTAAAGGGTACGGGCGACTGGCACGGTGG 2919
        | ||||| |||||||||||||||||||||||||| ||||||||||||||||| |
Db 2820 ATTGGGCCTTGGAGGCGTTGGTGTCCGGGTCAAATCCGTGCCGGCGTTTGGGCTCGGGTGG 2879

Qy 2920 TTGAGTGCTGTGTGATGGGCGGCGGAGAAGGCCACCACCATCCGGTCTCCAAGATGT 2979
        |||||||||||||||||||||||||||||||||| |||  |||||||||||||||||
Db 2880 TTGCTTTCACAAGGATCACGAGCGACTCACTGGCCGTGGTCGTCCCCGCTGGTCTTCCAAGATGT 2939

Qy 2980 GCGCAAGAGGGGCCCACCTGTTGACCACATGGGCTCTTTCTGCGCGCGTGTCAAGGAGC 3039
        | | |||||||||||  ||||||||||||| | |||||||||||| | ||||||||||||
Db 2940 GTGCGAGAGGAGCTCATTTGTTCGATCATATGGGCTCATTTTCGTGGCTGTGTGTCAAGGAGC 2999
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Qy 3040 GCTTGTTGGAATGGACGCGGCGGCTTGGCCCTTGTCATTCACTAGGACGGACTGTCGCA 3099
        |||||||||||  ||||||   |||||||||||||||||||||||||||||||||||||
Db 3000 GCCTGTTGGAATGGACGCGGCGGCTTGAACCTTCGTGTCATTCACTAGGACGGACTGTCGCCA 3059

Qy 3100 TCATCAGAGATGCCGCGAGGACCCGTCCTGCGGACAGTCGCGTGCGTCATCACGTGG 3159
        ||||| |  ||||| | ||||  |||  |||| |||||| |||||| | |||||||||
Db 3060 TCATACGGGATGCCGCGAGGACTTGTCCTGCGGCAATGCGTCATGGGTTTACCCGTGTG 3119

Qy 3160 TAGCACGGCGCGGTGATGAGGTTCTCATCGCGGCTCTTCAGATGTGAATCATTTGCCTC 3219
        | |   |||  |  ||| |||||||||| ||||||||||||||||||||||||||||||||
Db 3120 TTGCGGCGGTGTTGATGATGAGGTTCTCATCGGGCTCTTCCAGGATGTGAATCATTTGCCCTC 3179

Qy 3220 CCGGGTTGTCCGCCGACTGCACCAGTGTCATCCGTCGGTGCGGAAAGGGCTTCCTGGGGG 3279
        ||||||||||| ||||||||||||||||||||||||||| |||||||||||||||||||||
Db 3180 CCGGGTTTGTTGCCACCGCGCCCTGTTGTCATCCGTCGGTGCGGAAAGGGCTTCTTGGGGG 3239

Qy 3280 TCACGAAGGCAGCCTTGACCAGGATAGGGATCCTCGACTTCACATCCGGAACGTCATGGTGT 3339
        ||| ||| ||||||||||||||||  |||| ||  |||  ||||||||||||||  ||||||
Db 3240 TCACAAAGGCTGCCTTGACACAGGTCGGGATCCTCACTTCACCAGGAACGTCATGGTGT 3299

Qy 3340 TGGGGACGCTACGTCACGAAGCATGGGCACATGTCTCGAATGGCCTGCTGTTCACAACTT 3399
        |||||||| | | ||||| |||||||||||| |  ||||||||| |||||| |||||||||
Db 3300 TGGGGACGCTACGTCGCGAAGCATGGGCAACATGTCCTGTTCGTGTTTCACGACCT 3359

Qy 3400 TCCATGGGGCTTCATCCCGCGAACCATCGGCCGCACGCCCGTGGGGGGCCTTAATCCCAGGTGT 3459
        |||||||| |||||||| |||||||||||||| | |||||||||||||||||||||||||| ||
Db 3360 TCCATGGGGCTTCATCCCGCGAACCATCCGCGCGTCACCCGGGGGCCCTTAATCCCAGGATGT 3419

Qy 3460 GGTCAGCCAGTGACGATGACGTCACGGTGTACCCGCTTCCAGATGGGCAACTTCGTTGACGC 3519
        |||||||||||| |  |||||||| ||||||| ||||| ||||||||||| |||||||  |||
Db 3420 GGTCAGCCAGTGATGTCGATGATGTCACGGTGTATCCCCGGATGGGCTGTTCGTTTAAGC 3479

Qy 3520 CCTGCACTTGCCAGGGAGTCCTTCGTTTATTAGATCCGACGGGCTTTGTGCCATG 3579
        | || ||||||||||| ||| ||| || ||| ||||| |||||| ||||||||||
Db 3480 CTTGTACTTGCCAGGCAGATCCGTGGTCATCAGATCCGACGGGCCCATGCCATG 3539

Qy 3580 GCTTGAGCAAGGGGACAAGGTTGAGCTGGATGTGGCCATGGACTTCCCGTG 3639
        |||||||||| |||||| ||||| |||| |||||||||||  |||||| ||
Db 3540 GCTTGAGCAAGGGGACAAGGTGAGCTGGATGTGGCCATGTCCCTGATTTCCGTG 3599

Qy 3640 GTTCGTCTCGTGGTTCACCGGTCCTTGCGACAAAGGGCAGCAGTAAGAATGCTCGGTGTCAG 3699
        |||||| |||  |||||||||||||||||  |||||| |||||  ||||| |||||||||| 
Db 3600 GCTCGTCTGCGGCTTCACCGGTCCTCCATGTGACGAGGGCACGCAGTAGGAATGCTCGGTGTCTG 3659

Qy 3700 TGCTCCACTCTGGCGCGCAGGGTTACTGCGGCGGCGATTCACTAGGCCGTCAAGGTAC 3759
        |||||||| |||||||||||| ||| | |||||| || ||| |||||| |||||||||
Db 3660 TGCTTCACTCCGGTGGTAGGCTTCAGTCTTGCGATGTCTTCAGTCTGTTCACTAGGCCGTGTTCAAGTGC 3719

Qy 3760 CAACAGATGCAAGACTACCACAGAGAACCCCTGGCTCGGGCAAAAGGAGTTTTCAAGG 3819
        ||||||||  ||| ||||||||| ||| ||||| |||| ||||||||||||||||||
Db 3720 CAACAGATGGCCAAAACCACCACTGAACCCCCCTCCGGTGCGGGCAAAGGAGTTTTCAAAG 3779

Qy 3820 AGGCCCCGTTGTTTATGCGAAGGTCTTCACAAGGATCACCCGCGCCGTACCGGTTGGAGTACG 3879
        ||||||||||||||||| |||  ||||||||||| | | |||| |||  |||||||||||||
Db 3780 AGGCCCCGTTGTTTATGCCTGAGCGGAGCGGACACTCGCCGTCCCCGTCGCCGTCCTGGAGTACG 3839

Qy 3880 GCAACATGGCCACAAGGTCTTCAGAGTCCCGTGGTCGTACCCGTGAGGGGCATGG 3939
        ||||||||| |||||||| | | |||||||| |||||| ||| || |||| ||||
Db 3840 GCAACATGGGCCACAAGGTTCAGTCTTGAACCTGTGGCCGTCGCTGTGCGGGCCAAGTGG 3899

Qy 3940 GCCCATACAATGAGCGGCGGCTGGCGGGGAAACACCCCAGTATTACTGTGGCCATGACACCA 3999
        ||||| | |  ||| |||||||  | |||| ||||||||||| |||||||||||||| | |
Db 3900 GCCCGTACAGCGAGCGGCGGGTTAAACATCCAAGTATATATACTGTGGCATGCATGATACAA 3959

Qy 4000 CTGCTTCACAAGGATCACCGCCCTTACGTATTCCACTTACGGAAGGTTTTGG 4059
        ||| ||||||||||| |||||| ||| |   ||||||| |  ||||||||||
Db 3960 CTGCTTTCACAAGGATCACTGACTCCCCCTGACGTATTCAACCTCAAGATGGAGGTTTTTGG 4019

Qy 4060 CCAACCCTAGGCAGATGCTGTGGGGGTGTCGTGCGCGCTGGTCATTTGATGACGAGTGCAGTC 4119
        |||||||||||||||||| | || |||||||  ||||||| ||||| ||||||||| |||||
Db 4020 CCAACCCTAGGCAGATGCTCACGGGGTCGTTCGGTGGTGTGCTCGTGTGCAAGGAGC 4079
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Qy   4120  ATGACTCAACTGTGTTGTTGGGCATTGGGCCTGTGCTGTTCAGGGAGCTGCGCGGAGGATGTGGAG  4179
            ||||||||| ||| |||| |||| |||| ||| || ||  || || ||||
Db   4080  ATGACTCAACCTGCTGTGTAGGCCATTGGGCATGGGCCTGCGCTGGGAGCTGCGCGGTGCGGAG    4139

Qy   4180  TGCAATTGGTGCTCTACACGCCACTGCCACCCTCACGCCTCCGATCCCCGATCCCCAGCGACACCCAT  4239
            ||||||| ||||||||||||||||||||||
Db   4140  TGCAACTAGTGCTCTACACGCCACTGCCACCCTCACGCCTCCGATCCCCATGACGCAGCACCCTT     4199

Qy   4240  CAATCATTGAGACAAAACTGGACGTGGAGAGATCCCCTCTATGGCATGGCATACCTC           4299
            |  ||||||||||||||||||
Db   4200  CCATAATTGAGACACAAAATTGGACGTGGGCGAGAITCCCTTTTAITGGGCACGGAATACCCCC    4259

Qy   4300  TTGACGGATGCGGACCGGAAGGCATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGC        4359
            | |||||||||||| ||||||||||||||||||||
Db   4260  TCGAGCGGGATGCGGAACCGGAAGGCCACCTGTTCGTCCTTGGCTCAGGCTCAAGACGGCCGAGC  4319

Qy   4360  GCCTGGCGGCCCAGTTTCGGCTAGGGGGTAAATGCCATCGCCTATTACAGGGGGAAAG        4419
            |  |||| ||||||||||||||||
Db   4320  GCCTTGCTGCGCCCCGCTAGGGGGTCAATGCCATTGCCTATTATAGGGGTAAAG              4379

Qy   4420  ACAGTTCTATCATCAAAGATGAGACCCTGGTGTGTGCTACAGACGCCACTATCCCACTG        4479
            |||||||||||||||||||||
Db   4380  ACAGTTCTATCATCAAAGGATGGGACCTGGTGGTCTGCGTCGTGCTGCTCTGGAGGACCGTGTCG   4439

Qy   4480  GGTACACTGGGAACTTCGATTCTGTCACCCGATTGTGGTTAGTGCTGGAGGAGGTCGTCG       4539
            |||||||||||||||||
Db   4440  GGTACACTGGAAATTTCGACTCCGTCACCACTGTGGATTAGTGCTGGAGGAGGTCGTTG        4499

Qy   4540  AGGTGACCCTTGATCCCCACCATTACCATCTCCCTGCGCACGGTGCCCGCTCGGCTGAAC     4599
            |||||||||||||||||||
Db   4500  AGGTGACCCTTGATCCTCACCATTACCATCTCCCGCGACAGTGCCTGCGCTGCTCGGCATCTG    4559

Qy   4600  TGTCGATGCAGCGGCGGAGGACGCACGGTCGGGGCGCTCGGGGCCGCTACTACGCCG       4659
            |||||||||||||||||||||||
Db   4560  TGTCGATGCAAAGACGAGGACGCACGGTCGGGGCAGGTCGGGGCCGCTACTACTACGCGG       4619

Qy   4660  GGGGCGCTCAAGGCCCCTGCTGGTGTGCGCTCCAGGTCCTCTGGCGGTGGAAG           4719
            |  || |||||||||||||||||||||||||||
Db   4620  GGGTGCCAAAGCCCCTGCTGGTGGGTGCGCTCCAGGTCCTCTGGCGGTGGAAG             4679

Qy   4720  CCGGTGTGACCTGGTACGCGGAATGGAACCTGACTGACAGCAAACTACTGAGACTTACG      4779
            | ||||||| |||||||| |||||||||
Db   4680  CTGGAGTGACCTGGTACGCGGAATGGAACCTGACTTGACAGCTAACCTAACCTGAGACTTACG    4739

Qy   4780  ACAACTGCCCTCACCCGACCGGCCAGCCGTCGCAGCTGCTGGGGAGAGCCGCGGTGTCTTTT     4839
            ||||||||||||||||||| ||||||||
Db   4740  ACGACTGCCCCTCTTCGTTGGGCCAGCCGTCGCGGCTGTGATCCGGAGAGCCGCGGTGTGTTTCT  4799

Qy   4840  CGGGGGCTTGCCCCGTTGAGGGATGGCATCGCCCATGTGGTTAGCTGGCAAAAGTTCGCGCGGTCA  4899
            |  |||||||||||||||||||||
Db   4800  CTGGCGGCTTGCCCCGTTGAGGGATGGCATCGCCCCTGTGGTTTGGTTTGTATTCGGTCGGCGGTCA 4859

Qy   4900  ACTGGCCCTTCTCTGTTCAGCGGACCGTGTCAGCGGACCATGTGCCGGAAACACTGTCTCCGGCC   4959
            |||||||||||||||||||||||||||
Db   4860  ACTGGCCCCTCTTCGTTGTGGTTCAGCGGACCGTGTCAGCGGACCATGTGCCGGAAACACTGTCTCCGGCC 4919

Qy   4960  CATCGGATGACCCCAGGCTGGAAGGGCCGAATCCTGTCCCACTCCTGCTGAA             5019
            |||||||||||||||||||||||||||||||
Db   4920  CATCGGATGGACCCCAAATGGGCCGAATCCTGTCCCACTCCTGCTGA                   4979

Qy   5020  GGTGGGGCAATGATTACCATCTAAAGTGCCGCGGCCATCACACATCGTGACGACCTGGTCC      5079
            |||||||||||||||||||||||||||||||||
Db   4980  GGTGGGGCAATGATTACCATCTAAAGTGCCGCGGCCACCACCATAGTGGACGACCTGGTCC      5039

Qy   5080  GTAGGCTCGGGGGGTACGTCGCCCCATCTTGATGGTGG                           5139
            ||| |||||||||||||||||||
Db   5040  GGAGACTCGGTGTGGGGGGTACGCGCCGGATCTTGATGATCG                       5099

Qy   5140  GCCTCGCTATTGCGGGGATGCATGATCTCATACACCGGGTCTCTCGTGTGGTTA           5199
            |||| |||||||||||||||||||||
Db   5100  GTCTAGCTATCGCGGGGGAATGATCTCTACACCGGGTCGCCTAGTGCGTGGTGA            5159

Qy   5200  CAGACTGGGATGTGAAAGGGGTGCAGCCCCCTTTATCGGCATGGAACCAGGCCACGC          5259
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5160  CAGACTGGGATGTGAAGGGGTGCAGCCCCCTTTATCGGCATGGAGACCAGGCCACGC         5219

Qy   5260  CCCAGCCGGTTGTGCAGGTCCCCGGTAGACCATCGGCGGGGGGAGAGTCTGGCGCCAT        5319
            | ||||||| |||| |||| |||| ||||||||||||
Db   5220  CTCAGCCGGTGGTTCCTCCGGTTGCAGGTCGAATCAGCACCACCAT                   5279

Qy   5320  CGGATGCCAACACAGTGACAGATGCGGTGCGCGCCATCCAGTCAGTTGCCGATTGGTCAG      5379
            |||||||||||| |||||||||| |||||| || ||||||||||||||||
Db   5280  CGGATGCCAAGACAGTGACAGATGCGGTGGCAGCGATCCAGTCCAGTGCTGCCGATTGGGACTA  5339

Qy   5380  TCATGACCGTGTCGATGCTGGGGAAGTGCTGTCTGCCAGGCCTAAGAGCGGCCGAGGCCT      5439
            |||||||| || ||||| ||||||||
Db   5340  TCATGACTCTGTCGATGCCGGAGAAGTGTTGTCCTTGGCTCAGGCTCAAGACGGCCGAGGCCT   5399

Qy   5440  ACGCAGCTACCACCAAGTGCCTTGCTGCTCTACACGGGGACCCTGTACGGGCGGCCGTCCCCACTG  5499
            || |||| |||||||||||| || || |||||||||||
Db   5400  ACACAGCAGCCACCAAGTGCCTGCTCGTATGGCCCTGGCCCGTGTACGGGCCGGCCTTCCCACTG   5459

Qy   5500  TTTCAATTGTTGACAAGCTCTTCGCCGGGCTGGGCTCGGCGGTGGGGCTGGGGCTGGGTAGGCCATTGCCACA  5559
            || ||| |||||||||||||||||||||
Db   5460  TATCCATTGTTGACAAGCTCTTCGCCGGGCTGGGTGGGCCATTGCCACA                 5519

Qy   5560  GTGTAATAGCGTGCGGCAGTGGCGGCCTATGGGGTCTAGGAGCCCTCCAGTGGCTGCTGTG     5619
            ||||||||||||||||||||| ||||||||||
Db   5520  ACGTGATTGCTGCCGGCAGTGGCGGCCTTCAAAGAGCCCGTTGGCAGCCG              5579

Qy   5620  CCGCTTCCTACCTCATGGGCGTTGGGCGTCGGAGGCAACGCGCCAAACCCGCTTAGCCTCCG    5679
            |  || ||||||||||||||||||||||||||||||||||||
Db   5580  CGGCTTCCTACCTCGTGATGGGCGTTGGGCGTTGGAGGCAACGCGTCTCAGACGCGTCTGCATCTG 5639

Qy   5680  CTCTCCTACTAGGGGCCGCTGGGACCCGCTGGGACCGCGCCGTCGTGGGGTTAACCATGG      5739
            | |||| ||||||||||||||||||||||||||||
Db   5640  CCCTCCTATTGGGGCGCCCTTGGGCCACTCCGTGGGCTTGCGGCTTGACCGGG            5699

Qy   5740  CGGGGCGTTCATGGGAAGTGCTAGCGCCAGTGTCTCCCCCCTTTGCTGCTGCCACCATTTTACTGGGGG      5799
            | |||||| |||| |||| ||||| || || || |||||||
Db   5700  CAGGTGCGTTCATGGGGGGCCAGTCTCCCCCCTTGGCTCACCATTTTATTGGGGG           5759

Qy   5800  CCGTGGGGGCTGGGGCGCTGGAGGGGGCGCTAGCGTGAATGCGGGCTTATGGCGG           5859
            |  |||||||||||||||| |||||||
Db   5760  CCGTCGGAGGGTGGAGGGGTGTCTTGACTTCTTTGACTTCATGGCGG                   5819

Qy   5860  GGAAACTAATCATCAGAAGAATCTGTGTATGCCATCCAGTCGTAACCACCTCAACGTGCCGCAG    5919
            ||||||||||||||||| |||| |||| ||| |||||| ||||||||
Db   5820  GGAAACTTTCATCAGAAGAATCTCATCAGAAGAATCTGTGTATGCCATCCAGTCGTGACTGACCAGTTACT 5879

Qy   5920  GACTTGCGGGGATCGCCCCTCGGGTTGTACTCAGCTGAACAACTCTGCACTACCA           5979
            ||||| |||| || || |||||| || ||||||| ||||||| |||||||||||||
Db   5880  GCCTTGCGGGGATCGCTCTCGGGTTGGTTTTGTATTCAGCTGACTGACCAGTTACT          5939

Qy   5980  CTTGGTTGAACCGTCTGCTGACTACAGTCCTGACTGCTCCAAGTCCTCATTGCGTCCCTGACAGTTACT      6039
            ||||| |||| |||| |||| | |||||||||||||||||||||
Db   5940  CTTGGTTGAACCGTCTGCTGACTACAGTCTTCATTCATCTGTATCCCGACAGTTACT         5999

Qy   6040  TTCAGAGGCCGATTACTGTGACAAGTCTCAGGCCTTGAGCCTTGACTCCTCACTC           6099
            ||||||||||| |||| |||||||||||||||||||||||||
Db   6000  TTCAGCAAGTTGACTATTGGACAAGTCTCAGGCCTTGAGCCTCCACCCC                 6059

Qy   6100  GCACCCTGGTTGCCCTGGTCAACAGGGAGGCTAAGGTGGATGAGGTCAGGTGGGGTACG       6159
            | || |||||||||||||||| |||||||||||||||||
Db   6060  GCAACAGTGGTTGCCCTGGTCAACAGGGAGGCTAAGGTGGATGAGGTACAGGTGGGGTATG      6119

Qy   6160  TCTGGGACTTGTGGGAGTGGATGAATCATGGCCGTGGGCGGCATGGTACGTCGGG           6219
            ||| ||||||| |||| |||||||| |||||||||||||||||||||
Db   6120  TCTGGGACCTGTGGGAGTGGGTGTCATCATGGCCGTGGTCGCGTCATTATGGGGAGGTGTCGG    6179

Qy   6220  CCCTCTGCCCCCGTGGTGCATTGCTGCTGCGCGGGAGGGGTGTGTCCGGAGAAT           6279
            |||| || ||||| ||||||||||||||||||||||||||||
Db   6180  CCCTCTGCCCCCGGTGGTGTCATTACCCTTGTGGCACTGCGGGGAGGGGTGGTGTCCGGGGAAT  6239

Qy   6280  GGTTGTTGGACGGCCATGTTGAGAGTCGTTGCTTTTGTTGGTGTTGCGTGATCACCGGTGATG   6339
            ||||| || |||||||||||||||||||||||||||
Db   6280  CAGACTGGGATGTGAAGGGGTGCAGCCCCCTTTATCGGCATGGAGACCAGGCCACGC
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Db  6240 GGTTGCTTGACGGTCATGTTGAGAGTCGCTGCCTCTGTGGCTGCGCGGATCACTGGTGACG 6299

Qy  6340 TTTGAATGGGCAACTCAAAGATCCAGTTTACTCTACCAAGCTGTGCAGGCATTATTGGA 6399
         |||||||||||||||| || |||||||||||||| |||| ||||
Db  6300 TTCTGAATGGGCAACTCAAAGAACCAGTTTACTCTACCAAGCTGTGCCGGCACTATTGGA 6359

Qy  6400 TGGGACAGTCCCTGTGAACATGCTGGGCTATGGCGAGACGTCGCCTTTGCTCGCCTCAG 6459
         |||||| ||||||||||||| ||||| ||| || ||||||||||| || |||  |||
Db  6360 TGGGACTGTCCCTGTGAACATCTGGGTTACGGTGAAACGTCGCCTCCTCGGCCTCCG 6419

Qy  6460 ACACCCGAAGGTGGTACCATTCGGGACGTCTGGTGGCTGAGGTGGTTGGTGACCCCTA 6519
         |||||||||||| |  ||| |||||||||||||||||| |||| |||||| |||||
Db  6420 ACACCCGAAGGTTGTCCCTCGGGACGTCTGGTGGCTGAGGTGGTTGGTGACCACTA 6479

Qy  6520 CCCACGTTGTGATCAGGCGAACATCCGCCTACAAAACTGTGCGCCCAGCAAATCCTGTGG 6579
         ||||||||||  ||||| |||  |||| || || |||||||||||  ||| |||| |||
Db  6480 CCCACGTTGTAATCAGGAGAACCTCCGCCTATAAGCTGTGCGCCCTAGCAAATCCTATCGG 6539

Qy  6580 CTGCTGTTGCTGAGACCCTATTACGTCGACGGCATACCGGTCTCATGGGACGCGGACGCGC 6639
         ||||||||||||||||||||||| || |||||  |||||||||||||||||||||  |||
Db  6540 CTGCTGTACTGAGACCCTACTACGTCCGGTCTCATGGGACGCGGACGCGC 6599

Qy  6640 GAGCGGCCTGCCATGGTCTATGGCCCTGGGCAAAGTGTCACCATTGACGGGGAACGCTACA 6699
         ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  6600 GTGCGGCCGCCATGGTCTATGGCCCTGGGCAAAGTGTTACCATTGACGGGGAGCGCTACA 6659

Qy  6700 CCCTTCCGCCATCAACTGCGGCGCTTAGGAATGTGGCGCCCCTCTGAGGTGTCATCCGAGGTGT 6759
         |||||||||| ||||||||| ||| |||||||| |||||||||||||||||||||||||||||
Db  6660 CCCTTCCGCCATCAACTGCAGGCTCAGGAATGTGCGCGCCCCTCTGAGGTTTCATCCGAGGTGT 6719

Qy  6760 CCATTGACATTGGGACGGAGACTGAAGACTCAGAACTGACAACTGGGGGCCTGCGCCGG 6819
         |||||||||||||||||||||||||||||||||| |||| ||||||||||||||||||
Db  6720 CCATTGACATTGGGACGGAGACTGAAGACTCAGAACTGACAACTGGAGGCCGATCTGCCGCCGG 6779

Qy  6820 CGGCTGCGAGCCCTTCAGGCTGTCTATCGAGAATGCTGCGAGAATTCTTGAACCTCACATAGATG 6879
         ||||||||||||||||||||| ||||||||||||||||||||||||||||||||| |||||||||
Db  6780 CGGCTGCGTGCTCTCCAAGCGATCGAGAATGCTGCGAGGATTCTTGAACCGCACATTGATG 6839

Qy  6880 TCATCATGGAAGATTGCAGTACACCCCTCTCTTGTGGGAGTAGCCGAGAGATGCCTGTGT 6939
         |||||| |  |||| | ||||||||||||||||| ||||||||||||||||||||||||
Db  6840 CCATCATCAGCAGTACACCCTCTCTTGTGGGAGTAGCTATGGGGACGATGAGAGATGCCTGTAT 6899

Qy  6940 GGGGAGAAGACATACCCCGCACTCCATCCGCCAGCACTTCGGTTACTGAGAGCAGCC 6999
         |||||||||||||||||||||||||||||| || |||||||||||||||||||||||
Db  6900 GGGGAGAAGACATCCCCCGCACTCCATCCGCCAGCACTTCGGTTACTGAGAGCAGCT 6959

Qy  7000 CAGATGAAGAGACCCTCGGTGCTTCCTCCGCAGGACGATACCCCGTCTTCTGACTCAT 7059
         |||||||||||||||||| |||||| |||| |||||||| |||||||||||||||||||
Db  6960 CAGATGAAGAGACCCTCGGTGCTTCCTCCGCAGGACGATACCCCGTCTTCTGACTCAT 7019

Qy  7060 TCGAGGTCATCCAAGAGTCCGACAGAGTCCGAGACAGCAGCGGAAAGCGTCTTCAACGTGGCTC 7119
         |||||||||||||||||||| |||||||||||||||| ||||||||| |||| |||||||||||
Db  7020 TCGAGGTCATCCAAGAGTCCGAGACAGCAGCGGAAAGCGTCTTCAACGTGGCTC 7079

Qy  7120 TTTCCGTACTAAAAGCCTTGTTTCCACAGAGGCGATGCCCAAGAAAGCTTACCGTTAAGA 7179
         |||||||||| ||| ||||||||||| ||||| ||| ||| |||||||||||||||||||
Db  7080 TTTCCGTATTAGAAGCCTTGGGCTCATTTGGGCGTGGCAATGACCCAGCAAGCTTACCGTCAAGA 7139

Qy  7180 TGTCATGCTGTGTTGAGAAGAGACCGTCGGGTCATTGGGATTGACGGTGGCGCTG 7239
         |||||| || || |||||||||||| ||||||||||||||||||||||||||||||
Db  7140 TGTCGTGCTGCGCGTTGAGGCTGTCGGGTCAGTTCATTGGGTGTGACGGTGGCGTG 7199

Qy  7240 ACGTTGCAAGCCTGTGTGAGATGATGGCAAGATCCAGAATCCAGACCATAGGTGACAAGGTGC 7299
         | || ||||||||| || || ||||||| |||| ||||||||| |||| || ||||||||||
Db  7200 ATGTTGCTAGCCTGTGTGAGATGATGGCAAGATCCAGAATCCATACAGCCTATTGTGACAAGGTGC 7259

Qy  7300 GCACTTACCTTGAATTGCAGTTGGGCAATGAACTTTACCTTTGAATGTG 7359
         ||||||||| |||||||||| ||||||||||||||||||||||||||||
Db  7260 GCACTTACCTTGAATTGCAGTTGGGTGTGGGCAATGAACTTTACCTTTGAATGTG 7319

Qy  7360 ACAAGTGTGAGGCTAGGCAAGAGACCCTTGGCTTCCTTCTTCTTACATTTGGTCTGGGGTGC 7419
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Db  7320 GCAAGTGTGAGGCTAGGCAAGAGAAACCCTTGGCTTCCTTCTTCTTTACATTTGGTCTCGGAGTGC 7379
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Qy  7420 CACTGACGAGGGCCACTCCGGCCAAGCCCCTGTGTGAGGCCGGTTGGCTCCTTGCTGCTG 7479
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Db  7380 CGCTTGACTAGTAGGGCCACGCCAAGCCTCCCGTGTGAGGCCGGCGGTTGGCTGGCTCTTTATTAG 7439

Qy  7480 TGGCCGACACCACCAAGGTGTATGTGCCCTAGGTTCATGACAAATTCCTCGTGGACAGAGTTGACA 7539
         |||||||||||||||||||||||||| ||||||||||  ||||||||| ||||||||||||||||
Db  7440 TGGCCGACACTACTAAGGTGTATGTTACCAATCCAGACACAATGTGGGACGAGGGTGGACA 7499

Qy  7540 AGGTTACCTTCTGGCTGCTGGGCCCTAGGTTCATGATGACTCCTGGGACTCCATAGAGC 7599
         ||||   |||||||||| |||||||  |||||| |||||||||||||||||||||||||
Db  7500 AGGTGACCTTCTGGCTGCTGGGCTCCTAGGTTCATGATGACTCCTGGGACTCTATTGAGC 7559

Qy  7600 GCGCTAAGAGGGCAGCTCAAGCCTCAGCCTGCCTAAGCCTGGTTACACTTATGAGGAGCAATAA 7659
         |||| ||||||||||||| || ||||||||||||||||||||||  ||| |||||||||||||
Db  7560 GCGCTAAGAGGGCCGCTCAAGCCTGCCTAAGCCTGGTTACACTTATGAGGAGCAATAA 7619

Qy  7660 GGACTGTAAGGCCACATGTCCCCATGTGCCCATGTGGGATCTAAGGTGTCGGTCATGGTCGGTCAAGGACCTCG 7719
         |||||||||||||| ||||| |||||| ||||| |||||||||||||| ||||||||| |||||| ||||||||
Db  7620 GGACTGTAAGGCCACTGTCCCATGTGCCCATGTGGGATCTAAGGTGTCGGTTAAGGACTTAG 7679

Qy  7720 CCACCCCTGCGGGGAAGATGGCTGTGTCATGACCGGCTCCAGGAGATGACCGGACGACGC 7779
         |||||||| |||||||||||||||| || |  ||||||||||||||  |||||| |||||
Db  7680 CCACCCCCGCGGGGAAGATGGCCGTCCCAGACCGGCTCCAGGAGATACCGGACGACTC 7739

Qy  7780 CAGTCCCTTTACTCTTACTGTGAAAAAGAAGTGTTCTTCAAAGACCGAAAGAAGAAGA 7839
         ||||  ||||||||||||||||||||||||||||||||||||||||||||||| |||
Db  7740 CGGTCCCTTTACTCTTACTGTGAAAAAGAAGTGTTCTTCAAAGACCGGAAGGAGGAGG 7799

Qy  7840 AGGCCCCCCCTCTCATTGTGTTCCCCGCTTGTGGACTTCCGGATAGCTGAAAAGCTTATTC 7899
         |||||||||||||||||||||| ||| |||||| |||||| |||||||||||||||||||
Db  7800 AGGCCCCCCCTCTCATTGTGTTCCCCGCTTGTGGATATGCTAGAGGAGGACGATAGCTGAAAAGCTCATCT 7859

Qy  7900 TGGGAGACCCTGGACGTGTTGGGGTAGCCAAGGCGGTGTTGGGGGCCGCCTTCCAGTACA 7959
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Db  7860 TGGGAGACCCTGGACGTGTTGGGGTAGCCAAGGCGGTGTTGGGGGCCTACGCGTTCCAGTACA 7919

Qy  7960 CCCAAAATCAGCGAATTAGGGAGATGCTCAAACTGTGGGAATCAAAGAACACCATGTCGCG 8019
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Db  7920 CCCAAAATCAGCGAGTTAAGGAGATGCTAAGAAGAAGACTAAGAAGAAGACCCCTGCGG 7979

Qy  8020 CCATCTGTGTGGACGCCCACCAGTAGCTTCGACAGTAGCTTCTCGACGATAACTGACATCAAGGTGA 8079
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Db  7980 CCATCTGTGTGGACGCCCACTAGTAGCTTCTCGACAGTAACTGAAGAGGACGGTGGCTTTGG 8039

Qy  8080 AGACAGAGCTTATGCCTGCTTCCTGCTTCCGAGGCGATACCCGTCTTCTTGACTTCAT 8139
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Db  8040 AGACAGAGCTGTACGCCTGCTCTGGCCTCTGACCCTCGACCCGTCTTCCATAGCTTTGGGAAAT 8099

Qy  8140 ACTATGCCTCTGGCACAATGTCAACCCCCGAGGGTGTGCCAGTGGGTGAGAGGTATTGTA 8199
         ||||||||||| |||| |||||||||  |||||| |||||||||| ||||||| ||||
Db  8100 ACTATGCCCTCAGGCACCATGTCACCCCGGAGGGGTGCCCCGGTGAGAGGTATTGCA 8159

Qy  8200 GATCCTCAGGGTGCTTGACCAGTTCGGCGCAACTGCTTGACTTGCTATATCAAGGTGA 8259
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Db  8160 GATCCTCGGGTGTCCGAACTAGCGCGCAACTGCTTGACTTGCTCACATCAAGGTGA 8219

Qy  8260 AAGCCGCCTGTGAGAGGGTGGGCTGAAAAATGTCTGCTCCTCATCGCTGCGATGACT 8319
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Db  8220 AAGCCGCCTGTGAGAGGGTGGGCTGAAGAATGTCTGAAGAATGTCTCTCTCATAGCCCGATGACT 8279

Qy  8320 GTTTGATCATATGCGAACGGCCTGTGTGCGATCGGCCTTTGGGCACGACGCTTGGGAGAGCCCTGGCA 8379
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Db  8280 GCTTGATCATATGTGATCATATGTGACGCGGCCAAGCGACCACGACGCGTTTGGCAGAGCCCTAG 8339

Qy  8380 CGAGCTACGGGTACCGACGAGCCTTCGTATCATCGGACAGCGCCCCCTTCT 8439
         ||||| ||| ||||||| |||||||||| ||||| ||||||||||| |||
Db  8340 CGAGCTATGGGTACCGACGCGCCGAGCCCTCATATCATCCTTGGACACGGCGCCCCCTTCT 8399

Qy  8440 GCTCCACTTGGCTTGCTTCTGAGTGCAATGCAGATGGAAAACGCCATTTCTTCCTGACCACGGC 8499
         ||| ||||| |||| || ||||||||||| ||||| |||||||||||| ||||| ||||||||
Db  8400 GCTCCACTTGCTTGCTTCTGAGTGCAATGCAGATGGGAGCAGCGCCATTTCTTTCCTGACCACGG 8459
```

```
NUMBER OF SEQUENCES: 277
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Dehlinger & Associates
    STREET: 350 Cambridge Ave., Suite 250
    CITY: Palo Alto
    STATE: CA
    COUNTRY: USA
    ZIP: 94306
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/485,910
    FILING DATE:
    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/389,886
    FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/357,509
    FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/329,729
    FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/344,271
    FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/285,558
    FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/285,543
    FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/246,985
    FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
    NAME: Fabian, Gary R.
    REGISTRATION NUMBER: 33,875
    REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 324-0880
    TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 234:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 9327 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
    INDIVIDUAL ISOLATE: 3ZHGV-6, HGV FROM PNF2161
US-08-485-910-234

Query Match 83.9%; Score 7885.6; DB 2; Length 9327;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;

Qy     40 GCAAGCCCATAAACCGACGCCTATCTAAGTAGACGCCAATGACTCGGCGCCGACTCGGCG 99
          |||||||| ||||||  |||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAAGCCCAGAAACCGACGCCTATCTAAGTAGACGCCAATGACTCGGCGCCGACTCGGCG 60

Qy    100 ACCGGCCAAAAGGTGGTGGATGGGTGGTGGTGGTCGTAGGTCGTAAATCCGGTCAT 159
          |||||||||||  ||||||||  ||||||||||  ||||||||||||||||||||||
Db     61 ACCGGCCAAAAGGTGGTGGATGACGTGGGTGGTGGTGATGACTCCGGTCAC 120

Qy    160 CCTGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTCGCGGC 219
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTTAAGATTCCTCTTGTGCCTCGGGC 180
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Qy   8500 ACTTTCGGAGGCCCCTCGCTCGAGCGAGTACAGTGACCCAATGGCTTCGGCCA 8559
          |||| ||||||||||||||||||||||||||||||||| |||| ||||||||||
Db   8460 ACTTCCGGAGGCCGCCGCTCGAGCGAGTATAGTGACCCGATGGCTTCGGCGA 8519

Qy   8560 TCGGTTACATCCTCCTATACCCTTGGCATCCTACACGGTGGTCATCATCCCTCACG 8619
          ||||||||||||||| ||||| || |||||||||||||| ||||||||||||||
Db   8520 TCGGTTACATCCTCCTTTATCCTTTGCACCCCATCACACGGTCATCATCCCTCATG 8579

Qy   8620 TGCTCACCTGGCCGGTTAGGGGTGGTGGCACACCCTCTGATCCTCGTGTGTGGCCAGGTAC 8679
          |||| ||  |||||||||||| || ||||||||||||| |||||||||||||||| |||||
Db   8580 TGCTAACGTGGCCATTCAGGGGTGGAGGCACACCCGTTTGTGTCATCCGTTTGTGTGCCAGGTAC 8639

Qy   8680 ATGGTAATTACTACACAGTTTCCACTGACAAACTGCCTAACATCATCGTGCCCCTCCACG 8739
          |||||||| |||||| |||||||||||||||||||| |||||||||||||||||||||||
Db   8640 ATGGTAACTACTACACAGTTTCCACTGACAAACTGCCTAACATCATCGTGCCCCTCCACG 8699

Qy   8740 GACCAGCAGCGTTGAGGGTTACCCGACACAACTAAGACAACAAAAATGGAGGGCTGCAAGG 8799
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Db   8700 GACCAGCAGCGTTGAGGGTTACCCGAGCAGACACAACTAAAAACAAAGATGGAGGGCTGTAAGG 8759

Qy   8800 TGCTGAGCGACCTCAAGCTCCCTGCCTTAGCCAGTCCACCGGAAGAAGGCCGGGGGCATTGC 8859
          | ||||||||||||||||||||||| ||||| |||||||||||||| ||||||||||||||
Db   8760 TTCTGAGCGACCTCAAGCTCCCTGCTTTAGCAGTCCACCGAAGCAGGCCGGGGGCGTTGC 8819

Qy   8860 GAACCGTATGCTCCGGTCCGCGCGTTGGGCTGAGTTGGCTAGGGGGCTCTTGTGGCGTC 8919
          ||||||||||| |||||||||||||||||||||||||||||||||||| |||||||||||
Db   8820 GAACACGCATGCTCCGCGCCGCGCGTTGGGCTGAGTTGGCTAGGGGGCTTGTTGTGGCATC 8879

Qy   8920 CAGGCCTGCGGCTTCCCCTCCGGAGATTGCTCGGTTATCCCGGGGGTTTCCCCTTTTCCC 8979
          ||||||||||||||||||||  ||||| || |||||||||||||||||||||  ||||||
Db   8880 CAGGCCTACGGCTTCCTCCCCTGAGATTCTGGTATCCGTGGGGGGTTCCTCTCCCCC 8939

Qy   8980 CCCCTATATGGGGGGTTGGTTCATCAATTTGATTTCACAAGCCAGAGAGTCGCTGGCGGT 9039
          ||||||||||||||  |||||| || |  |||| | |  ||||||||||||||||||||||
Db   8940 CCCCTATATGGGGGGTTGGTACACCAATTTGATTTTACAGGCCAGAGAGTCGCTGGCGGT 8999

Qy   9040 GGTTGGGGTTCTTAGCCCTGCTCATCGTAGCCCTTCTTCGGGTGAACTAAATTCATCTGTT 9099
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9000 GGTTGGGGTTCTTAGCCCTGCTCATCGTAGCCCTTCTTCGGGTGAACTAAATTCATCTGTT 9059

Qy   9100 GCGGCAAGGTCCGGTGACTGATCATCACTGGAGGAGGTTCCCGCCCCTCCCCGCCCAGGG 9159
          ||||||||||||| ||||||||| ||  ||||||||||||||||||||||||||||||||
Db   9060 GCGGCGAGGTCGTGTGACTGATCGTCACCGGAGGAGGTTCCCGCCCCTCCCCGCCCCAGG 9119

Qy   9160 GTCTCCCCGCTGGGTAAAAAGGGCCCGGCCTTGGGAGGCATGGTTACTAACCCCCTG 9219
          |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||
Db   9120 GTCTCCCCGCTGGGTAAAAAGGGCCCGGCCTTGGGAGGCATGGTTACTAACCCCCTG 9179

Qy   9220 GCAGGGTCAAAGCCTGATGGTGCTAATGCACTGCACTCCGCTCGGTGGGGTCGCTACCTTA 9279
          ||||||||||||||||||| ||||||||||||||||||| ||||||||||||||||||||
Db   9180 GCAGGGTTAAAGCCTGATGTGCTAATGCACTGCACTTCGGTGGGGTCGCGTCGCTACCTTA 9239

Qy   9280 TAGCGTAATCCGTGACTACGGGCGTGCTCCGGAGCCCTCCGAGAGCCCTCCGATGGGCACAGTGCAC 9339
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   9240 TAGCGTAATCCGTGACTACGGGCGTCTCGCAGCCCTCCGAGAGCCCTCCGATGGGCACAGTGCAC 9299

Qy   9340 TGTGATCTGAAGGGGTGCACCCCGTAA 9367
          |||||||||||||||||||||||  ||
Db   9300 TGAGATCTGAAGGGGTGCACCCCGGAA 9327
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RESULT 12
US-08-485-910-234
; Sequence 234; Application US/08485910
; Patent No. 5874563
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, LaVonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
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Qy    220 GAGACCGGCCACGTCCACAGGTTGCTGCCCCTACCGGTTGTGAATAAGGGCCCGACGTCAG  279
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Db    181 GAGACCGGCCACGTCCACAGGTTGGCCCCCTACCGGTTGTGAATAAGGGCCCGACGTCAG   240

Qy    280 GCTCGTCGTTAAACCGAGCCCGTCACCCACCTGGGCAAACGACGCCCACGTACGGTCCAC   339
          |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db    241 GCTCGTCGTTAAACCGAGCCCGTTACCCACCTGGGCAAACGACGCCCACGTACGGTCCAC   300

Qy    340 GTCGCCCTTCAATGTCTCTCTTGACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAGT   399
          ||||||||||||||||||||||||||| ||||  |  ||||||||||||||||||||||||
Db    301 GTCCCCCTTCAATGTCTCTCTTGACCAATAGGCCGGCCGGCGAGTTGACAAGGACCAGT   360

Qy    400 GGGGCGCGGGGTTATGGGGAAGGACCCCAAACCTGCCCTTCCCGGTGGCCCGGGAAAT    459
          ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGGGCGCGGGGCT-TGGAGAGGGACTCCAAGTCCCGGCCCTTCCCGGTGGCCCGGGAAAT   419

Qy    460 GCACCATAGCCGCTCAGGGTCATCCGGCTCCGGCGGGTAGCCCAAGAATCCTTCGGG      519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GCACCATAGCCACCAGCTCCGCGCCGGCGGGTAGCCCAAGAATCCTTCGGG           479

Qy    520 TGAGGGCGGTGGCATTCTCTTTCTATACCATCATGCAGTCCTTCTCGTCCTTCTCG      579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 TGAGGGCGGTGGCATTCTCTTTTCTATACCATCATGCAGTCCTTCTCGTCCTTCTCG     539

Qy    580 TGGTTGAGGCCGGGCCATTCTGCCCCGCCACCAGCTTGTCGAGCCAATGGGCAAT       639
          |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    540 TGGTTGAGGCCGGGCCATTCTGCCCCAGCTTGTCGAGCCGAATGGGCAAT            599

Qy    640 ATTTCCTCACAAATTGCTGCCCCGGAAGACATCGGGCTTCTGCCTGGAAGGCCGATGCC   699
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Db    600 ATTTCCTCACAAATTGTGTGCCCCGGGACTCGGGTTCTGGGTGTGAGGTGACTCGG      659

Qy    700 TGGTTGCCCTGGGGTGTTGCACGGTTTGCACCGACCGTTGCTGGCCACTGTATCAGGCGGGTT 759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 TGGTGCCCTGGGGTGTTGCACGATTTGCACTGACCAATGCTGGCCACTGTATCAGGCGGGTT  719

Qy    760 TGGCTGTGCGGCCTGGCAAGTCCGCGGCCCAGCTCGTTGGGGAACTGGGAGCCTGTACG   819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 TGGCTGTGCGGCCTGGCAAGTCCGCGGCCCAACTGGTGGGGAGCGTGGTGAGCCTATACG   779

Qy    820 GGGCCCTTGTCGGTCTCGGCTTACGGTAGCCGGGATCCGGTTTACTCCG            879
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Db    780 GGCCCCTTGTCGGTCTCGGCTATGTGGCGGATCCTGGGTGAGGTGTACTCGG          839

Qy    880 GGGTCCTGACAGTTGGTGTTGCGGTTGAGGCGCCGGGTCTACCTGATGCCCAACCTGAAGT 939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 GGTCCTAACGGTGGGAGTCGCGTTGAGGATGGGATCTACCCGGTTACCCGGCGTCAACCTGACGT  899

Qy    940 GTGCAGTAGAATGTAAGTGGAACGTTAAGTGGAAGTGGGAGTTTTGGAGATGGGACTGAGCAGTTGG 999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 GTGCAGTGCGTGTGAGTTAAAGTGGGAGTGGGAGTTTTGGAGATGGGACTGAACAGCTGG  959

Qy   1000 CCTCCAATTACTGGGATTTTGGAATACCTTTGGAATATTTTGAAGTTCCCATTGAGTTGG 1059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 CCTTCAACTACTCGGATTTCGGGAATACCTTCTGAAGGTCCCATTTGATTTCTGGAAGCG  1019

Qy   1060 TGATGAGCCTGACCCCTGTTGTGGGTTGGCCGTGGTGTACGGGATGGCGGGGAACAACGGA 1119
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Db   1020 TGATAAGCCTGACCCCTGTTTTGGTTCTTCTGTCTGGCATGGCGGGATGGTCCTTGAAGGCC  1079

Qy   1120 TTGTCATGGTTTTCCTGTCCCCGCGGTCCAGTGCAGTCATGCCTGGCAAGGCGCCCCCCGCCTCG 1179
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Db   1080 TTTGTATGGGTCTTTTCCTGTCGTTCCGGGCGGATGCCCGGGATGTGAAGTGCAGTGTTGAACCAGTTCG  1139

Qy   1180 TTTTTGGGGTCCCCGCCCCTTACTGGGATGGGAGTCGGAGACCGTTGGGGAAGTGCGGGGCCA 1239
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Db   1140 TTTTTGGGGTCCCCGCCCCTTGACTGGGATGGGAGTCGGAGAAGTGTGGGGCCA         1199

Qy   1240 ACGGGTCCGGTATTCCCCACTGGGGAGGGAGGGTGTCGAGGGAATGTCACGCTCTTGT     1299
          |||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 ACGGGTTCCGCGTTTTTTCGGACTGGGGAGGAGTGTGGGGAACGTTACGGCTTCAGT      1259

Qy   1300 GTGACTGCCCAACGGCCCTGGGTTCGGCAGGCGGTTGGGTGGG                 1359
          ||||||||||||||||||||||||||| |||||||| |  ||||
Db   1260 GTGACTGCCCTTAACGGCCCTGGGTGGTGTTGCCAAGCCTTTGCCAGCCAATCGGCTCGGG  1319

Qy   1360 GCGACCCCATCACCCATTGAGCACCACGGACAAAACCAGTGCCCCTATCATGCCCCCCAAT 1419
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 GTGACCCCATCATTACTGGGACCACGGGCAAAATCAGTGGCCTTTCATGCCCCCCCAGT    1379

Qy   1420 ATGTCTATGGGTCGTGTCCGTAACGTGCGTGGGGTTCCGTGGGGTTCCGCTTGGTTGCCTCGA 1479
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 ATGTCTATGGGTCGTGCTACAGTCACTTGCGTGTGGGTTCCGCTTCTTGGTTGTGCCTCCA   1439

Qy   1480 CCGGGCGGTCGTGATTCGAAGATCGATGTGTGGAGTTGGTGTCGGGATCGGTGGCCAGCT    1539
          ||  ||||| ||||||||||||  |||||||||||||||||||||||||||||||||||||
Db   1440 CCAGTTGCTCGGCGGACTCGGAGATCCGGGATCGGTGGGGAGTTTAGTGCCAGTGGCTCTGCCACCT  1499

Qy   1540 GCACCATAGCCGCTCTAGGGTCATCCGGATCGGGTCATCCGGACACGTGTTGAGCTCTCCGAGTGGG 1599
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 GCACCATAGCCACACTGGGGGGATCATCCGGGATCCGGACACGGCTCCGCCTCCGAGTGGG   1559

Qy   1600 GAGTCCGTGCTAACGTGTATTCTGGACCGGTCGGCCGCTTCATGTGCCACCTGTGTGC    1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 GAATCCGTGCTGCCGGTGTCGTGGACCGGTCGGCCGCCTGCTTCATGCGGCACCTGTGTGA  1619

Qy   1660 GGGACTGCTGGCCCGAAACCGGTCGGTTAGATCCGGTTCCTTCCATTCCATCCGTGCGCACGGGGC 1719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 GGGACTGCTGGCCCGAGACCGGGTCGGTTAGGTTCCGTGCGGCGCCGGTGGGGC        1679

Qy   1720 CTCGGCTGACAAAGGACTTGGAAGCTGTGCCTTCGTCAACAGGACAACTCCCTTCACCA   1779
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 CTCGGCTGACAAAGGACTTGGAAGCTGTGCCTTCGTCAATAGGACAACTCCCTTCACCA    1739

Qy   1780 TAAGGGCGCGGCTGGGCAAGAGGGCGAGAGGCAACCCGGTGCGGTCGCGCCCGGTTTTG   1839
          | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 TTAGGGGCCCCTGGGCAAGAGGGCGAGAGGCAACCCGGTGCGGTCGCGCCCGGTTTTG    1799

Qy   1840 GGTCCTACACCATGACCAAGATCCGGGATTCCGCGCATTTGTGAAATGTCCACACCACCAG 1899
          ||||||||||||||||||| ||||||||||  ||||||||||||||||||||||||||||||
Db   1800 GGTCCTACGGCCATGACCACATCCTGGTGGAGTGTGCGGAGTGTCCCACACCACCAG     1859

Qy   1900 CCAATAGAGCCTCCGACTGGAACGTTCGGGTTCTTCCCCGGAGTCCCGCCATTAACAAACT 1959
          || ||||||||||| ||||| |||||||||||  |||||||||| |||| ||||  |||||
Db   1860 CCATCAGCCCCTCCCCACCGACGCCTGATGGTTTGGTCTCTCGGGACGCCCGCCTCTCAACAACT  1919

Qy   1960 GCATGGCGCTAGGCACGGAAGTGTCTGAGGCATTGGGCGGGGCTGGGCGTTACGGGGGGT   2019
          |||| ||||  |||||||||||||||||||||||||||||||||||| |||||||||| 
Db   1920 GCATGCTCTTGGCACGGAAGTGTCCGAGGCACTTGGGGGCTGGGCCTGGCCCGTTGGGGGGG  1979

Qy   2020 TCTACCAGGCCTCTGGTTCGGCAGGTGTTCGGACTGATGGCAGCCGAAATCCGGTTTGCC  2079
          |||| ||||||||| |||||||| |||||||||||||||||||||||||||||||| |||||
Db   1980 TCTATGAACCCCTGGTGGTGCGCAGTGTCGGACTGATGGGACAGCCGAAATCCGGTTTGTC  2039

Qy   2080 CGGGGTACGGCCGATGGCTGTCCCTGGTTCCTCTGGTAGAGCCTGACCGCCAGGGGCACC   2139
          |||| ||||||||||||||||||||||||  |||||||||||||||||||||||||||  
Db   2040 CGGTGTTTGCAGCAACGTTGCGTATGGTTTATACATCGTGGTTTATACATGTCCAGGGTGCACT  2099

Qy   2140 TGCAGGAGGTGGATCGGGGCAACTTCATCCCCGGTTGCTCTTGGATTTTG           2199
          ||||||||||||||||| ||||||||||||||||| |||  ||||| |||||||
Db   2100 TGCAGGAGGTGGATCGGGGCAACTTCATCCCCGTGATGGTTGGTTGGTTGGGACTTTG   2159

Qy   2200 TATTTGTCCTCTATCTGATGAAGCTGGTTGCCGATGATCTTGC                 2259
          ||||||  ||||| |||||||||| ||||||||| ||||||||||
Db   2160 TATTTGTCCTGTTATACCTGATGAAGCTGGTGGCCGATGATCTTGC              2219

Qy   2260 TTCTGCTGTGGTGGTTGGCAGTTGGCGGGTGAACCAGTTGGCTGGCTGCCGGCGCTGGACGCTG  2319
          ||||||||| |||||||| |||||||||||||||||||||||||||||||||||||||||
Db   2220 TGCTGCTATGGTGGTGGTTGGTCAGTTGGGAACCAGCAGCTGGCCTTAGGGGCCGCCGGAAGCCG  2279

Qy   2320 CCGTGGCGGTGAAGTTTTTGCGGGGGCCTTCCACTG                         2379
          |||  ||||| ||||||| |  ||||||||||||||||
Db   2280 CCGTTGGCAGGTGAGGTTTCGCCGGGCCCTGTCTCGTGTCCTCGTGTCTCGGGGACTTTCAGT  2339

Qy   2380 TCAGTATGATACTAGTCTCAGCAAACCTGGTTGTTGTACTTTCGGTGATGGCCCTCAGC    2439
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Qy 4600 ... 4659
Db 4620 ... 4619

Qy 5680 ... 5739
Db 5640 ... 5699

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Qy  8980  CCCCCTATATGGGGGTGGTTCATCAATTGGATTCACAAGCCAGAGGAGTCGCTGGCGGT     9039
          ||||||||||||||||||||| ||||   ||||| |||||||||||||||||||||||||
Db  8940  CCCCCTATATGGGGGTGGTTGGTACACCAATTGGATTTTACAAGCCAGAGGAGTCGCTGGCGGT   8999

Qy  9040  GGTTGGGGTTCTTAGCCTGCTCATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTT     9099
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Db  9000  GGTTGGGGTTCTTAGCCTGCTCATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTT     9059

Qy  9100  GCGCAAGGTCCGGTGACTGATCATCACTGGAGGAGTTCCCGCCCCTCCCGCCCCAGGG      9159
          |||| ||||| |||||||||| |||| |||||||||||||||||||||||||||||||||
Db  9060  GCGCGGCAGGTCTGGTGACTGATCGTCACCGGAGGAGTTCCCGCCCCTCCCGCCCCAGGG     9119

Qy  9160  GTCTCCCCGCTGGGTAAAAAGGGCCCGGCCTTGGGAGGCATGGTGTTACTAACCCCCTG     9219
          |||||||||||||||||||||||||||||| |||||||||||||||  |||||||||||||
Db  9120  GTCTCCCCGCTGGGTAAAAAGGGCCCGGCCCTTGGGAGGCATGGTGGTTACTAACCCCCTG    9179

Qy  9220  GCAGGGTCAAAGCCTGATGGTGCTAATGCACTTCGTGCTGGGGTCGCTACCTTA          9279
          ||||||| |||||||||||||||||||||||| ||  |||||||||||||||||||||||
Db  9180  GCAGGGTTAAAGCCTGATGGTGCTAATGCACTGCCACTTCGGTGCTGGGGTCGCTACCTTA    9239

Qy  9280  TAGGTAATCCGTGACTACGGGCTGCTCGCAGAGCCCTCCCGGATGGGGCACAGTGCAC      9339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9240  TAGGTAATCCGTGACTACGGGCTGCTCGCAGAGCCCTCCCGGATGGGGCACAGTGCAC      9299

Qy  9340  TGTGATCTGAAGGGGTGCACCCGGTAA      9367
          || ||||||||||||||||||||| ||
Db  9300  TGAGATCTGAAGGGGTGCACCCGGGAA      9327
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;   FILING DATE: 03-AUG-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,543
;   FILING DATE: 03-AUG-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/246,985
;   FILING DATE: 20-MAY-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Fabian, Gary R.
;   REGISTRATION NUMBER: 33,875
;   REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 324-0960
;   TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 182:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 9103 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: both
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   INDIVIDUAL ISOLATE: HGV-JC Variant
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 276..9005
US-08-466-033-182

```
Query Match             82.6%;  Score 7760.6;  DB 1;  Length 9103;
Best Local Similarity   90.8%;  Pred. No. 0;
Matches  8264;  Conservative    0;  Mismatches  839;  Indels    0;  Gaps    0;

Qy   76  CAATGACTCGGCGCCGACTCGGCGACCGCCAAAAGGTGGTGATGGGTGGTGACAGGGT     135
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Db    1  CAATGACTCGGCGCCGACTCGGCGACCGCCAAAAGGTGGTGATGAGTGGTGATGACAGGGT    60

Qy  136  TGGTAGGTCGTAAATCCGGTCATCCTGGTAGCCACTATAGGTGGTCTTAAGAGAAGT     195
         ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   61  TGGTAGGTCGTAAATCCGGTCACCTTGGTAGCCACTATAGGTGGTCTTAAGAGAAGT      120

Qy  196  CAAGACTCCTCTTGTGCCTGCGGGAGACCGCGACGGTCCACAGTGCTGGCCTACCG      255
         ||| ||||||||||||||||||||||||||||||||||||||||||| ||||| |||||
Db  121  TAAGATTCCTCTTGTGCCTGCGGGAGACCGCGACGGTCCACAGTGTTGGCCCTACCG     180

Qy  256  GTGTGAATAAGGGCCCGACGTCAGGCTCGTCGTTAAACCGAGCCCGTCTCCTGACCAATAGGTTA     315
         ||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||||| |||
Db  181  GTGGGAATAAGGGCCCGACGTCGTCAGCTCGTCGTTAAACCGAGCCCGTCTCCTGACCAATAGGCTTA    240

Qy  316  AAACGACCCCACGTACGGTCACGGTCGCCCTCCAATGTCTCCTTCAATGTCTCTTGACCAATAGGTTTA    375
         ||||||| ||||||||||||||||||| || |||||||||| ||||||||| |||||||||||||| |||
Db  241  AAACGACGCCCACGTACGGTCACGGTCGCTCGTCGCTCCAATGTCGCTCTTGACCAATAGGCTTA     300

Qy  376  TCCGGCGAGTTGACAAGGACCAGTGGGGGCCGGGGGTTATGGGGAAGGACACCCCAAACCCT        435
         |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  301  GCCGGCGAGTTGACAAGGACCAGTGGGGGCCGGGGGTTATGGGGAAGGACCCCCAAACCCT       360

Qy  436  GCCCTTCCCGGTGGCCACCGGGAAATGCATGGGGCCCAGCTCCGCGGCGTCCGCAGCC            495
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  GCCCTTCCCGGTGGCCACCGGGAAATGCATGGGGCCCAGCTCCGCGGCGTCCGCAGCC           420

Qy  496  GGGGTAGCCCAAGAATCCTTCGGGTGAGGGGTGGCGGTGGCATTCTCTTTCTATACCATCA          555
         ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db  421  GGGGTAGCCCAAGAATCCTTCGGGTGAGGGGTGGCGGTGGCATTCTCTTCCTTATACCATCA       480

Qy  556  TGGCAGTCCTTCTGCCTTCCTTCTCGTGGTTGAGGCCGGGCCATTCTGGCCCGGCCACCC          615
         ||| || || || |||| ||||||||||||||||||||||||||||||||||||||||||||
Db  481  TGGAAGCCCTCTGCGTTCCTCTCGTGGGTGAGGCCGGGGCCATTCTGGCCCGGCCACCC        540

Qy  616  ACGCTTGTCGAGCGAATGCGCAATATTTCCTCACAAAATTGCTGTGCCCGGAAGACATCG          675
         |||||||||||||||||||||||| || |||||||||  ||| ||| |||||||||||||
Db  541  ACGCTTGTCGAGCGAATGGCAATATTTCCTCACAAACTGTTGTCTGCTCCAGAGACATTG       600
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RESULT 13
US-08-466-033-182
; Sequence 182, Application US/08466033
; Patent No. 5766840
GENERAL INFORMATION:
;   APPLICANT: Kim, Jungsuh P.
;   APPLICANT: Wages, John
;   APPLICANT: Young, LaVonne M.
;   APPLICANT: Fry, Kirk E.
;   APPLICANT: Linnen, Jeffrey M.
;   TITLE OF INVENTION: Hepatitis G Virus and Molecular
;   TITLE OF INVENTION: Cloning Thereof
;   NUMBER OF SEQUENCES: 277
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dehlinger & Associates
;   STREET: 350 Cambridge Ave., Suite 250
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/466,033
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/389,886
;   FILING DATE: 15-FEB-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/357,509
;   FILING DATE: 16-DEC-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/329,729
;   FILING DATE: 26-OCT-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/344,271
;   FILING DATE: 23-NOV-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,558

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Qy   676 GGTTCTCGCCTGGAAGGCGGATGCCTGGGCGGTGGCCCTGGGGGTGCACGGGTTTGCACCGACCGTT 735
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Db   601 GGTTCTCGCCTCGGAAGGCCGGTTGCCTGTGGGCCCTGGGCGGTTGCCGCAGTTGCACTGACCCAT 660

Qy   736 GCTGGCCACTGTATCAGGCGGTTGCGCTGTGTGCGCTTGGGCCAAGTCCGCGGCCCAGCTCG 795
         |||||||| |||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   661 GCTGGCCGCTGTATCAGGCGGTTGCGCTGTGTGCGCTGGGCCAAGTCCGCAGCCCAGCTGG 720

Qy   796 TTGGGAACTGGGGAGCCTGTACGGCGCCCTTGTCGGTCTCGGCTTACGTAGCCGGGATCC 855
         | ||| ||||||| ||||||||||||||||||||||||||||||||| |||| ||| ||||
Db   721 TGGGGCAACTGGGTGGCCTCTACGGCGCCCTTGTCGGTCTCGGCCTAGCTGGGCCGCATCC 780

Qy   856 TGGGTCTCGGCGAGGTTTACTCCGGGGTCCTGACAGTTGGTGTTGCGTTGACGGCGCCGGG 915
         |||||||||| ||||||| |||||| ||||||||||||||| |||||||||||||||||||
Db   781 TGGGCCTGGGTGAGGTGTACTCCGGGTGTCCTAACAGTTGGTGTTGCGTTGACGCCGCCGGG 840

Qy   916 TCTACCTGATGGCCAACCTGAACTGCACAGTGTCAGTAGAATGTGACGTTAAGTGGGAAGTGAGT 975
         |||||||||||||||||||||||||||||||| |||||| ||| |||||||||||||||||||||
Db   841 TCTACCCGATGGCCAACCTGAACTGCACAGTGTCAGCTGAGTGTGACGTTAAGTGGGAAAGTGAGT 900

Qy   976 TTTGGAGATGGACTGAGCAGTTGCCTCCAATTACTGATTTTGGAATACTTTGGAAAG 1035
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTTGGAGATGGACTGAGCAGCTGCCCTCCAATTACTGATTCTGGAATACTTTGGAAGG 960

Qy  1036 TCCCATTTGAATTTGGAGAGAGGATTGTCATGGTTTCCTGCTGCTGTGTGACGATGGCGGGGGA 1095
         | |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   961 TCCCGCTGCTGTGGAGAGGCGTGCTAAGCCTGACTTTGTGTTTCCTGCTGCTGTGACGATGGCGCCGGA 1020

Qy  1096 CATTGCTTTTGCTGGAGCAACGGATTGTCATGGTTTCTGCTGGTGTCCGCGCTCCGTTTGGGGTCC 1155
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Db  1021 CGTTGCTGCTGTGAGCAACGGTCTCCGCGCTCCGTTTGGGGTCC 1080

Qy  1156 TGTTGCAAGGCGCCCCGCCTCCGTTTTGGGGTCCGCGCCCTTTGACTACGGGTTGAAGT 1215
         | ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1216 GGCAGTCATGCTCTGCAGGGCTCGCCGTATTCCCACTGGGGGAGGAGGGTGTGGG 1275
         | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GGCAGTCGTGTTCCTGCAGGGCTCAATGGGCTCGCCGCCTATACTGGGGGAGAAGTGTGGG 1200

Qy  1276 ATCGAGGAAATGTCACGCGTCTTGTGTGACTGTGGGGCGCCCCCTGGGTTTGGGTCCCGG 1335
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Db  1201 ACCGTGCCGGTTGGTTGTTCCTGTGACTGCCTCCCCACCGGCCCCTGGGTGTGGTTGCCGG 1260

Qy  1336 CCTTTTGCCAGGCGGTTGGGTGGGGCGACCCCATCACCCCATTGGAGCCACGGACAAAACC 1395
         ||||| |||||||| | ||||||||||||||| ||||||||| |||||||||||||||
Db  1261 CCTTTTGCCAAGCAATCGGCTGGGATCCCCATCACTCACTACTGGAGCCACGGCCAAAATC 1320

Qy  1396 AGTGGCCCTATCATGGCCCCAATATGTCTATGGGTCTGTGTCCGTAACGTGTCGTGGG 1455
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Db  1321 GGTGGCCCCTCTCATGCCCCAGTGATTGTCTATGGGTCTCGTTTCAGTCACTTGCGTGTGGGG 1380

Qy  1456 GTTCCGTGTCTTGGTTTGCCTCGACCGGGGTCTGTGATTCGAAGATCGATGTGTGGGAGTT 1515
         ||||| || ||||||||||||||||||||| |||||| || | ||||||||||||||||
Db  1381 GTTCCGTGTCTCTTGGTTTGCCTGGGGTCTGCGACTGTGATGTGTGGGAGTC 1440

Qy  1516 TGGTGCCAGCGTGTGGATCTGCACCATAGCCGCTCTAGGGTCATCGGATCGGCGACA 1575
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Db  1441 TGGTGCCAGCGTGTTGCTCCCCCAGCTGTCTCGCATCCGTGGATCGGGACA 1500

Qy  1576 CGGTGGTTGGAGCTTCCGAGTGGGGAGTCCGTGTATTCTGGACCGTCGC 1635
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Db  1501 CGGTAGTTGGAGCTCTCCGAGTGGGGGACTCCGCGCGTGCAATTCTGGATCGTCGC 1560

Qy  1636 CTGCTTCATGTGGGCACCTGTGTCCGGGACTGGCTGCGCGAACCGGTCGGTTAGATTCC 1695
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Db  1561 CGGCTAGTTGAGCTGTGTGAGAGACTGCTGGCCCCGGAAACCGGGTCGGTTAGGTTTTC 1620

Qy  1696 CTTTCCATCCGGTGCCGCAGGGACTTGGAAGCTGTCCCTTCG 1755
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Db  1621 CATTCCATCCGGTGCGCGCACAAAGACTTGAAGCTTGCCCCTTCG 1680
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Qy  1756 TCAACAGGACAACTCCCTTCACCATAAGGGCGCCCCTGGGCAACCAGGGGAGGAGGCAACC 1815
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Qy  1816 CGGTGCGGTCGCCGGTTGCCTGGGCCCTGGGCGGTTTGGGTTTGGGCGTGGCGCGGATTCCCTGC 1875
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Db  1741 CGGTGCGGTCGCCGGTTGCCCTGGGTTTGGGTTTGGGCGTGGCGCGGTTCGGACTCCTTAC 1800

Qy  1876 ATTTGGTGAAAATGTCCCACACCAGCCATAGAGCCTCCGACTGGAACGTTCGGGTTCTTCC 1935
         ||||||||||||||||||||||||||||||| |||||||| |||| ||||||||||||||
Db  1801 ATTTGGTGAAAATGTCCCACACCAGCCATTGAGCCTCCCACCGGACGCGTTTGGGTTCTTCC 1860

Qy  1936 CCGGAGTCCGCGCCATTAACAACTGCATGCGCGTCAGGCACGGGAAGTGTCTGAGGCATTGG 1995
         |||||| ||||||||| |||| ||||||||||| || ||||||||||||||||||||| |||
Db  1861 CCGGAGTGCGCGCCTTCTTAACAACTGCCTGCTGTGTTGGGCACGGGAAGTGTCCGAAGCGCTGG 1920

Qy  1996 GCGGAGCTGGGCTTACGGGGGGGGTTCTACGAGCCTCTGGTTCGGAGCGTCCAGGTGTTCGGAGCTGA 2055
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Db  1921 GCGGGGCCGCGCTCACGGGGGGGGTTCTATGAACCCCTGGTGCGCCAGGCCGTTCATGGAGCTGA 1980

Qy  2056 TGGGACGCCGAAATCCGGTTGCCCGGGGTACGCATGGGTGTCCTCGTGGTAGACCTGACG 2115
         |||| ||| |||| ||||||||||||||||| | || ||| |||||||||||||||||||
Db  1981 TGGGCGCGCAAATCCGGTTTGCCCGGGGTTTGCATGGCGTGTCCTCGGGTCGACCTGACG 2040

Qy  2116 GGTTCATACACGTCCAGGGCACCTGCACGGAGGTGATGCGGCCAACTTCATCCCTCCTC 2175
         |||| ||| ||||||||| |||||||||||||||||||||| |||| ||||||||||
Db  2041 GGTTTATACACGTCCAGGGCCACTGCACGGAGGTGCGATGCGTCGATGCGTCATCCCTCCAC 2100

Qy  2176 CACCCTGGTTGCTCTTGGATTTTGTATTTGTCCTGCTCTATCTGATGAAGCTGGCTGAGG 2235
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Db  2101 CTCCGCTGGTTGCTCTTGGGACTTTGTGTTGTCCTCGTTATACCTGCTAGAAGCTGGCTGAGG 2160

Qy  2236 CACCGGTTGGTCCCGTGATCTTGGTGGTGGTGTGAACCAGTTGGGGTTC 2295
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Db  2161 CACGGCTGGTCCCGTGATCTTGGTGGTGGTGGTGAACCAGTTGGCAGTCC 2220

Qy  2296 TAGGACTGCCGGCTCTGGACGCTGCCGCTGGCTGGAGTTTTTGCGGGCCCTGCCTTGT 2355
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Db  2221 TTGGACTGCCGGGTGTGGACGCCGCCGTGGCTGGTGCTTCTTCGCGGGCCCTGTT 2280

Qy  2356 CATGTGTTTGGGCTTCAGCTGTCAGTGATATCTAGGTCTCAGACAAACCTGTGTTGT 2415
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Db  2281 CGTGTGTCTGGGCCTCCGTCCACCGTTAGTATGAATGATCCTGGGCTTAGCAAACCTGGTGTTGT 2340

Qy  2416 ACTTTCGGTGATGGCCCCTCATGTTCCTGCGTTGTGGAAGCTCGCTCGGG 2475
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Db  2341 ATTTCCGGTGGATGGCCCCAACGCCCTCATGTTCCTCGTTGTGGAAGCTCGCTCGGG 2400

Qy  2476 GAGCTTTCCCGCTGGCACTTTTGATGGGATTCGGCGACCCGGCCCACCTCTGTGC 2535
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Db  2401 GAGCCTTCCCGCTGCACTTTCGTGATGGGGGATCTCGACCGCCAACCCGCGGCGCCACCTGGGTGC 2460

Qy  2536 TCGGGGCCAGTTCTGCTTCGATGCGATCACATTGGGGCTGGGT 2595
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Db  2461 TCGGGGCCAGTTCTGCTTCGATGTGCATCACATTCGGACACGTCGGGTTTGGGCTGGGG 2520

Qy  2596 TGGTGCCAGCGTGTGGCTTGGCTTGGGCCATAAGCTCAATGAGCCAGGGGGT 2655
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Db  2521 TGGTGCCAGCGTGTGGTAGCCTGGGCCATTGCCGCATGAGCCGATGAGCGGAGGGGT 2580

Qy  2656 GGAAGCACAAAGGCCGTGATCTATAGGACGTGGTGTAAAGGTACCCAGCCAGA 2715
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Db  2581 GGAGGCACAAGGCCCGTGATCTATAGGACGTGGTGTAAGGGGTACCAGCCAAAC 2640

Qy  2716 GGGTGTGCGGAGCCCCCTCGGGGAGGGGCGCCCTACCAAGTTCGCCGTGGT 2775
         ||||||||||||| |||||||||| |||||||||||||| ||||||||| |
Db  2641 GGGTGTGCGGAGCCCCCTCGGGGAGGGGCGGCGCCACCAAACCCTTGACGTTCGCCGTGGT 2700

Qy  2776 GCTTGCCTCATACATCGGCCGGATGCTGTGATGATGGTGTCCTCC 2835
         ||||||||||||||| |||||||||||| |||||| || |||||
Db  2701 GCTTGCCTCATACATCGGCCGATGCTGATGATGGTGTGGTAGCCTTGGTCTCC 2760

Qy  2836 TCTTCGGCCTGTTCGACGCACTGGACTGGGCCCTGCGAGAGCTCCTGGTCTCCCGCCCT 2895
         |||||||||| || ||||||||||||||||||||||||||||||||||||||
Db      TCTTTCGGCCTGTTCGGAGCTCTTGGAGCTTGCCCTTGGTCTCCCGCCCCT
```

Nucleotide sequence alignment (Qy / Db rows with match bars). Left panel spans positions 2761–3975; right panel spans positions 3841–5055.

This page is a nucleotide sequence alignment (Query "Qy" vs Database "Db") printed in a rotated, densely packed layout. The alignment consists of paired rows labeled **Qy** and **Db** with flanking position numbers and match bars (|). Representative position markers visible include:

Left column (Qy/Db start–end positions):
5056, 4981, 5116, 5041, 5176, 5101, 5236, 5161, 5296, 5221, 5356, 5281, 5416, 5341, 5476, 5401, 5536, 5461, 5596, 5521, 5656, 5581, 5716, 5641, 5776, 5701, 5836, 5761, 5896, 5821, 5956, 5881, 6016, 5941, 6076, 6001 (with paired end positions 5115, 5040, 5175, 5100, 5235, 5160, 5295, 5220, 5355, 5280, 5415, 5340, 5475, 5400, 5535, 5460, 5595, 5520, 5655, 5580, 5715, 5640, 5775, 5700, 5835, 5760, 5895, 5820, 5955, 5880, 6015, 5940, 6075, 6135, 6060).

Right column (Qy/Db start–end positions):
6136, 6061, 6196, 6121, 6256, 6181, 6316, 6241, 6376, 6301, 6436, 6361, 6496, 6421, 6556, 6481, 6616, 6541, 6676, 6601, 6736, 6661, 6796, 6721, 6856, 6781, 6916, 6841, 6976, 6901, 7036, 6961, 7096, 7021, 7156, 7081, 7216 (with paired end positions 6195, 6120, 6255, 6180, 6315, 6240, 6375, 6300, 6435, 6360, 6495, 6420, 6555, 6480, 6615, 6540, 6675, 6600, 6735, 6660, 6795, 6720, 6855, 6780, 6915, 6840, 6975, 6900, 7035, 6960, 7095, 7020, 7155, 7080, 7215, 7140, 7275).

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     TTTCTTTTGGGGTGACCGGTGGCTGATGTGGCCAGTCTGTGTGAGATGGAGATCCAGAACC   7200
Qy 7276 ATACAGCCTATTGTGACAAGTGCGCACTCCGCTTGAATTGCAGGTTGGGTGCTTGGTGG   7335
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Db 7201 ATACAGCCTATTGTGACAAGTGCGCACTCCGCTTGAATTGCAAGTTGGGTGCTTGGTGG   7260
Qy 7336 GCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAGAGACCTTGGCTTCCT   7395
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Db 7261 GCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAGAGACCTTTGGCCTCCT   7320
Qy 7396 TCTCTTACATTTGGTCTGGGGTGCCACTGACAGAGGGCCACTCCGGCCCAGCCCCTGTGG   7455
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Db 7321 TCTCCTATATTTGGTCTGGGGTGCCATTGACTAGGGCCACACCGGCCTAAACCACCTGTGG   7380
Qy 7456 TGAGGCCGGTTGGCTCCTTGCTGGTGGCCGACCACCAAGGTGTATGTCACCAACCCGG   7515
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Db 7381 TGAGGCCGGTTGGCTCCTTGTTGGTGGCTGACCACCACGAAGTGTATGTCACAAACCCGG   7440
Qy 7516 ACAATGTTGGGGAAGAGTTGACAAGGTTACCTTCTGGCGTGCCCCTAGGGTTCATGACA   7575
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Db 7441 ACAATGTTGGGGAAGAGTGACAAGGTGACCTTCTGGCGCGCCCCCAGGGTCCATGACA   7500
Qy 7576 AATTCCTCGTGACTCCATAGAGCGCGCTCAAGAGGGCAGCTCAAGCCTGCCTAAGCATGG   7635
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Db 7501 AATATCTCGTGACTCCATCGAGCGTGCCAAGCGTCCAAGCTGCCAAAGCATGG   7560
Qy 7636 GTTACACTTATGAGGAGCCAATAAGGACTGTAAGGCCCATGTGGCCATGGGCTGGGGAT   7695
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Db 7561 GTTACACTTATGAGGAGCAATAAGGACTGTTAGGCCACATGCTGGCCATGGGCTGGGGAT   7620
Qy 7696 CTAAGGTGTCGGTCAAGGACCTTGCGCCACCCCTGCGGGAAGATGGCTGTCATGACCGGC   7755
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Db 7621 CTAAGGTGTCGGTCAAGGACCTTGGCCACCCCTGCGGGAAGATGGCCCTCCACGACCAC   7680
Qy 7756 TCCAGGAGATACTTGAAGGGACGGCCAGTCCCTTTACTCTTACTGTGAAAAAGGAAGTGT   7815
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Db 7681 TTCAGGAGATACTTGAGGGGACTGCCAGTCCCGGTCCCTTTACTCTTACTGTGAAAAAGGAGGTGT   7740
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Db 7741 TCTTCAAAGACCGAAAGGAAGGAGAGGAAGAAGGCCCCCCCCATCGTGTTGTTCCCCCCTGGACT   7800
Qy 7876 TCCGGATAGCTGAAAAGCTTATTCTGGGAGACCCTGGGACGGCTAGCCAAGGCGGTGTTGG   7935
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Db 7801 TCCGGATAGCTGAGAAAGCTTATTCTGGGAGACCCGGGGTGGCCAAGGCCGGTGTTGG   7860
Qy 7936 GGGGGGCCTACGCCTTCCAGTACACACCCCAAAATCAGCGGAATTAGGGAGATGCTCAAACTGT   7995
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Db 7861 GGGGGGCCTACGCCTTCCAGTACACCCCCAAAATCAGCGAGTTAAGGAGATGCTCAAACTGT   7920
Qy 7996 GGGAATCAAAGAAGACACCATGCGCCCACATGCTGTGGACGCCACATGCTTGCGACAGTAGCA   8055
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Db 7921 GGGAGTCAAAGAAACACCTTGCGCCCACATCGTGTGGACGCCACTTGCTTGCGACAGTAGCA   7980
Qy 8056 TAACTGAAGAGGACGTGCGCGCTGGGGAAATAACTATGCCTCTGCCACAATGGTAACCCCGAGGGGG   8115
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Db 8041 AGTGGGGTGCGAGCTTTGGGAGTACTTGGGAGGTATTGTAGAGCCGTATGGGGTCACCCCTGAGGGGG   8100
Qy 8176 TGCCAGTGGGTGAGAGGTATTGTAGATCCTCAGGGGGTCTTGACCACCAGTGCGAGCAACT   8235
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Db 8101 TTCCCGTAGGTGAGAGGTATTGTAGATCCTCAGGGCGTTTGACTACCAGCGCGAGTAACT   8160
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Db 8161 GCCTGACCTGCTACATCAAGGTGAAACGCCGCTTGTGGGGGCTGAAAAATGTCT   8220
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Db 8221 CGCTTCTCATAGCCGGCGGATGACTGTTTGATCATATGCGAACGGCCAGTGTGCGACCCTT   8280
Qy 8356 GCGACGCTTTGGGCAGAGAGCCCTGCCGAGCTACGGGTACGGCATGGACGCATGCATGCTTCGTATCATG   8415
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Db 8281 GTGACGCCCTGGGCAGAGCCCTGGCAGTATGGCTTGCGAGGCCTTGCGCCATCCATCA   8340
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Db 8341 CATCACTGGACACGGCGCCCCCCCTTCTGCTCCACTTGGCTCCACTTGGCCAACGCAGATGGGA   8400
Qy 8476 AACGCCATTTCTTCCTGACCACGGACTTCGGAGGCCCCCTCGGCTCGCATGTCGAGCGAGT   8535
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Db 8461 ATAGTGACCCAATGCTTCGGCCATCTCCTCGTATCCCTGTCGGCATCCCATCA   8520
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Qy 8656 CTGATCCTGTGTGTTGCCAGTACAGTAATTACTACAAGTTTCCACTGGACAAACTGC   8715
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Qy 8776 AGACAAAAATGGAGGCTGGCAAGGTGCTGAGCGACCTCAAGCTCCCCTAGGCTAGCAGTCC   8835
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Db 8761 ACCGGAAAGAAGGCCCGGAGCACTGCGGAACACGCATGCTTCGGTCGGCGGTTGGGCCGAGT   8820
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Qy 8956 TCCCCGGGGTTTCCCCCTTTCATCAATGGGGTTGTTCATCAATTGGATTTCA   9015
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Db 8881 TCCCCGGGGTTTCCCCCTCTCCCCCCCCCTACAATGGGGTGCATCAATTGGATTTTA   8940
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Qy 9076 TCGGGTGAACTAAATTCATCTGTGCGGCAAGGTCCGGTGACTGATCATCACTGGAGGAG   9135
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Db 9001 TCGGGTGAACTAAATTCATCTGTGCGGCAAGGTCCAGTGACTGACTGATCATCACTGGAGGAG   9060
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RESULT 14

US-08-444-733-182

; Sequence 182, Application US/08444733

; Patent No. 5824507

; GENERAL INFORMATION:

;   APPLICANT: Kim, Jungsuh P.

;   APPLICANT: Wages, John

;   APPLICANT: Young, LaVonne M.

;   APPLICANT: Fry, Kirk E.

;   TITLE OF INVENTION: Linnen, Jeffrey M.

;   TITLE OF INVENTION: Hepatitis G Virus and Molecular

;   Cloning Thereof

;   NUMBER OF SEQUENCES: 277

;   CORRSPONDENCE ADDRESS:

```
;     ADDRESSEE:  Dehlinger & Associates
;     STREET:  350 Cambridge Ave., Suite 250
;     CITY:  Palo Alto
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  94306
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/444,733
;     FILING DATE:
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/389,886
;     FILING DATE:  15-FEB-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/357,509
;     FILING DATE:  16-DEC-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/329,729
;     FILING DATE:  26-OCT-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/344,271
;     FILING DATE:  23-NOV-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/285,558
;     FILING DATE:  03-AUG-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/285,543
;     FILING DATE:  03-AUG-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/246,985
;     FILING DATE:  20-MAY-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Fabian, Gary R.
;     REGISTRATION NUMBER:  33,875
;     REFERENCE/DOCKET NUMBER:  4600-0201.36/G100P11
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 324-0880
;     TELEFAX:  (415) 324-0960
; INFORMATION FOR SEQ ID NO: 182:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  9103 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  both
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
;   ORIGINAL SOURCE:
;     INDIVIDUAL ISOLATE:  HGV-JC Variant
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  276..9005
US-08-444-733-182

Query Match         82.6%;  Score 7760.6;  DB 1;  Length 9103;
Best Local Similarity   90.8%;                  Pred. No. 0;
Matches  8264;  Conservative    0;  Mismatches  839;  Indels    0;  Gaps    0;
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Qy   76 CAATGACTCGTCGTAAATCCCGGTCATCCTGGTAGCCACTATAGGTGGTCGTTGACAGGGT  135
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Db    1 CAATGACTCGGCCGCCGACTCGGCGACCGGCCAAAAGGTGGTGATGACAGGGT   60

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Qy  196 CAAGACTCCTCTTGTGCCTGCGGCGGAGACCCGCACGGTCCACAGGTGCTGGCCCTACCG  255
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Qy  256 GTGTGAATAAGGGCCGACGTCAGGCTGCGTCGTTAAACGAGCCCGTCACCCACCTGGGC  315
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Qy  496 GGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGCATTTCTCTTTCTATACCATCA  555
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Db  541 ACGCTTGTCGAGCGAATGGGCAATAATATTCCTCACAAACTGTGTGCTCCAGGACATTG  600

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Qy 1216 GGCAGTCATGCTCCTGCAGGGCTAACCGGTCGCGTATTCCACTGGGCGGAGAGGGTGTGGG  1275
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Db 1141 GGCAGTCTTGTCCGTTCCTGCGCAGGGCTAACTGGGTCGCGCTATACTACGGGGAGAAGGTGTGGG  1200

Qy 1276 ATCGAGGGAATGTCACGCTCTTTGTGTGACTGACCCAACGGCCCCTGGGTTTGGTTGCCCGG  1335
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Db 1201 ACCGTGGAAGTCACGCTCGGTGTGACTGACCCAACGGCCCCTGGGGTTGCCCG  1260
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Qy   1336 CCTTTTGCCAGGCGGTTGGGTGGGGCGACCCCATCACCCATTGGAGCGACCACGGACAAAACC 1395
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Qy   1936 CCGGAGTCCCCGCCATTAACAACTGCATGCATGCGTCCTAGGGGGGTTCTGCAGAGCCTC 1995
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Qy   1996 GCGGAGCTGGGCTTACGGGGGTTCTCGCAGAGCCTCTGGTTCCTCAGGGTGTTCCGAGCTGA 2055
          |||| |||| |||| | ||| |||||  ||||| || |||||||| ||| ||||||||||||
Db   1921 GCGGGGCCGCGGGGCTGTTCCTGGTCACGGCCGGTTCGGAGCTGA 1980

Qy   2056 TGGGACGCCGGAAATCCGGTTTGCCCCGGGGTACGCGTCCTCTGGTAGACCTGACG 2115
          ||||||| ||||||||||| |||||| || | || || ||||||||||  ||||||
Db   1981 TGGGGCCGCGGAAATCCGGTTTGCCCCGGGTTCATGGCTGCTCCTCGGTCAGCCTGACG 2040

Qy   2116 GGTTCATACACGTCCAGGGGCACCTGGCGGGCCAACTTCATCCCCTCCTC 2175
          || || | ||||||||||| ||||||||||||||||||| |||||| | |
Db   2041 GGTTTATACACGTCCAGGGGGCACCATGCCGATGCCAACTTCATCCCCTCCAC 2100

Qy   2176 CACGGTTGCTTGCTCTTGGATTTGTATTTGTCCTATCTGATCGAAGCTGGCTCAGG 2235
          ||||| || | |||| || || |||| || ||| || ||| || |||| ||||||
Db   2101 CTCGGCTTGCTTGCTCTTGGACTTTGTGTTTGTCCTGTTGTTATACCGGTCGGCTGAGG 2160

Qy   2236 CACGGTTGGTTGTCCGGTTGATCTTGCTTGTCTCTGCCGCGTCGGTGGTTGGCCGTTC 2295
          ||||  || |||||| || ||||| ||||| ||||| || |||  || |||| || ||
Db   2161 CACGGCTGGTTGTCCGGTTGATCTTGCTTGTCTCTGCCGCGTCGGTGGTTGGCCGTTC 2220

Qy   2296 TAGGACTGCCGTGAGCCTGTGGCGTCCTGGAAGTTTTGGGGTGCTTGCCTTGT 2355
          | |||| || || ||| |||||||| ||||| |||| | |||||||| ||||
Db   2221 TTTGGACTGCCGTGACCTGTGGCGTCTTGGGGGGTGCCAGTCCTGCCCTGT 2280

Qy   2356 CATGGTTGTTTGGGTTCTCGGCGCGTTCGGCGTATGATCCGTTAGTATGCAGTTGGTGTTGT 2415
          | |||| || | ||| || |||||| | ||| | |||||||| || || | | |||| |||
Db   2281 CGTGGTTGTCTTGGGGTCTCGGCGCGTTCGGCTGTCAGTATGATCCGTTAGTATGCAGTTGGTGTTGT 2340
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Qy   2416 ACTTTCGGTGGATGGGCCCTCAGCGTCCTCGTGTTGTGGAAGCTCGCTCGGG 2475
          | |||||||| | ||||||| || |||| |||||||||||||||||||||||
Db   2341 ATTTCCGGTGGATGGGCCCCCAACGTCCTCGTGTGTGGAAGCTCGCTCGGG 2400

Qy   2476 GAGCTTTCCCGCTGGCACTTTGATGGGGATTTCGGCGACCCCGGGCCGGCCACCTCTGTGC 2535
          ||| || || || ||||| || | |||||||||| |||| ||||||||||||||||  |||
Db   2401 GAGCCTTCCCGCTGCACTTCTCGTGATGGGGATCTCGGCGACTCGGCAACCGGGGCGCACCTCGGTGC 2460

Qy   2536 TCGGGGCCCAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCGGTTGTTGGGCTGGG 2595
          ||||||| |||||||||||||| || ||||||||| |||||| ||||||| ||||||||||
Db   2461 TCGGGGCCGAGTTCTGCTTCGATGTCACATTCGAGGTGGACACGTCGGTTTTGGGCTGGG 2520

Qy   2596 TGGTGGCCAGCGTGTGGCCGTTGGGCCTGGTTCCTGAGCTCGCGCTCCTGAGCGCAGGGGGT 2655
          || ||||||| ||||||||| || || || || || ||| ||||| || || ||||||  ||
Db   2521 TGGTGGCCAGCGTGTGGCCGTTGGGCCTGGTTCCTGAGCTCGCGCTCCTGAGCGCCGGGGAGGGT 2580

Qy   2656 GGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCAGGCTGTGCCGCCAGA 2715
          ||| ||||||||| || |||| |||||||||||| ||| |||||| |||| || ||||| |
Db   2581 GGAGGCACAAGGCCGTGATCTATAGGACGGTGGTGTAAGGGGTACCAATACGCCCAAC 2640

Qy   2716 GGGTGGTGCGGAGCCCCTCCGGGGAGGGGCGTCTCCTACCAAGCTTCTGACGTTCCGCCTGT 2775
          |||| |||||||||||||||||| ||||| |||||||||||||||| | |||| || || ||
Db   2641 GGGTGGTGCGGAGCCCCTCCGGGGAGGGGCGTCTCCCGCCACCAAACCCTTGACGTTGCTTGGT 2700

Qy   2776 GCTTGGCCCTCATACATCTGCCCGATGCTGTGATGATGCTGAGGGCCTGTTGACCACATGGGCT 2835
          |||||||| |||| |||||||||||||| | ||||||||||||| ||| |||||||| ||||
Db   2701 GCTTGGCCCTCATACATCTGCCCGATGCTGTGATGATGGTGGTCCTTGGTGTCTCC 2760

Qy   2836 TCTTCGGCCTGTTCGACGCCACTGGACTGGGCTCTCCGGGAGGAGCGGCTCCTGGTTCTCCCGGCCCT 2895
          || || |||| ||||||| ||||| || |||||| ||| |||| |||| | |||| || ||||||| |
Db   2761 TCTTTGGCCTGTTCGACGCCGTTGGACTGGGCTTTGGGTGTCTCCGGCCCT 2820

Qy   2896 CGTTACGGCGACTGGCACGGGCGTGTGAGCGTGTGATGGCGGAGAAGGCCACCA 2955
          ||||| ||||| || | ||| || |||  || || |||| ||||||||||||||
Db   2821 CGTTACGGCGTCTGGCACGGGCGTGTGAGTGTGTGATGGCGGAGAAGGCCCACA 2880

Qy   2956 CCATCCGACTGGTCTCCAAGAGTGCGCAAGAGGGGCCTACCCGTTGACCACATGGGCT 3015
          || || ||||| || |||||| ||||||| || ||  || |||  | |||| |||| |
Db   2881 CCGTCCCGCTGGTCTCCAAGAGTGCGCAAGAGGGGCCTATTTGTTGTTGACCATATGGGCT 2940

Qy   3016 CTTTCTCGCGCGTCAAGGACGCCGGCTTGTTCAAGGACGCGGGCTTTGGAGCCCTTGT 3075
          ||||| | |||||| || || |||| | |||||| || ||||  |||||||||| | |
Db   2941 CTTTTTCGCGGCGGTCAAGGACGCTCACTAAGGCTGTCACTAAGGCCTTTTGGAACCCCGT 3000

Qy   3076 CATTCACTAGGACGGACTGTCGCATCATCATCAGAGATGCCCGGAGGAGCCCGTCCTGCGGAC 3135
          ||||||||||||| |||||| || ||||||| || ||||||||||||||| | || || |||
Db   3001 CATTCACTAGGACGGACTGTCGCATCAGTCATTAGATGCTCGGGCGCCCCGTCGGCCTGCGGACT 3060

Qy   3136 AGTGCGTCATGGGTTTACCCGTGATGAGGTTCTCATCGCGCGTCT 3195
          |||||||| |  ||||| || ||| ||||||| |||| |  ||||
Db   3061 AGTGCGTCATGGGTTTACCCGTGGTGAGGTTCTCATCGCGCGTGTCT 3120

Qy   3196 TTCAGGATGTGAATCATTTGCCTCCCGGGGTTGCCTCCCGGCAACTTCATCCCGTC 3255
          |||||| |||| |  || || || ||| || |||||||| |||||||| |||||||
Db   3121 TTCAGGATGTGAACCATTTGCCTCCCGGGGTTGCCTCCCGGCAACTTCATCCCCAC 3180

Qy   3256 GGTGCGGAAAGGCTTCCTGGGGGTCACGGAGCCAGCCTTGACAGGTAGGAGGCTGACT 3315
          |||| ||||||||||||| | ||||||||| | |  || |||| ||||| |||||||
Db   3181 GGTGCGGAAAGGGGTTCTGGGGGTCACTAAGGTCAGCTCGGATCGGCTGACT 3240

Qy   3316 TACATCCAGGGAACGTCATGGTTGTTGGGGACGGCTACGTCACGAAGCATGGCACATGTC 3375
          || |||||||| |||| ||||||| |||||||| || || ||||| ||||||| || ||
Db   3241 TACATCCAGGGAACGTCATGGTTGTTGGGGACGGCTACGTCGCGAAGCATGGGGACATGCC 3300

Qy   3376 TGAATGGCCTGCTTCACAACTTTCCATGGGCTTCATCCGGAACCGATCGCCACGACGCCCCG 3435
          | ||||||| | || |||| |||| ||||| ||||||| || |  || | |||||  ||||
Db   3301 TGAACGGCCTGCTTCACGACTTTCCATGGGCTTCATCCGGAACCATCCGGACAACCATCGCCACGACGCCCCG 3360

Qy   3436 TGGGGGCCCTTAATCCCAGGGTACCCGCCTTC 3495
          ||||| |||| || ||||| || |||||| ||
Db   3361 TGGGGGCCCTTAATCCCAGGGTACCCGCCTCC 3420

Qy   3496 CAGATGGGGCAACTTCGTTGCACCGCCCTGCCACTGGCGGGAGTCCTCGTTGGGTTATTA 3555
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Left column:

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         |  |||||||||||| |||||||||||||||||||||||||||| ||||| ||
Db 3421  CGGATGGGGCAACCTCGTTGACGCCCTGCCAGCCGCTGAGTCCGTTGGGTCATAC        3480

Qy 3556  GATCCGACGGGGCTTTGTTGCCCATGGCTTGAGCAAGGGGACAAGGTTGAGCTTGGATGTGG  3615
         |||| ||||||||| |||||||||||||||||| ||||| |||||| ||| ||||| |||||||
Db 3481  GGTCCGACGGGGCTTTGTTGCCCATGGCTTGAGTAAGGAGACAAGGTGGAGCTGTAGGATGTGG 3540

Qy 3616  CCATGGAGGTCTTGACTTCCGGTTCGTTCACGGTCTTGTTCACCGGTTCTTTTGCGACAAAGGGC  3675
         |||||||| |||| ||||||| |||||||||||| ||||||||| ||||||| ||||||||||||
Db 3541  CCATGGAGGTCTCAGATTTCCGGTCGTCGCCGCTCACCGTCTCACCGGTCACCGTGTCGACGAGGGC 3600

Qy 3676  ACGCAGTAAGAATGCTCGTGTCAGTGCTCCACTCTGGCGGCAGGGTTACTGCGGCGCGAT  3735
         |||||| ||||| ||||||||||||||||||||||||||| ||||| ||||||||||| ||
Db 3601  ACGCAGTAGGAATGCTCGTGTCGGCTGCTCCACTCGGGTGGTCGGCTCCACCGCGCTCGAT 3660

Qy 3736  TCACTAGGCCGTGACTCAAGTACCAACAGATGCCAAGACCACCACAGACACCCCTCCGG  3795
         |||||||||||||| | |||||| |||| ||||| || ||||||| |||||||||||||
Db 3661  TCACCAGGCCGTGACCCGGGTTCCCAACAGATGCTAAGACCACCACACTGAACCCCTCCGG 3720

Qy 3796  TGCCGGCAAAAGGAGTTTTCAAGGAGGCCCCGTTTTATGCCTACGGGCGGCGGAAAGA  3855
         |||||||||| ||||||||||||||||||| |||||||||||||| ||||||| |||||||
Db 3721  TGCCGGCAAAAGGAGTTTTCAAGGAGGAGCCCCACTTTATGCCCACCGGGCGGCAGGAAAGA 3780

Qy 3856  GCACCCGGCCTACCGGTGGAGTACGGCAACATGGGCCCACAAGGTCTTGATCTTGAACCCGT  3915
         |||||| | ||||||||||||||||||||||||| ||||| ||| ||| |||||||| |||
Db 3781  GCACGCGGCCTCCCCGTTGGAGTATGGCAACATGGGGCACAAGGTCCTGATTTTGAACCCCT 3840

Qy 3916  CGGTAGCTACCGTGAGGGCCATGGCCCATACATGGAGCGGCTGCGGGTGCGGGAAACACCCCA  3975
         |||||||| |||||||||||| |||||||||||||| |||||||||||||||||||||||||||
Db 3841  CGGTTACTGTGAGGGCCAGTGGCCCATGGCCCCTTTACATGGAGCGGCTGCGGGTGCGGGAAAACATCCAA 3900

Qy 3976  GTATTACTTGTGGCCATGACACCACTGCTTTCACAAGGATCACTGACTCGCCCCTTACGT  4035
         ||| ||||| | |||| |||| ||||| | ||||||||||||||||||||||| ||||||||
Db 3901  GTATTCACTGTGGCCATGACACCACTGCTTCACAAGGATCACTGACTCGCCCCTTAACGT 3960

Qy 4036  ATTCCACTTACGGAAGGTTTTGCCCAACCCTAGGCAGATGCTGAGGGTGTGTCGGGTGG  4095
         | || ||||| ||||| ||||||||||||||||||| ||||| ||||||||||| |||||
Db 3961  ACTTCACCTATGGGAGGGTTTCTGCCAACCCTAGGCAGATGCTGCGAGATGGGTGTGTCGGGTGG 4020

Qy 4096  TCATTTGTGACGAGTGCCACCAGTCATGACTCAACTGTGTTGGGCCATTGGGGCCGTGTCA  4155
         |||| | |||| |||| |||||||||| |||||||| || |||||||| || |||
Db 4021  TCATTTGCCGATGAATGCCATACCCCAGTCATGACTCAACTGTCCCACTGTGTTGGGACGGGGTCC 4080

Qy 4156  GGGAGCTGGCGCGGAGGATGTGGGCGTGCAGGTGCAGTTTCTACGGCCACTGCCACCCCCG  4215
         |||||||||| ||||||||||||||||||||||| || | ||||||||||||||||||||
Db 4081  GGGAGCTGGCGCACGAGTGTGGGCGTGCAGGTGCAGTTGTCTCTCACGGCCACTGCCACCGCCTG 4140

Qy 4216  GATCCCGATGACCCAGCCAGCACCCATCAATCATTGGACGTGGGAGAGATCC  4275
         | |||| ||||||||||||| |||| |||| ||||| ||||||| || |||
Db 4141  GGTCCCCATGACTCAGCACTGTCAATCACTCATTGGGACCAAATTGGATGTGGGTGAGATTC 4200

Qy 4276  CCTTCTATGGGCATGGCCACTATCCTCTTGAGCGGATGCGGACGTCCGGAAGGCATCTCGTATTCT  4335
         |||| ||||| |||||||||||||||||| ||||||| |||||||||||||||||||||||||
Db 4201  CCTTCTATGGGCATGGCCATAGCCCTCGAGCGGATGCGGACGTCCGGAGGCATCTCGTATTCT 4260

Qy 4336  GGCCACTCCCAAGGCTGAGTGCCGACGCCGCTTGGCGGCGCTGGCGCCAGTTTTCGGCTAGGGGGTAAATG 4395
         || ||||| ||| ||| |||||||| ||||||| ||||||| ||||| |||
Db 4261  GCTACTCTAAGGCAGAGTCGAGCGGCGTCGCCGAGGTCCAGTGCGCTCAGTTTCTGCTAGGGGGTTAACG 4320

Qy 4396  CCATCGCCTATTACGCACTCCACTGGGAAAGATGATCATCAAAGATGGAGACCTTGGTGTGT  4455
         | ||||| |||| || ||| |||||||||| ||| | ||| |||| ||||||||||||||||
Db 4321  CCATAGCCTATTACGCCACCGCCACTGGGAAAGATCAGGACCCAGATCTGGTGGTGT 4380

Qy 4456  GTGCTACAGACGCACTACTCCACTGGTACTTCGATTCTGTCACCGATTGTG  4515
         || | | | ||||| || |||||||||||||| |||||| ||||||||||||
Db 4381  GCCGGACCACCGCCTATCCCGTGATACCCTCGAGTTCTGATCCACCGACTGTG 4440

Qy 4516  GGTTAGTGGTGGAGGAGGTCGTCGAGGTTGACCCTGACCCTTTGACTCCACCATCTCCCGC  4575
         || |||||||||| ||||| |||||||||| |||||||||||| |||| ||||||||
Db 4441  GGTTAGTGGTGGAGGAGGTCGTCGAGGTCAGGTCGAGGTCACCCTTGATCCCACCATTACCCCCTGC 4500

Qy 4576  GCACGGTGCTGCCCGGGCTGCGAACTGTCGATGCAGAGACGCGCGAGGGCACCGGGTAGGGGCA  4635
         || | ||||||||||||||||||
Db 4576  ACGCTCAGAGCTTCGGCGTTTTTGGCGTGGCGTGTTGGGCGGTGGCGGGACCCGCTTGGGGCA    (continued right)
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Right column:

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Db 4501  GGACAGTGCCGCGTCGGCAGAACTGTCGATGCAGAGACGAGGACGCACGGGTAGGAGGCA  4560
Qy 4636  GGTCTGGGCGGCCTACTACTACGCGGGGTCGGCAAGGCCCCTGCTCGTGTGTGCCTCAG   4695
         ||||| |||||||||||||||||||||||||| || ||||| || |||||| ||||||
Db 4561  GGTCTGGGCGGCCTACTACTACGCGGGGTCGGCGAAAGCCCCGGGTGTGCGCCTCCGG   4620

Qy 4696  GTCCTGTCTTGGTCGGCGGTGGAAGCCGGTGAACCTGGTACGGAATGGAACCTGACCTGA  4755
         |||||||||||||||||||||||| |||| ||| ||||| |||||||||||||||| |||||
Db 4621  GTCCTGTCTTGGTCGGCGGTGGAGGCGGGTGAGCAGGTGATGGAATGGAACCTGACTTGA  4680

Qy 4756  CAGCAAACCTACTGAGACTTTACGACAACTGCCCTTACACCGCAGCCGTCGCAGCTGACA  4815
         |||| ||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Db 4681  CAGCTAACCTATTGAGACTTTACGACGACTGCCCTTACACCGCAGCCGTCGCAGCTGACA  4740

Qy 4816  TTGGGGAAGCCGCGGTGTCTTCTTTTCGGCGGTCGCCCGTTGCCCGTTGAGGATGCATCC  4875
         | |||||||||||||| | || | ||| ||||||| ||||||||||||||||||||||
Db 4741  TCGGTGAAGCCGCGGTGTTTTTTCTCCGGGCGTCAACTGCCCGTTGAGGATGCATCC    4800

Qy 4876  GCTGGGCAAAAGTTCGCGGCGTCAACTGCCCTTCGTGGTGTGTTCAGCGGACCATGT    4935
         ||||||||||||| |||||||||||||||||||| |||||||||||||||| |||||||
Db 4801  GCTGGGCAAAAGTGCGCGGCGTCAACTGGCCCTCGTTGGTGGTTCAGCGGACCATGT    4860

Qy 4936  GCCGGAAACACTGTCTCCCGGCCATCGATGACCCCAGTGGGCAGGTCTGAAGGGCC    4995
         ||||||||||||| ||||||||||||||||| |||||||| ||||||||||||||||
Db 4861  GCCGGGAAACACTGTCTCCCGGACCATCGACGACCCCAATGGGCAGGTCTGAAGGGCC    4920

Qy 4996  CGAATCCTGTCCCCACCTCCTGCTGAGGTGGGCAATGATTTACCATCTAAAGTGGCCGGCC  5055
         |||| || ||| |||||||||||| |||||||||||||| ||||||||| ||||||||||
Db 4921  CGAATCCTGTTCCACTACTGCTGAGGTGGGCAATGATTTACCATCAAAAGTGGCCGGCC  4980

Qy 5056  ATCACATCGTGGACGACCTGCGTCCTAGGCTCGGGGGTTACGTCCGCTGCG    5115
         ||| ||| ||||||||||||||| |||||||||| ||||||| |||||||||
Db 4981  ACCACCATTGTGACGACCTGGTCGTCCTAGGCTGGGGAGGGTTATGTCCGCGCG    5040

Qy 5116  ATGGGGGACCCATCTTGATGGTGGGCCTTAATGCTGGGGGGATGATCTATTGCGTCAT    5175
         ||||||||||||||||||| | ||||||||||||||| ||||| |||||||||||||||
Db 5041  ATGGGGGACCCGATCTTTAATGCTCGGCCTCCGTATCCGGGGGATGATCTACACGCCATCTT  5100

Qy 5176  ACACCGGGCTCTCGTGGTTACGACTGGGATGGCATTGGGCGTGTCA    5235
         ||||||||||||||||| |||||||||| |||||||| |||||||||
Db 5101  ACACCGGGCTTTAGTGGGTGGTTGACAGACTGGGATGGCATTGGGCAGCCCTCTT    5160

Qy 5236  ATCGGCATGGAGACCCAGGCCACGCCCCCAGCCGGTTCGTGCAGTCCCCGTAGACCATC  5295
         ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db 5161  ATCGGCATGGAGACCCAGGCCACGCCCCCACAGCCGGTTGTGCAGTCCCCGTAGACCATC  5220

Qy 5296  GGCCGGGGGGGAGAGTCTGCCGCCATCGATGCCAACACAGTGCCGGCCGGCCA    5355
         ||||| ||||||||||||||||| ||||||| || ||||||||||||||||||||
Db 5221  GGCCGGGGGGGAGAGTCTGCCGCCTCCGATGCACAGTGCCAAGACAGTGCCGGCCGGCCA  5280

Qy 5356  TCCAGGTGGATTGCCGATTGCCAGTCAGTCATCAGCACCGTCGATCGGGAAGTGCTGTCCTTGG  5415
         |||||||||| ||||||| |||| | |||||||||||||||||| ||| | ||| |||||
Db 5281  TCCAGGTGGATTGCCGATTGCCAGTCAGTCATGACCCGTCGATCGGGAAGTGCTGTCCTTGG   5340

Qy 5416  CCCAGGCTAAGACGGCGCCGGCCGGCCTTGCTGCCAGCTACCACCAGCTGGCTTGCTGGCTGCTCTACA  5475
         | |||||| || | |||||||||| ||||||||||||||||||| ||| ||||||||||||||||||
Db 5341  CTCAGGCTAAAACAGCTGAGGCCGGCCGTTCCTCCTACTCGATGGCTGGCTGCTCGCGTGGCTGCTACA  5400

Qy 5476  CGGGGACGGCGGGCCGTCCGCCACTGTTCAATTGTTGACAAGCTCTTCGCCCGGGGTGGG  5535
         || |||||||||||||||||||||| | |||||| |||| |||||| |||||||||||||
Db 5401  CGGGGACGGCGGGCCGTCCGCCACTGTTTCAATTGTTCACAAGCTCTTTGCCCGGAGGTGGG  5460

Qy 5536  CGGCCGGTGGTAGGCCATTGCCACACTGTAATAGCTGCGGCGGCTATGGGGCTT    5595
         || |||||| || |||| ||||||||||| || |||| ||||||||| |||||||
Db 5461  CGGCTGTGGTTGGTGCCACTGTTCACAGCGTCATAGCTGCGGCGGTGCCTACGGGGCTT  5520

Qy 5596  CTAGGAGCCCTCCATTGGCTGCCGCCTTCCATTGGGTTGCTTGGGCGTCGGAGGCA    5655
         | ||||| ||| ||| ||||||||||||| ||||||||| ||| |||||||||||||
Db 5521  CCAGGAGTCCTGGGACTGGCTGGCGCGCCGCCTCCTGCTGATGGGACTGGGCGTCGGAGGCA  5580

Qy 5656  ACGCGCAAACCCGCTTAGCCTCCGCTCGCCGCGAGACGCGCCGAGGGTCTGGGCA    5715
         || |||||| ||| || |||| |||||||||||||| |||||||||||||
Db 5581  ACGCTCAGAGCTTGGCGTCTGCCCGCTTGTTGGGCGCTGGCACCGCCCTGGGCA   5640
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Qy  5716 CGCCTGTCTGTGGGTTAACCATGGCGGCGCCGTTCATGGGAAGTGCTAGCGTCTCCCCCT 5775
         ||||| |||| ||||||||||||||||||  || |||||||||||| |||||||||||| |
Db  5641 CTCCCGTCGTGGGTTAACCATGGCGGGGGCCGGTTCATGGGAAGGGCTAGCGTCTCCCCT 5700

Qy  5776 CCTTGGTCACCATTTTACTTGGTGGGGGCCGTGGGGGCGTGGATGGCTGGAATCGGCTA 5835
         |||||||||| ||||| || ||| ||| ||||||||||| ||||||||||||||||||||
Db  5701 CCTTGGTCACCATTCTTGCTGGGGGGCCGTGGGGGCGTGGATGGCTGGAATCGGCTA 5760

Qy  5836 GCCTTGTCTTCGACTTTATGGCGGGAAACTATCATCAGAGATCGTGTATGCCATCC 5895
         ||||||||| |||| |||||||||||||||||||||||||||||||| ||||||||
Db  5761 GCCTTGTCTTTGACTTCATGGCGGGAAACTATCGTCAGAGATCTGTGGTACGCCATCC 5820

Qy  5896 CAGTGCTAACCAGTCCGGGGATCGCCTTGCGGGGATCGCCCTTGGGTTGGTGTTGTTACT 5955
         |||||||||||||||||||||||||||| |||| ||||||||||||||||||| |  |||
Db  5821 CAGTGCTCACCAGCCCGGGGATCGCCCTTGGGTTGGTGCTGTTACT 5880

Qy  5956 CAGCTAACAACTCTGGCACTACCACTTGGTTGAACCGTCTGCTGACTACAATTGCCAAGGT 6015
         |||||||||||||||| ||||||||||||||||||||| ||||||||||||  | |||||
Db  5881 CAGCTAACAACTCTGGTACTACCACTTGGTTGAACCGTCTGCTGACTACGGTTACCTAGGT 5940

Qy  6016 CCTCATGCATCCCTGACAGTTACTTTCAGCAGGCCGATTACTGTGACAAGGTCTCAGCTG 6075
         ||  || |||||||||| ||||  || || |||||||||||||||||||||||||||| ||
Db  5941 CTTCTGCATCCCTGACAGTTACTTTCCAACAGGCCGATTACTGTGACAAGGTCTCGGCCG 6000

Qy  6076 TGCTTCCGACGCTTGAGCCTTGTCCACTCGCACCGTGCCTCGGTTGCCCTGGTCAACAGG 6135
         ||| |||| | | || ||||||||||||||||||| ||| | |||| | ||| |||||||
Db  6001 TGCTTCGCACTGACTGAGCCCTCCACTCGTGGTCGCCCACTGTGGTCAATAGGGAACCCAAGG 6060

Qy  6136 TGGATGAGGTTCAGGTGGGGTACCTGTGGGACTTCGGGCCCTCTCCCCGTGTGTTCAGCTGC 6195
         |||||||||||||||||||||||||| || ||||||||||||||| |||||||||||||| ||
Db  6061 TGGACGAGGTACAGGTGGGGTACGTGTCTGGGGATCTCTGGGACCTGTCTCCGGGATCTCAAGTGC 6120

Qy  6196 GCATCGTGATGGCCAGACTTCGGGCCCTCTCGGCCCCTGTGTCATTACCCTTATGGCACT 6255
         ||||| |||||| |||||| |||| ||| | ||| | |||||||||||||  | ||||||
Db  6121 GCATGGTCATGGCCAGGCCAGGCCTCGCCCCGTGTCACTGCCTTTTGTGGCACT 6180

Qy  6256 GCGGGGAGGGGTGGTCCGGAGAATGGTTGTTGGACGGCCATGTTGAGAGTCGTTGTCTTT 6315
         |||||||||||| ||||||| || ||||||| ||||| |||| |||||||||| |||| |
Db  6181 GCGGGGAGGGGTGGTCCGGAGAGTGGTTGTTGGACGGCCATGTTGGACGGCCGTGTCTTT 6240

Qy  6316 GTGGTTGCGTGATCACCGGCGATGTTTTGAATGGGCAACTCAAAGATCCAGTTACTCTA 6375
         | | ||||| |||||||| |||||| ||| |||| |||||| ||||| ||||| | ||||
Db  6241 GCGCGGTGCCGTGATCACCCGCGATGTTTTCAATGGGCAACTCAAAGAGCCAGTTCACCTA 6300

Qy  6376 CCAAGCTGTGCCCTTTGCTGCCCTCAGACACCCCGAAGGTGGTACCATTCGGGACGTCTGGGT 6435
         | |  || |||| ||| ||||| || |||||| |||||||||  |||| |||||||| | |
Db  6301 CAAAGTGTGCCGCCGTTCCTGTGAACATGGCAACTCAAAGAGCCAGTTCACCTA 6360

Qy  6436 AGACGTCGCCTTTGCTGCGCCTCTTGCGTCAGAAGGTGGTGACCCCACGTTGGTACCGCCT 6495
         |||| | || |||   ||  || |||| |||||| |||| |||||||  | |||||| ||
Db  6361 CAAAGTTGTGCCGCACCCCTCTGCGACCCCCGAAGCGTGGTGGTGGACGTCGGGGCT 6420

Qy  6496 GGGCTGAGGGTGGTGGTGACCCCTACCCACGTTGTGATCAGGCGAACATCCGCCTACAAAC 6555
         |||||||||||||||||||| |||  |||| | ||||||||  |||| || |   ||||
Db  6421 GGGCTGAGGGTGGTGGTGACCCCTACCCACGTTGTGATCAGGCGAACAACCTCTCCCCTACGAGT 6480

Qy  6556 TGCTCGCGCAGCAAATCCTGTCGCTGTTGCGCCTATTACGCTCGACGGCATAC 6615
         ||||||||||||||  |||| |||| ||||  | ||||||||||||||||||
Db  6481 TGCTGCGCCAACAAATCCTATCAGCTGCTGTTTATGTCGACGGCATAC 6540

Qy  6616 CGGTCTCATGGACGCGGACGCGGCAGCGCCTCATGGTCTCTATGGCCCTGGGCAAAGTG 6675
         ||||||||||||| ||||| |||| |||||| || ||  ||  ||| |||| |||||||
Db  6541 CGGTCTCATGGACGCGGACGCGGCTCGTGCGCCTGCCATGCGGCTCAGGAGGCTGGGCAAAGTG 6600

Qy  6676 TCACCATTGACGACGGGAACGCTACCACCTACCCTTCCGGCTTAGGAATGTGGGCGC 6735
         |||||||||||||||||||| ||||||||||  ||| ||||||| ||| || |||||
Db  6601 TTACCATTGACGACGGGAGCGCTCAACTCGCGCTCCGGCTCAGGAGGACTGAGACTCAGAAC 6660

Qy  6736 CCTCGAGGTGTCATCCGAGGTGTCCATTGACAATTGGGACGAGGACTGAAGACTCAGAAC 6795
         |||||||||| |||||||||||||||| |||| ||||| ||||||||||||||||||||
Db  6661 CCTCGAGGTTCATCCGAGGTGTCCATAGACACATTGGGACGAGGACTGAAGACTCAGAAC 6720
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```
Qy  6796 TGACTGAGGCGACCTGCCGCCGGCCGCGGCCGTCAGCCTGCAGCCCTCAGGCTATCGAGAATGCTGCGA 6855
         |||||||||||||||||||| ||||||  || |||  |||||||  |||| |||| ||||||  ||||||
Db  6721 TGACTGAGGCGACCTGCCGCCGGCCGCGGCCGTCAGCCTGCAGCCCTCAGGCTATCGAGAATGCTGCGA 6780

Qy  6856 GAATTCTTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTACGACACCCTCTTTGTG 6915
         || ||||||||| | || || || ||||||||| |||||||||||||||||||||||||||
Db  6781 GGATTCTTGACCTCATATTGATGTCATCATGGAAGATTGCAGTACGACACCCTCTTTGTG 6840

Qy  6916 GGGAGTAGCCGAGAGATGCCTGTGTGGGAGAAGACATACCCCGCACTCCATCGCCACCAC 6975
         ||| |||||||||||||||||| |||||| ||| |||| |||| | |||||||||||||||
Db  6841 GTGAGTAGCCGAGAGATGCCTGTGTGGGAGAAGACATCCCCCGCACTCCATCGCCAGCAC 6900

Qy  6976 TTATCTCGGTTACTGAGAGCAGCCCAGATGAGAAGACCCCGTCGGTGTCTTCCTCCGAGG 7035
         ||||| | |||||| ||||||||||||||| ||||| |||| |||||||| || |||||||
Db  6901 TTATCTCGGTTACCGAGAGCAGCAGATGAGAAGACCCCGTCGGTGTCCTCCTCCGAGG 6960

Qy  7036 AGGATACCCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCGAGACAGCCGAAGGGG 7095
         ||||||||||| | | |||||| || ||||||||||||||||| |||||| |||| |||
Db  6961 AGGATACCCCGCCCTCTGACTCATTCGAGGTCATCCAAGAGTCTGAGACACGTGAAGGAG 7020

Qy  7096 AGGAAAGCGTCTTCAACGTCGTTCTTCCGTACTAAAAGCCTTGTTCCACAGAGGCGGATG 7155
         ||||||||||||||||| ||| |||||||||||||||||||||||||||||||| ||||||
Db  7021 AGGAAAGTGTCTTCAACGTCTTTCCGTACTAGAAGCCTTGTTCCACAGAGTGATG 7080

Qy  7156 CCACAAGAAAGCTTACCGTTAAGATGTCATGCTGTGTTGAGAGAGCGTAACACGCTTCT 7215
         |||| ||||||||||||| || | |||  || ||||||||||||||| || ||  |||
Db  7081 CCACTAGAAAGCTTACCGTTCAGGATGAATTGCTGTTGAGAAGGCGTTCACGCGCTTCT 7140

Qy  7216 TTTCATTGGAATTGACGGTCGCTGGCAAGCCTGTGTGTGAGATTGGAAATCCAGAACC 7275
         ||||| | ||| || ||||| |||||||||| ||||| ||||  ||||||||||||||||
Db  7141 TTTCTTCTTTGGGCTGGCGTGGCCAGTGTCTGTGTGAGATGGAGATGGAGATCCAGAACC 7200

Qy  7276 ATACAGCCTATTGTGACAAGGTGCGCCACTCCGCTTAAGATGTCATGTGTTGGCTGGCACT 7335
         ||||| ||||||||||||||| ||||||||| ||||  ||||||||| ||||| ||||||
Db  7201 ATACAGCCTATTGTGACAAGGTGCGCCACTCCGCTTCCGCCTCGTGTGTCAAGTGCTGGCACT 7260

Qy  7336 GCAATGAACTTACCTTTGAATGTGACAAGTGTAGGCTAGCAAGAGACTTGGCTTCCT 7395
         |||||||||||||||| | || |||||||| |||| |||||||| ||||||||||||
Db  7261 GCAATGAACTTACCTTTGAATGTGATAAGTGTAGGCTAGCAAGAGACTTGGCCCCT 7320

Qy  7396 TCTCTTACATTTGGTCTGGGGTGCCCACTGACGAGGGCCACTCCGGCCAAGCCCCCTGTGG 7455
         |||||| | || ||| | ||||||||||||||||||||||||| |||| | ||||||||||
Db  7321 TCTCCTATATTTGGTCTGGGGTGCCCATTGACTGACGGGCCACACGGCCTAAACCACCTGTGG 7380

Qy  7456 TGAGGCCGGTTGCCTCCTTGTCTGGTGCCGCACCACCAAGGTTACCTTCTGCGTCTCACCAACCCGG 7515
         |||| |||| ||||  || || ||||| ||||| ||||| | ||   |||| |||| ||||||| |||
Db  7381 TGAGGCCGGTTGCCTCCTTGTCTGGTGCTGACAGCTGTGACACGAAAGTGTATGTCACCAAACCCGG 7440

Qy  7516 ACAATGTTGGGAGAGTTGACAAGGTTACCTTCTGCGTCTGCCCCGGTTCATGACA 7575
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Db  7441 ACAATGTTGGGAGAGTTGACAAGTGACCTTCTGGCGCAGGGTCCATGACA 7500

Qy  7576 AATTCCTCGTGGACTCCATAGAGCGTGCGATAGAGCGTGACCTGCCTAAGGCATGG 7635
         || ||||| ||||| ||||| ||| ||| ||||||||||  |||||||| ||||||
Db  7501 AATATCCTCGTGGACTCCATCGTGCAGCGTGCGATAGAGCCGGAGGAGGCGGCCTGCCAAAGCATGG 7560

Qy  7636 GTTACACTTATGAGGAGGCAATAAGGACTGTAAGGACTGCTGCCATGCTGCGGGGAT 7695
         ||||||||||||||||||||||||| ||| || ||| ||||||||||||||| |||||
Db  7561 GTTACACTTATGAGGAGGCAATAAGGACTGTTAGGCTTAGGCCACATGCTGCGGGGAT 7620

Qy  7696 CTAAGGTGTCGTCAAGGACCTGCCCACCCTGCGGGGAGAATGGCTGTGTCCATGACCCGGC 7755
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Db  7621 CTAAGGTGTCGTCAAGGACTTGGGGCCCTTGCGGGGAGAATGGGGAAGAGGGAGTGT 7680

Qy  7756 TCTTCAAAGACCGAGAAGGAAAGAGGCCCCCCTCATTGTTCCCCCCCTGACT 7815
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Db  7681 TTCAGGAGATACTTGAGGGGACTTGAGGGGACTTTTCACTTTACTCTTTACTGTGTAGAAAGGAGTGT 7740

Qy  7816 TCTTCAAAGACCGAGAAGGAAAGAGGCCCCCCTCATTGTTCCCCCCCTGACT 7875
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Db  7741 TCTTCAAAGACCGAGAAGGACGAGAAGGAGAAGACTCAGAAC 7800

Qy  7876 TCCGGATAGCTGAAAAGCTTATTCTGGACGGGTAGCGAGGCCAAGGCGGTGTTGG 7935
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Db 7801 ||||||||||| |||||||| |||||||| ||||||||||||||||||||||
Qy 7936 GGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAGTGCTCAAACTGT 7995

Db 7861 ||||||||| ||||||||||||||||| ||| |||||||||||||||||
Qy 7996 GGGAATCAAAGAAGACACCATGCCCATCTGTGTGACGGCCACATGCTTCGACAGTAGCA 8055

Db 7921 |-||||||||||||||||||||||||||||-|-||-|||-||||||||||
Qy 8056 TAACTGAAGAGACGTGGCGCTGGAGACAGAGCTTTATGCCCTTCAGACCATCCAG 8115

Db 7981 |-||||||||||||||||||||||||||||| ||||||||||||||||||
Qy 8116 AATGGGTGCGTGCCCTGGGAAATACTATGCCTCTGCACAATGGTAACCCCCGAGGGGG 8175

Db 8041 |-|||||| |-|||||||| |||||| |||| |||||| |||||
Qy 8176 TGCCAGTGGGTGAGAGTATTGTGATCCTCAGGGGTCTTGACCACCAGTGCGAGCAACT 8235

Db 8101 ||||||| ||-|-|||||||||||| |||||| |-|||||||||
Qy 8236 GCTTGACTTGCTATATCAAGGTGAAAGCCGCTGTGGGGCTGGGGCTGAAAAATGTCT 8295

Db 8161 |||| |||||||||||||||||||||||| |||||||||||||
Qy 8296 CGCTCCTCATCGCTGGCGATGACTGTTGATCATATGCGAACGGCCGTGTGTGCGATCTA 8355

Db 8221 |||| ||| |||||||||||||||| |||||||| |||||||||
Qy 8356 GCGACGCTTTGGCCAGAGCCCTGGCGTACGGCCTTCGTTGCGACCCTT 8415

Db 8281 |-||||||||||||||| |-||||||||||||||| |||||||||
Qy 8416 CATCACTCGGACACGGCCCCCCTCTGCCACTGGCTAGCTGAGTGCAATGCAGATGGGA 8475

Db 8341 |||||||| |||||||||| |||| ||||||||||
Qy 8476 AACGCCATTTCTTCCTGACCACGACTTCGGAGGCCCCTGCCTCGCATGTCAGCCAGT 8535

Db 8401 |||||||| |-||||| |||| |||||| ||||| |||||||||
Qy 8536 ACAGTGACCCAATGGCTTCGGCCATCTTCGGCCATCTTCTCATATCCTCTTACACTCCTATCA 8595

Db 8461 ||||||||| |||||||| |||||| |||||||||
Qy 8596 CACGGTGGTCATCATCCCTCACCTGCGCGTTTAGGCGGTGGTGCCACACCGT 8655

Db 8521 ||||||||||| |||| |||||||||||||||
Qy 8656 CTGATCCTGTGTGGTGCCAGTGGTAATTACTACAAGTTCCACTGACAAACTGC 8715

Db 8581 ||||||||||| |||||| |||||||||
Qy 8716 CTAACATCGTCGGCCCTGGCCCCACCGGTTGAGGGTTACCGCAGACACAACTA 8775

Db 8641 ||||||||||| ||||||| ||||||||
Qy 8776 AGACAAAATGGAGGCTGGCAAGCTGCTGAGCGACCTCAAGCTCCCTGGCCTAGCAGTCC 8835

Db 8701 ||||||||||| || ||||||| ||||||||
Qy 8836 ACCGGAAGAAGGCCGGGCAATTGCGAACGGCTATGCTCCGGTCGCCGCGCGGTTGGGCTGAGT 8895

Db 8761 ||||||||||| ||| ||||||||||||||||||
Qy 8896 TGGCTAGGGGGTGTGTGGCGGTCTTCCCCCTTCCCGGCTCCCGGGAGATTGCTGGTA 8955

Db 8821 ||| ||||||||||| |||||||||||||||||
Qy 8956 TCCCGGGGGTTCCCCCTTTCCCCCCTATATGGGGGTGTTCATCAATTGGATTTCA 9015

Db 8881 TCCCGGGGGGTTCCCCCTCTCCCCCCCCTACATGGGGGTGGTGGTGTCATCAATTGGATTTA 8940

Qy 9016 CAAGCCAGGAGGAGTCGCTGGCGGTGGTTGGGGTTCTTAGCCCTGCTAGCCCCTCT 9075
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Db 8941 CAAGCCAGGAGGAGTCGGTCGGCTGGGGTTGGGGTTCTTAGCCCTGCTAGCCCCTCT 9000

Qy 9076 TCGGGTGAACTAAATTCATCTGTTGCGGCAAGGTCCGGTGACTGATCATCACTGGAGGAG 9135
                 |||||||||||||||||||||||||| |||||||||||||||||||||||
Db 9001 TCGGGTGAACTAAATTCATCTGTTGCGGCAAGGTCCAGTGACTGATCATCACTGGAGGAG 9060

Qy 9136 GTTCCCGCCCTCCCCGCCCCAGGGGTCTCCCCGCTGGGTAAAA 9178
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Db 9061 GTTCCCGCCCTCCCCGCCCCCAGGGGTCTCCCCGCTGGGTAAAA 9103

RESULT 15
US-08-464-134-182
; Sequence 182, Application US/08464134
; Patent No. 5849532
; GENERAL INFORMATION:
;   APPLICANT: Kim, Jungsuh P.
;   APPLICANT: Wages, John
;   APPLICANT: Young, LaVonne M.
;   APPLICANT: Fry, Kirk E.
;   APPLICANT: Linnen, Jeffrey M.
;   TITLE OF INVENTION: Hepatitis G Virus and Molecular
;   TITLE OF INVENTION: Cloning Thereof
;   NUMBER OF SEQUENCES: 277
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dehlinger & Associates
;   STREET: 350 Cambridge Ave., Suite 250
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/464,134
;   FILING DATE:
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/389,886
;   FILING DATE: 15-FEB-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/357,509
;   FILING DATE: 16-DEC-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/329,729
;   FILING DATE: 26-OCT-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/344,271
;   FILING DATE: 23-NOV-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,558
;   FILING DATE: 03-AUG-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/285,543
;   FILING DATE: 03-AUG-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/246,985
;   FILING DATE: 20-MAY-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Fabian, Gary R.
;   REGISTRATION NUMBER: 33,875
;   REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 324-0880
;   TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 182:

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SEQUENCE CHARACTERISTICS:
;    LENGTH: 9103 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: both
;    TOPOLOGY: linear
     MOLECULE TYPE: cDNA
.    HYPOTHETICAL: NO
;    ANTI-SENSE: NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE: HGV-JC Variant
;    FEATURE:
;      NAME/KEY: CDS
;      LOCATION: 276..9005
US-08-464-134-182

Query Match         82.6%;  Score 7760.6;  DB 2;  Length 9103;
Best Local Similarity  90.8%;  Pred. No. 0;
Matches  8264;  Conservative  0;  Mismatches  839;  Indels  0;  Gaps  0;
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Qy    76 CAATGACTCGGCGCGCGACTCGGCGACCGGCCAAAAGGTGGTGGATGGTGGTGACAGGGT 135
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Db     1 CAATGACTCGGCGCGCGACTCGGCGACCGGCCAAAAGGTGGTGATGGGTGATGACAGGGT 60

Qy   136 TGGTAGTCGTAAATCCGGTCATCCTGGTAGCCACTATAGGTGGTCTTAAGAGAAGGT 195
         ||||||||||||||||||||||||| | |||||||||||||||||||||||||||||
Db    61 TGGTAGTCGTAAATCCGGTCACCTTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGT 120

Qy   196 CAAGACTTCCTCTTGTGCCTGCGCGAGACCGGCCACAGTGTGCTGGCCCTACCG 255
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Db   121 TAAGATTCCTCTTGTGCCTGCGCGAGACCGGCCACAGTGTTGGCCCTACCG 180

Qy   256 GTGTGAATAAGGGCCCGACGTCAGGCTCGTCGTCGTTAAACCGAGCCCGTCACCCACCTGGGC 315
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Db   181 GTGGGAATAAGGGCCCCGACGTCAGGCTCGTCGTCGTTAAACCGAGCCCGTAACCCCCTGGGC 240

Qy   316 AAACGACGCCCACGTACGGTCCACGTCGCCCTTCAATGTCTCTTGACCAATAGGTTTA 375
         ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   241 AAACGACGCCCACGTACGGTCCACGTCGCCCTTCAATGTCGCTCTTGACCAATAGGCTTA 300

Qy   376 TCCGGCCAGTTGACAAGGACCAGTGGGGGCGGGCATGGGGAAGGACCCCCAAACCCT 435
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Db   301 GCCGGGCCAGTTGACAAGGACCAGTGGGGGCGGGGTTATGGGGAAGGACCCCCAAACCCT 360

Qy   436 GCCCTTCCCGTGTGGGCCCGGGAAATGCATGGGGCCACCCAGCTTCCGCGGCGGCCTGCAGCC 495
         |||||||||||||||||||||| | |||||||||||||||||| ||||||||||||||||
Db   361 GCCCTTCCCGGGCGGACCGGGGAAATGCATGGGGCCACCCAGCTTCCGCGGCGGCCTGCAGCC 420

Qy   496 GGGGTAGCCCAAGAATCCTTCGGGGTGGTGCATTTCTTTTCTATACCATCA 555
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Db   421 GGGGTAGCCCAAGAATCCTTCGGGGTGGTGCATTTCTCTCTTTTCCTATACCATCA 480

Qy   556 TGGCAGTTCCTTCTTCTCTGCGGTTGAGGCCGGGCCCAATTCTGCGCCCCGCCACCC 615
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Db   481 TGGAAGCCCTTCCTCCTCTGTTCCTCGGGGTGAGGCCGGGTTATGGGGAAGGACCCCCAAACCCT 540

Qy   616 ACGCTTGTCTGCGAGCGAATGGCAATATTTCCTCACAAATTGCTGCGCCCCGGAAGACATCG 675
         |||||| | ||||||||||||||||||||| | |||| ||||||| |||||||||||||
Db   541 ACGCTTGTCGAGCGAATGGGCAATATTTCCTCACAAACTGTTGCTGCAGAGGACACAATTG 600

Qy   676 GGTTCTGCCTGAAGGCCGGATGCCTGGTGGCCGTTGCACCGGTT 735
         |||||||||||||||||||||| ||||||||||||||||||||||
Db   601 GGTTCTGCCTGAAGGCCGGTGGCCCTGGGTGGCCGTTGCACTGACCGAT 660

Qy   736 GCTTGGCCACTGTATCGGCGGGGTTGTGGCCTGCGTGTGGGCCTGGCAAGCTCG 795
         |||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db   661 GCTTGGCCGCTGTATCGGCGGGGTTGTGGCCTGCGTGTCGGCTTGGGCAAGCTGG 720

Qy   796 TTGGGAACTGGGACCTGTACGGCGCCCTGTACGGGCCCTGTCCGGCTTCGGTCTCCGGGGATCC 855
         ||||||||| |||||||||||||||||||||||| |||||||||||||||||||||| |||||
Db   721 TGGGGCAACTGGGTGGCCTCTACGGGCGCCCTGTTCGGTGTCCGGCTACGGGCCGGCCATCC 780

Qy   856 TGGGGTCTGGGGCGAGTTTACTCCGGGTCCTGACAGTTGGGTTGCGTTGAGGCGCCGGG 915
         |||| ||||| |||||| ||| || |||||||||| ||||||||||||||||||||||||
Db   781 TGGGGCAACTGGGTGGCCTCTACGGGCGCCCTGTTCGGTGTCCGGCTACGGGCCGGCATCC 840
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Db   781 TGGCCTCGGTGAGTGTACTCGGGTGTCCTAACAGTTGGTGTGTTGCGTTGCGTTGACGCGCCGGG 840

Qy   916 TCTACCTGATGCCCAACCTGAGTGTGCAGTAGAATGTGACGTTAAGTGGGAAGTGAGT 975
         ||||| |||||||||||||||| |||||||||| ||||||  |||||||||| |||||
Db   841 TCTACCCGATGCCCAACCTGACGTGTGCAGTAGAGTGTGAGCTTAAGTGGGAAAGTGAGT 900

Db   976 TTTGGAGATGGACTGAGCAGTTGGCCTCCAATTACTGGATTTTGGAATACCTTTGGAAAG 1035
         ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Qy   901 TTTGGAGATGGACTGAGCAGTGGCCTCCAATTACTGGAATTCTGGAATACCTTTGGAAGG 960

Qy  1036 TCCATTTGAATTTTGGAGAGGAGTGATGAGCCTGACCCCTCTGTTGGTTTGGGTTGGCCG 1095
         |||||||||||| ||||||||| |||||||||||||||||||||||||||||||||||||
Db   961 TCCCGTTTGACTTCTGGAGAGGCGTGTAAGCCTGACCCCTGCTGGTTTGCGTTGGCCCG 1020

Qy  1096 CAATTGCTTTTGCTGGAGCAACGGATTGTCATGGTTCTTCCCGCCCCTTTGCTGCTGGTTGAAGT 1155
         ||||| ||||||||||||||||||||| | ||||||||||||||||||| |||||||||||||||
Db  1021 CGTTGCTGCTGCTGGAGCAACGGACGGATTGTCATGGTTCTTCCCGCCCCTTTGACTACGGTTGACAT 1080

Qy  1156 TGTTGCAAGGCGCCCCGCCCGTTTGGGTCCGCGTATTCCCACTGGGAGAGGGTGTGGG 1215
         ||| ||||||||||||||||||||| |||||||| ||||  |||| || |||||||||
Db  1081 TGTCGCAAGGCGCTCCGGCCTCCGTTTGGGTCTGCGTAATACTACTGGGAGGAAGGTGTGGG 1140

Qy  1216 GGCAGTCATGCTCCTGCAGGGCTAACGGCGTCGCGTATTCCCACTGGGAGAGGGTGTGGG 1275
         ||||||||||||| |||||||| ||||||||||||||| | ||| |||||||||||||||
Db  1141 GGCAGTCGTTGTTCCTGCAGGGCTAATGGCGTCGCGCTATACTACTGGGGAGGAAGTGTGGG 1200

Qy  1276 ATCGAGGGAATGTCACGCTCTTGTGTGACTGCGGGCGCCCCCAACGGCGCCCTGGGTTTGGGTCCCGG 1335
         |  || ||||||| | | |||||||||||||||||||||||||||||||||||||||||||
Db  1201 ACCGTGGAACGTCACGCTCCTGTGTGACTGCGGGCGCCCCAACGGCGCCCTGGGTGGTTGCCGG 1260

Qy  1336 CCTTTGCCAGGCGGTTGGGTGGGGCGACCCCATCACCCATTGGAGCCACGGACAAAACC 1395
         || ||||||||| | || |||||| ||||||||||| | ||||||||||||||||| ||
Db  1261 CCTTTTGCCAAGCAATCGGCTGGGGCGATCCCATCATTGGAGCCACCAGCGCCCAAAATC 1320

Qy  1396 AGTGGCCCCTATCATGCCCCAATATGTCTATATGGTCTGTGTCCGTAACGTCGTGTGTGGG 1455
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Db  1321 GGTGGCCCCTCCTCATGCCCCAGTATGTCTATGGTGTCTGTTCAGTCACTGCTGTGTGTGGG 1380

Qy  1456 GTTCCGTCGTTGTTGCCTCGACCGGCGGCTCGTGATTCGAAGATCGATGTGTGGAGTT 1515
         ||||||||||||||||||||||||||| || | || |||||||||||||||||||||
Db  1381 GTTCCGTCTCTTGGTTGCCTCGACCGGCGGCTCGTGAGATCGAAGATCGATGTGTGGAGTC 1440

Qy  1516 TGGTGCCGGTTGGATCTGCCAGTTGCCACCATAGCCGCTCTAGGGTCATCGGATCGCGACA 1575
         |||||||||||||| |||||||||||||||||||||||||| | |||||||||||||||||
Db  1441 TGGTGCCGGTTGGTTCCCGGAGTTGCCACCATAGCCGCTCTTGGATCGTCGGGATCGGGACA 1500

Qy  1576 CGGTGGTTGAGCTCTCCGAGTGGGGAGCTCCGTGCGTAACGTGTATTCTGGACCGTCGGC 1635
         | |||||||||||||||||||||| |||||||| |||||| ||||||||||||||||||
Db  1501 CGGTAGTTGAGCGTCTCCGAGTGGGGAGCTCCGTGCGCAACGTGCATTCTGGATCGTCGGC 1560

Qy  1636 CTGCTTCATGTGCGGGACTGTGTGGCCTGTGAGGCCGGACTGTCGGTTAGATTCC 1695
         ||||||||| | ||||||||||||||||||||||||| |||||||||| ||||||
Db  1561 CGGCCTCGTGTCGCGGGCACCTGTGTGAGACTGCTGTGCGCCCCGAAACCGGGTCGGTTAGGTTTC 1620

Qy  1696 CTTTCCATCGGTGCGGCACGGGGCCCTCGGCTGACAAAGGACTTGAAGCGTGTGCCCTTCG 1755
         | ||||||||| |||||||||||||| || ||||||| ||||||||||||||||||||| |
Db  1621 CATTCCATCGGTGCGGCACGGGGCCGGGCCTAAGCTGACAAAGGACTTGAAGCGTGTGCCCTTCG 1680

Qy  1756 TCAACAGACAACTCCCTTCACCCATGGGCCCCCTGGGCAACCAGGGGAGGCAACC 1815
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Db  1681 TCAATAGGACAACTCCCTTCACCCATAAGGGCCCCCTGGGCAACCAGGGCAACCAACC 1740

Qy  1816 CGGTGCGGTCGCCCCCTGGGTTTGGTCCTGCCTGTGTGCCTGGCAAGAATCCGGGATTCCCTGC 1875
         ||||| ||| ||| ||| |||||||| ||||| ||||||| | |||||||||||||||||||||
Db  1741 CGGTGCGGTCGCGGCTGGGTTTTGGTCCTGCCTGTGTGCCATGGCAAGAATCCGAGACTCCTTAC 1800

Qy  1876 ATTTGGTGAAATGTCCACCAGCCATAGAGCCTCGGACTTCGGGTTCTTCC 1935
         ||||||||||||||||||||||| ||||||| | |||| |||||||| ||
Db  1801 ATTTGGTGAAATGTCCACCAGCCATTGAGCCTCCCACCGGGACGTTTGGGTTCTTCC 1860

Qy  1936 CCGGAGTCCCGCCCATTAACAACTGCAATGCCGTCGTTGGGCACGGCGCCGGG 1995
         ||||| | ||||| | | |||| ||||| | ||||| ||||||||||||||||
Db  1861 CCGGAGTCCCGCCCTTAACAACTGCTGTTTAACAACTGCTCCGTGTTGGGCACGGCGCTG 1920
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Right column (positions 3001–4215):

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Qy   3076 CATTCACTAGGACGGACTGTCGCATCATCAGAGATCGCGGAGGACCTGTCCTCGCGGAC 3135
          ||||||||||||||||||||||||||||||| ||||||| ||||||| ||||||||||
Db   3001 CATTCACTAGGACGGACTGTCGCATCATCAGAGATGAGCTGCGGAGGACCTGGCCTGCGGGC 3060

Qy   3136 AGTGCGTCATGGGTTTACCCGGTTAGCACGGCGCGGTGATGAGGTTCTCATCGGCGTCT 3195
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   3061 AGTGCGTCATGGGTTTGCCGTGGTAGCGCCGTGTGTGACGGAGGTTCTTATCGGTGTCT 3120

Qy   3196 TTCAGGATGTGAAATCATTGTCCTCCGGTTGTCCGACTGCACCAGTTGTCATCCGTC 3255
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   3121 TTCAGGATGTGAACCATTTGCCTCCCCGGATTCGTCCCGACCCGCACCCGTTGTCATCCGGC 3180

Qy   3256 GGTGCGGAAAGGGCTTCCTGGGGTCACGAAGGCAGCCTTGACAGGTAGGGATCCTGACT 3315
          |||||| |||||| |||||||||||||||||||||||||||||||||||||||||
Db   3181 GGTGCGGGGAGGGGGTTTCTGGGGGTTCTGGGGTCACTAAGGCTGCCTTGACTGGTCGGGGATCCTTGACT 3240

Qy   3316 TACATTCCAGGGAACGTCATGGTGTTGGGACGGCTACGTCACGAAGCATGGCACATGTC 3375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TACATTCCAGGGAACGTCATGGTGTTGGGACGGCTACGTCGCCGAAGCATGGGACATGCC 3300

Qy   3376 TGAAATGGCCTGCTGTGTTCACAACTTTCATGGGGCTTCATCCCGAACCATCGCCAGCCCG 3435
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGAACGGCCCTGCTGTGTCACGACTTTCATCGGGGCTTCATCCCGAACCATCGCCACGCCCG 3360

Qy   3436 TGGGGGCCCTTAATCCCAGTTGGTGGTCAGCCAGTGGTGACGCCCTGACGTGTACCGGCTTC 3495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TGGGGGCCCTTAATCCCAGTGGTGTCCCCGAGTGGTGTCGCCCTGACGTGTACCGCCCTCC 3420

Qy   3496 CAGATGGGGCAACTTCGTTGACGCCCCTGCACTTGCCAGGCGGGAGTCCTGTTGGGTTATTA 3555
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   3421 CGGATGGGGCAACCTCGTCAGATTCCCTGGCCTGCCAGGCTGAGTCCTGGGTCATCAC 3480

Qy   3556 GATCCGACGGGGCTTTGTGTCCATGGCCTTGAGCAAGGGGACAAGGTGAGCTGGATGTGG 3615
          || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GGTCCGACGGGGCTTTGTGTGCCATGGCCTTGAGTAAGGGAGGAGACAAGGTGGAGCTAGATGTGG 3540

Qy   3616 CCATGGAGTCTCTGACTTCCGTGGTTCGTCTGGTTCACCGGTCCTGTTGGGACAAAGGGC 3675
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   3541 CCATGGAGTCTCAGATTTCCGTGGCTCCTGGCTGCGTCCTGTCGTTGGGAGGGGGC 3600

Qy   3676 ACGCAGTAAGAAATGCTCGTGTCAGTTCGCAGTTTCGGGTTTACTGCGGCGCCGAT 3735
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   3601 ACGCAGTAGGAAATGCTCGTGTCGGTGCTCCACTCGGTGGTGTGCGGCGGCGTCGAT 3660

Qy   3736 TCACTAGGCCGTGACTCTATAGGACCTGGTGTAAAGGGTACCAGGCTGTGCCGGCCAGA 3795
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TCACCAGGCCGTGGACCCGGGATAGGGACCTGGGTTGCAACAGATGCTAAGACCACTGAACCCCCTCCGG 3720

Qy   3796 TGCCGGCAAAAGGAGTTTTCAAGGAGGCCCCGTTGTTTATGCCCATCACGGGGGCGGAAAGA 3855
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TGCCGGCAAAGGGAGTTTTCAAGGAGCCCCACGTGTTTATGCCCCACAGGGGCGCAGGAAAGA 3780

Qy   3856 GCACCCGGTACCGGTTGGAGTACGGCAACATGGGCAACAAGGTCTTGAACCCGT 3915
          |||||||||||||||||| ||||||||||||||||||||||||| |||||||||
Db   3781 GCACCGCGGTCCCGTTGGAGTATGGCAACATGGGGCAACAAGGTCCTGATTTTGAACCCCT 3840

Qy   3916 CGGTAGCTACCGTGAGGCCCATGGGCCGGCCGGGCGGCTGGCGGGGAAACACCCCA 3975
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 CGGTGGCAGTGCGACAGTGAGGCCCATGGGCCCTTACATGGCCGGGGGAAAAACATCCAA 3900

Qy   3976 GTATTTACTGTGGCCATGACACCACTGCTTTCACAAGGGCGCCCCCTTACGT 4035
          |||||||||||||||||||| |||||||||||||||||| ||||||| |||||
Db   3901 GTATCTACTGTGGCCCATGACAACACCACTGCCTTCACAAGGATCACTACTGATTCCCCCCTTAACGT 3960

Qy   4036 ATTCCACTTACGGACGTCTCCAAGGTTTTTGGCCAACCCTAGGCAGTCTTGACATGGGCT 4095
          |||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||
Db   3961 ACTCTACCTATGGGAGTTTCTGGCCAACCCTAGGCAGTCTTGACCATATGGGCT 4020

Qy   4096 TCATTTGTGACGAGTGCCACAGTACTCAACCTGTGTTGTTGGGGTGTGTCA 4155
          |||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   4021 TCATTTGCGATGAATTGCCACAGTCATGATTCCACTGTTGTTGGGGATTGGGACGGTCC 4080

Qy   4156 GGGAGCTGGCCGCCGAGGATGTGAGTGCAATTGGTGTGCTCTACGCCACTGCCACCCCTCCCG 4215
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CTTTTTGCGCCGCGTCTCGACCGCCGCTGTCAAGGAGCGCCTGCGCGGGATTGGGATTGGACGGGTCC 3000
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Left column (positions 1921–3075):

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Qy   1996 GCGGAGCTGGGCTTACGGGGGGTTCTACGAGCCTCTGTGTTCGGGTGTTGTTCGGAGCTGA 2055
          |||||||||||||| || ||||||||||||||||||||| ||||||||||||||||||||
Db   1921 GCGGGGGCCCGCTCACGGGGGGGTTCTATGACCCTGGTGCGCAGGACCTTGGCCTGCGGGGCTGA 1980

Qy   2056 TGGGGCAGCCGAAATCCGGTTGCCCGGGTACCGCATGCGGTTGTCCTCGCGGTAGACCTGACG 2115
          |||||||||||||||||||||| |||||||| || |||||||| ||||||||||||
Db   1981 TGGGGCCGCCGAAATCCGGTTTGCCCGGGTTTGCATGGCTGTCCTCGGGGTCGGACCTGACG 2040

Qy   2116 GGTTCATACACGTCCAGGGCACCTGCAGGAGGTGGATGCGGCAACTTCATCCCTCCTC 2175
          |||| ||||||||||||||||||| || |||||||||||||||||||||||||||||
Db   2041 GGTTTATACACGTCCAGGGCCACTGCAGGAGGTCGCAATGCTGGCCAACTTCATCCCTCCAC 2100

Qy   2176 CACGTCGGTTGCTCTTGGATTTTGTATTTGTCCTGCTCTATCTGATGAAGCTCCTGACT 2235
          ||||||||||||| | ||||| || |||| || | |||||||||||||| |||||||
Db   2101 CTCGCTCGGTTGCTCTTGGACTTTGTGTTGTCCCTGTTATACCTGATGAAGCTGCTGAGG 2160

Qy   2236 CACGGTTGGTCCGTGATCTTCGCTTGCTCCGGGGTACCGCAGTTGGCGGTTC 2295
          |||||||||||||||||||||||||||||| ||||||| ||||||||||||
Db   2161 CACGGTTGGTCCGTTGATCTTCGCTTCTGCTGGTTGGTGGGTTGGGTGAACCAGTTGGCAGTCC 2220

Qy   2296 TAGGACTGCCTGTGGACGCTCGCCGTGCGGGTGAAGTTTTTGCGGGCCCCTGCCTTGT 2355
          | |||||| ||||| |||||||||| |||| |||||||||| ||||||||||||||||
Db   2221 TTGGACTGCCTGTGGGACGCCGGCCGGCGGGTCTTCGCGGGCCCCGCCCTGT 2280

Qy   2356 CATGGTGTTTGGGCCTTCCCCACTGTCACGTGTATGAGCTCTAGCACGTCTGTGTTGT 2415
          ||||||| ||||||||||||||||||| ||||| ||| |||||| ||||||||||||
Db   2281 CGTGGTGTCTGGGCCTCCCCAAGCCCTCACCGTGTAATCTGGGCTTAGCAAAACCTGTGTTGT 2340

Qy   2416 ACTTTCGGTGGATGGGCCTCAGCGCCTGTTCCTCCTGTGTGTGGAAGCTCGTCGGG 2475
          | |||||||||||||||||||| |||||||||| |||||||||||||||||||||||||
Db   2341 ATTTCCGGTGGATGGGCCTCCCAAGCCCTCATGTTCCTGCGTGTTCGTGGAAGCTCGCTCGGG 2400

Qy   2476 GAGCTTTCCCGTGCACTTTGATGGGGATTTCGGCGACCCGGCGCGCCACTCTGTGC 2535
          ||||||||||||||||||||||||||| ||||||||||||| ||||
Db   2401 GAGCTTTCCCGTGCACTTCTGATGGGGATCTCGCCGCTCGATGAGCGCGGGTGC 2460

Qy   2536 TCGGGCCGAGTTCTGCTTCGATGTCACATTCGAGGTGTCACACTTCGGTGTTGGGCTGGG 2595
          |||||||||| ||||||||||||||||||||| ||||||| |||||||||||||||||||
Db   2461 TCGGGTGGATGGGTCTCAGATTCGAGGTGTCACATTCGAGGTGTCACACCTCGGGCTGGG 2520

Qy   2596 TGGTGCCAGCGTGGCTTGGGCCGCCATAGCGCTCCTGAGCCTCCAATGAGCGCTCCTGTGC 2655
          ||||| |||||||||||||| |||||| | | | |||||||||||||||||
Db   2521 TGGTGGCCAGCGTGGCTTGGGCCATGGCCTTGGGGAGGCGGCGGGAGGGT 2580

Qy   2656 GGAAGCACAAGGCCGTGATCTATAGGACGGTGGTTGTAAAGGGTACCAGGCTGTGGCCGCCAGA 2715
          ||| ||||||||||||| |||||||| |||||| |||||||||||||||||||||||
Db   2581 GGAGGCACAAGGCCGTGATCTATAGGACGGTGTGTAAAGGGTACCAGGGCAATACGCCCAAC 2640

Qy   2716 TCTTCGGCCTGTTGGGGTCTCGGGGAGGCGCTCCTACCAGCTTCTGACGTTCGCCTGT 2775
          ||||| |||||||||| || |||||||||||| |||||| | ||||||||||||| ||||
Db   2641 GGTGTGGCCAGCGTGGTAGCCGGAGGGGGCGGCGGCCACCCCAAACCCTTGACGTTTGCTTGGT 2700

Qy   2776 GCTTGGCCCATACATCTGCCCGGATGCTCGTGATGATGGCGGGTTGGCCTTGGTCTCTCC 2835
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   2701 GCTTGGCCCATACATCTGCCCGGATGCTCGTGATGGTGTGTAGGCCTTGGTGCTCC 2760

Qy   2836 TCTTCGGCCTGTTCGACGCACTGACTGGAGGAGTCTTGGAGGCTCCCGGCCCCT 2895
          ||||| |||||||||||| |||||||| ||||||||||||| ||||| |||||
Db   2761 TCTTTTGGCCTGTTCGACGCTTGGACTGGAGGTGTCTTGGAGTGTCTTGGAACCCCCTGT 2820

Qy   2896 CCATCCGACTGGCCACGATGTGGGTTGTCGCCGAGAGAAGGCCACCA 2955
          |||||||| |||||||||||||| ||||| ||||||||||||||||||
Db   2821 CGTTACGGCGTCTCGCCGCGCTATTTGTTGTCGTGGAGGGAAGGAGCCACACA 2880

Qy   3016 CTTTCTCGCGCGTGACTTGTCAGGAGCCGCTTTGGACGCCGTTTGGAGCCCTTGT 3075
          |||| |||||||||||||||| ||||||||||| ||||||||||||||||||| ||
Db   2941 CTTTTTGGTCGCGTGACTTGTCAGGAGCCGCCCGTCGGGGACGCCCCGTTTGGAACCCCTGT 3000
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Db 4081  |||||||| |||| |||||| ||||| ||| |  |||||||||||| ||||||
         GGGAGCTGGCACGAGAGTGTGGGTCAGGCTTGTGCTCTACGCCACGCCTCCTG 4140

Qy 4216  GATCCCCGATGACCCAGCACCCATCAATCATTGAGACAAAACTGGACGTGGGAGATCC 4275
         |||| || |||||| |||| ||| ||||||||||| ||| |||| ||||| |||||
Db 4141  GGTCCCCCATGACTCAGCGATCCATCATCAATCATTGGATGTGGGTGAGATTC 4200

Qy 4276  CCTTCTATGGGCATGGCCACTATCCACTGGGTACACTTCGATTCTGTCACCGATTCT 4335
         |||||||||||||||||| |||||||||||||||| ||||||||  |||||||||||
Db 4201  CCTTCTATGGGCATGGCCACTATCCCTCCAGCGGATGCGGACCCGATAGCCGTATTCT 4260

Qy 4336  GCCACTCCAAGGCTGAGTGCGCCGAGCCGCTGGGCGCCAGTTTTCGGCTGGGGGTAAATG 4395
         || ||| |||||||||||| || ||||||||||||| |||| |||| || |||||
Db 4261  GCTACTCTTAAGGCAGAGTGTGAGCGGCTAGCCGGTCAGTTTTCTGCTAGGGGAGTTAACG 4320

Qy 4396  CCATGCCTATTTACAGGGGAAAGACAGTTCTATCATCAAAGATGGAGACCTGGTGGTGT 4455
         |||| ||||||||||||| |||| |||| || ||||||||||||||| |||| ||||| |
Db 4321  CCATAGCTATTTACAGGGGAAAAGACAGTTCTATCATCAAGGACGGAGATCTGGTGGTGT 4380

Qy 4456  GTGCTACAGACGCACTATCCACTGGGTACACTTCGATTCTGTCACCGATTGTG 4515
         | ||| ||||| || |||||||||||||| ||||| ||||||||||||||||
Db 4381  GGGCGACCGACGCCATCCCGCTGGATACACTTCGATTCTGTCACCGACTGTG 4440

Qy 4516  GGTTAGTGGTGGAGGAGTCGTCGAGAGTCGCTGAACTTCAGCCCTGTGAGTCGCGCTCAG 4575
         ||||| ||||||||||||||||||||||| |||||||||| ||||| ||||||||| |||
Db 4441  GGTTAGTGGTGGAGGAGTCGTCGGCCGGTCAGTTTTACGTTGGTGTCGCCAAGGCCCGGG 4500

Qy 4576  GCACGGTGCCCCGCTCGGCTGAACTGTCGATGCAGCGGCACGGCGCAGGGGCA 4635
         ||| ||||||| ||||| |||||||||| ||| || ||||| | ||| |||
Db 4501  GGACAGTGCCCCGCTCGGCTGAACTGTCGATGCAGCGGCACGGCGCAGGAGGCA 4560

Qy 4636  GGTCTGGGCGCTACTACCGCGGGGTCGGCAAGGCCCTGCTCGTGTGGTGGCGCTCAG 4695
         |||||||| | |||||| | |||||||| |||| || || ||||| |||||| || ||
Db 4561  GGTCTGGGCGCTACTACCGCGGGGTCGGCAAGGCCCTGCTCGTGTGGTGGCGCTCGG 4620

Qy 4696  GTCCTGTCTGGTCGGCGGTGAAGCCGGTCGTGTGACGTGGTTACGGACGGAATGGAACCTGACCTGA 4755
         ||| ||||||||| ||| || || ||| || || ||||| ||| |||||||||||||||||||||||
Db 4621  GTCCTGTCTGGTCGGCGGTGAAGCCGGTCGTGTGTATGGAAGTTCAGCCGGAATGGAACCTGACTTGA 4680

Qy 4756  CAGCAAAACTACTGAGACTTTACGACAACTGTCTCGGGGATGACCCCGAGCTCGCAGACA 4815
         ||||||||||||| ||||||||| |||| |||| ||||| || ||||| || ||||||||
Db 4681  CAGCTAACCTATTGAGACTTTACGACAACTGTCTCCACCGACCTCGAGCGTCGCAGACA 4740

Qy 4816  TTGGGGAAGCCGCGGTTGTTCTTTTCGGGGTTGTCCCCGTTGCCCGGTCATCCCGATGTTA 4875
         || ||||||||||| | |||||| ||  ||||| ||| | ||| ||||||||||||||||
Db 4741  TCGGTGAAGCCGGGGTGTTTTTCTCCGGGGTGTCGCCGCTGCCCGGTCAGCCATCCCGATGTTA 4800

Qy 4876  GCTGGGCAAAAGTTCTCGGGCCGGTCAACTGGCCCGTCAACTGGCGGCCTAGGGGCGACCATGT 4935
         ||||||||||||||||| || ||||| || |||| ||||| || |||| || ||||||||
Db 4801  GCTGGGCAAAAGTTCTCGGCGCCGGTCAACTGGCGCCGTCAACTGGCGGCCGACCATGT 4860

Qy 4936  CAGCGGGAAAACACTGTCTCCCGGGCCCATCGGATGACCCCAGTGGCTCGAAGGGCC 4995
         ||||||||||||||||||||| ||| |||| |||| ||||| || |||||||||||
Db 4861  CAGCGGGAAAACACTGTCTCCCGGCCCATCGGACGACCCCAGGTCTCGAAGGGCC 4920

Qy 4996  CGAATCCTGTCCCACTCCTGCTGAGGTGGGCCAATGATTTACCATCTAAAGTTGGCCGCGCC 5055
         |||||||||||| |||||||| |||| |||||||||||||||||||||||| ||||||||||
Db 4921  TCGGTGAAGCCGGGGTGTTTTTCTCCGGGCTAGCCCGCTGGGCCAATGATTTACCATCAAAAGTTGGCCGCGCC 4980

Qy 5056  ATCACATCGTGACGACCCATCTTGGTGCCTAGGGCTCGGGGCTAGGTTCCGCTGCCG 5115
         || ||| |||||| |||||||| |||||||||||| ||||||| ||||||||||||
Db 4981  ACCACATTGTTGACGAACTGTTGGTGCCTAGGGTTGGTGCCGGAGGGGTATGTCCGCTGCCG 5040

Qy 5116  ATGCGGGACCCATCTTGATGTGGGGGCCTATTGCGGGGGCATGATCTATGCGTCAT 5175
         |||||||||| | ||||| || |||||||| || || |||||||| ||  |||||
Db 5041  ATGCGGGGCCGATCTTAATGTGGTGTTCGGCCTCCGCTCATCGCGGGATGAATCTTACGGACCATCTT 5100

Qy 5176  ACACCGGGTCTCTCGTTGGTGGTGTTTACAGACTGGGATGTGAAGGGGTGGCAGCCCCCTTT 5235
         ||||||||||| |||||||||||||||||||||| ||||||||||||| |||||||||| ||
Db 5101  ACACCGGGTCTTGTTTAGTGGTGGTGACAGACTGGGATGTAAAGGGGGGGCAGCCGGCCCTTT 5160

Qy 5236  ATCGGCATGGAGGACCAGGCCACGCGCCCAGCCAGCCGGTTGTGCAGGTCCCCGGTAGACCATC 5295
         |||||||||||| ||||||||||||||||||||||||||| |||||||||| ||||| |||||
Db 5161  ATCGGCATGGAGGACCAGGCCACGCGCCACGCCAGCCGGTTGTGCAGGTCCCCGGTAGACCATC 5220
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Db 5161  ATCGGCATGGAGGACCAGGCCACGCGCCACGCCAGCCGGTTGTGCAGGTCCCCGGTAGACCATC 5220

Qy 5296  GGCCGGGGGAGAGTCTGCCATCGATGCCGCCATCGGATGCCAAGACAGTGACGATGGGGCCA 5355
         |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db 5221  GGCCGGGGGAGAGTCTGCCATCGATGCCGCCATCGGATGCCAAGACAGTGACGATGGGGCCA 5280

Qy 5356  TCCAGGTGGATTGCGATTGGTCAGTCATGCAGCCTGTCGATGCCCTGTGCTGCGGGGAGTGTCCTTGG 5415
         |||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||
Db 5281  TCCAGGTGGATTGCGATTGGTCAGTCATGCAGCCTGTCGATGCCCTGTCGGCGGAAGTGTCCTTGG 5340

Qy 5416  CCCAGGCTAAGACGGCCGAGGCCTACGCAGCTACGCCAAGTGGCTTGCTCGGCTGCTACA 5475
         || |||||||||||||||||| |  |||| |||||||||| |||||| ||||||||||||
Db 5341  CTCAGGCTAAAACAGTGAGGCCCAACCGCCAAGTGGCTCGCGGGTCGGCTGGCTGCTACA 5400

Qy 5476  CGGGACGGCGGCGGCCGTTCCCCACCTTCAATTGTGTGTTCAAATTGTTGACAAAGCTCTTCGCGGC 5535
         ||||||| ||||||||| ||  || || ||||| | |||||| || |||||||||||||  |
Db 5401  CGGGGAGTCGCCGGCGCCGTTCCCCACCTCTTTGCCGGAGGTCTTTGACAAGCTCTTTGGGCGGC 5460

Qy 5536  CGGCGGTGTAGGCCATTGCCACAGTGTAATAGCTGCGCGGCCGTATGGGGGCTT 5595
         ||||| || |||||| || | |||| ||||| | | ||||| |||||||||||
Db 5461  CGGCTGTGTTGGCCACTGTCACAGCGCATAGTCGGGCCGTGCCGGGGGCTT 5520

Qy 5596  CTAGGAGCCCTCCATTGGCTGCTCCGCTTCCTACCTCATGGGGTTGGGGCGTCGGAGGCA 5655
         | ||||||| || || ||||||||||||||| |||| || ||||| ||||| |||||||
Db 5521  CCAGGAGTCGCCGGCCGCGGCCGTTCCTACCTGATGGGGACTGGGGGTCGGAGGCA 5580

Qy 5656  ACGGCCAAACCCGCTTAGCCTCCTCCGCTCGGGACCGGCCGCTCTGGGCA 5715
         ||| || || || || || || ||||| || || ||| |||| ||||||
Db 5581  ACGCTCAGACGCGTTTGGCGGTCTGTTTGGGCCGGTGGCCGCTGGGCACCCCTGGGCA 5640

Qy 5716  CGCCTGTCTGGGTTAACCAGTACCATGCGGGGCCGTTCATGGGGAAGTGCTAGGTCTCCCCT 5775
         |||| |||||||||||||||||| |||| |||||  |||||| ||||| ||||| ||||
Db 5641  CTCCCGTGTGGGTTTAACCAGTACCATGCGGGGATCCGGGTGCCTGCGGGTGCTAGGTCTCTCCCT 5700

Qy 5776  CCTTGGTCACCATTTACTGGGGCCGTGGTAGTAGCGGCGTGGTGAATGCGGCTA 5835
         ||||| ||||||| || ||||||||| |||||| ||| | ||| ||||||||||
Db 5701  CCTTGGTCACCATCTGTTGGGGTACGGTGGTACTGTTGTCGTTCAACGCTGCTA 5760

Qy 5836  GCCTTGTCTTCGACTTTATGGCGGGAAACTATCATCAGAAGATCTGTGTATGCCATCC 5895
         ||||||||||||||||||||||||||||||||||||||| ||||| | ||| |||||
Db 5761  GCCTTGTCTTTGACTTCATGGCGGGAAACTATCATCAGAAGATCTGTGTACGCCATCC 5820

Qy 5896  CAGTGCTAACCAGTCCGGGGATCCGCCCTGCGGGGGATGCCCTGGTGGTGTTGTTACT 5955
         ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db 5821  CAGTGCTAACCAGTCCGGGGATCCGCCGGGGGGATGCCCTGGTGGTGTTGGTGTGTACT 5880

Qy 5956  CAGCTAACAACTCTGGCACTACCACTTGGTTGAACCTGTTGACTACCATTGCCCAAGGT 6015
         |||||||||||||| |||||||||||||| ||||| ||| |||||| |||||||||||
Db 5881  CAGCTAACAACTCTGTGGTACTACCACTTGGTTGAACCTGTTGCTGCTGACTTACCTAGT 5940

Qy 6016  CCTCATGCATCCCTCGACAGTTACTTCAGCAGGACCAGGCCCGATTACTGACAAGGTCAGCTG 6075
         ||||| ||  |||  ||||||||||||| ||||||||||||||||||||||| |||||||||
Db 5941  CTTCTTGATCTCGACAGCTATTTCCAACAGGCCCGATTACTGTGACAAGGTCAGCGCCG 6000

Qy 6076  TGCTCCGACGCTTGAGCCTGACTGCCATCCGGCGTTGCCCTGGTTGCCCAACAGGGAGCCTAAGG 6135
         |||| | |||||| |||| ||| ||||||| ||||||||||| || ||||||||| |||||||||
Db 6001  TGCTTCGCACTGTCGAGCTGTCTCCAGCCGTGGTTGCCCTAGTTGGTGCCCTAGTCAATAGGAACCCAAGG 6060

Qy 6136  TGATGAGGTTCAGTGGGTACGTCTGTGGGAGTTGTGATCATGCTCAAGTGC 6195
         |||| || || ||||||| |||| ||||| || ||||||||||||||||||
Db 6061  TGGACGAGGTACAGGTGGGTACGTCTCTGGGATCTCTGGGAGTTCTCAGCTGGATCATGCTTCGTTACGTAGGT 6120

Qy 6196  GCATGGTGATGGCCAGACTTCGGGCGCTCATTACCCTTATGGCCACT 6255
         || |||||| ||||||||||||| | ||| || || |||||||||||
Db 6121  GCATGGTCATGGCCAGGCTCCGGGGGCATGATCTATTCACTGCTCCTTTGTGGCACT 6180

Qy 6256  GCGGGGAGGGGTGTCCGGAGAATGGTTGTGTTGACACGGGTGGCCATGTTCAACAGGGAGCAGCTAAGG 6315
         ||||| ||||| ||| ||||||||||||| |||||||| |  ||||||||||||||||||||| ||||
Db 6181  GCGGGGAGGGGTGTCCGGAGAGTGGTTGTGTTGACACGGGTGGCCATGTTCAATAGGAGAGTCGCTGTCTTT 6240

Qy 6316  GTGTTGCGTGATCACCGTGATGTTTCAATGGGCAACTCAAAGATCCAGTTTACTCTA 6375
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 6241  GCGGGTGCCTGATCACCGCGATGTTTCAATGGGCAACTCAAAGAGCCCAGTTTACTCTA 6300
```

Qy 7456 TGAGGCCGGTTGGCTCCTTGCTCGGTGGCCGACACCACCAAGGTGTATGTCACCAACCCGG 7515
        ||||||||||||||| |||||| | ||||||| |||||| ||||||||||||||||||||||
Db 7381 TGAGGCCGGTGGGGGCCCTTGTTGGTGGCCGACACCACGAAAGTGTATGTCACAAACCCGG 7440

Qy 7516 ACAATGTTGGGAGAAGAGTTGACAAGGTTACCTTCTGGCGTCGCCCCCAGGGTTCATGACA 7575
        ||||||||||||||||||||||||||||||| ||||||||| |||||||||| ||||||||
Db 7441 ACAATGTGGGAGAAGAGTGGACAAGGTGCAAGGTCACTTCTCGGCGCGCCCCCAGGTCCATGACA 7500

Qy 7576 AATTCCTCGTGGACTCCATAGAGCGCGCTAAGAGGCAGCTCAAGGCTGCCTAAGCATGG 7635
        || |||||||||||| || || | || || |||||||||| | |||| ||||||||
Db 7501 AATATCTCGTGGACTCCATCGAGCGTGCCAAGAGGCGGCTCAAAGCATGG 7560

Qy 7636 GTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCAATGCTGCCATGGGCTGGGGAT 7695
        ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db 7561 GTTACACTTATGAGGAGGCAATAAGGACTGTGTAGGCCACATGCTGCCATGGGCTGGGGAT 7620

Qy 7696 CTAAGGTGTCGGTCAAGGACCTCGGCACCCCTGCGGGGAAGATGGCTGTCCATGACCGGC 7755
        ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db 7621 CTAAGGTGTCGGTCAAGGACCTCGGCACCCCTGCGGGGAAGATGGCCGTCCACGACCGAC 7680

Qy 7756 TCCAGGAGATACTTGAAGGGACGCCAGTCCCCTTTACTCTTACTGTGAAAAAGGAAGTGT 7815
        |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db 7681 TTCAGGAGATACTTGAGGGGACTCCGGTCCCTTTTACTCTTACTGTGAAAAAGGAGGTGT 7740

Qy 7816 TCTTCAAAGACCGAAAGGAAGAAGAGAGGCCCCCCGCCCTCATTGTGTTCCCCCCCTGGACT 7875
        ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db 7741 TCTTCAAAGACCGTAAGGAGGAGGAGAGGCCCCCCGCCCTCATTGTGTTCCCCCCCTGGACT 7800

Qy 7876 TCCGGATAGCTGAAAAGCTTATTCTGGAGACCCTGGACGGGTAGCCAAGGCGGTGTTGG 7935
        |||||| |||||||||||| || |||||||||||||||||||||||||||||||||||||
Db 7801 TCCGGATAGCTGAGAAGCTTATCCTGGAGACCCGGGGCCGGTGGCCAAGGCGGTGTTGG 7860

Qy 7936 GGGGGCCTACGGCCTTCCAGTACACCCAAATCAGCGAATTAGGAGGATGCTCAAACTGT 7995
        | |||||||||||||| ||||||||||||||||| | |||||||||||| |||||||||||
Db 7861 GGGGGCCTACGGCCTTCCAGTACACCCAAATCAGCGAGTTAAGGAGGATGCTCAAACTGT 7920

Qy 7996 GGGAATCAAAGAAGACACCATGCCCATCTGTGTGGACGCCACATGCTTCGACAGTAGCA 8055
        | || || ||||||||||||||||||||||||||||||||| |||||||||||||||||
Db 7921 GGGAGTCAAAGAAGAAAAAACACCTTGCCCATCTGTGTGGACGCCACTTGCTTCGACAGTAGCA 7980

Qy 8056 TAACTGAAGAGGACGTGGCCCTGGGGAAATACTATGCCTCTGGCACAATGTAACCCCGAGGGGG 8115
        | |||||||||||| |||| | || ||| | ||| || || ||| | |||||||||||||
Db 7981 TTACTGAAGAGGACGTGGCGCTGGGGAAGTAGTACTATGCCTCAGGCGTTTGACTACCAGCGAGTAACT 8040

Qy 8116 AATGGGTGCGTGGCCCTGGGAGAGTACCTGTGAGAGGGTAACCCCGAGGGGG 8175
        ||| ||||||||||||||||||||||||||| ||||||||||||||||||||
Db 8041 AGTGGGTGCCGAGCTTTGGGAAGTACTATGCCTCAGGCGTTTTGACTACCAGCGAGTAACT 8100

Qy 8176 TGCCAGTGGGTGAGAGGTATTGTAGATCCTCAGGGGTCTTGACCAGTGCGAGCAACT 8235
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Db 8101 TTCCCGTAGTGGAGAGTATTGTAGATCCTCAGGCGTTTGACTACCAGCGAGTAACT 8160

Qy 8236 GCTTGACTTGCTATATCAAGGTGAAAGCCGGCCTGTGAGAGGTGGGCTGAAAAATGTCT 8295
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Db 8161 GCCTGACCTGCTACATCAAGGTGAAAGCCGGCCTGTGTGAGAGTGGGGCTGAAAAATGTCT 8220

Qy 8296 CGCTCCTCACATGCCTGCGATGACTGTTGATCATATGCGAACAGCGTGTGCGATCCTA 8355
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Qy 8356 GCGACCGCTTGGGCACGAGCGCCCCCTTCTGCTCCACTTGGGTTACGGCGTACGCATGCGTATCATG 8415
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Qy 6376 CCAAGCTGTGCAGGCATTATTGATGGGGACAGTCCCTGTGACACATGCTGGGCTATGGCG 6435
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Qy 6436 AGACGTCGGCCTTGCTCGCCTCAGACACCCGAGGTGTACCATTCGGGACGTCTGGGT 6495
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Qy 6496 GGCTGAGGTGGTGGTGACCCCTACCCACGTTGTGATCAGGCGGAACATCCGCCTACAAAC 6555
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Qy 6556 TGCTGCGCCAGCAAATCCTGTCGGCTGCTGTTGCTGACCCTATTACGTCGACGGCATAC 6615
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Db    8461 ATAGTGACCCAATGGCTTCGGCCATAGTTACATCCTCCTGTATCCCTGGCATCCCATCA 8520
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Qy    8596 CACGGTGGGTCATCATCCTCACGTGCTCACCTGCGCGTTAGGGGTGGTGGCACACCGT 8655
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Qy    8656 CTGATCCTGTGTGCGTGCCAGGTACATGGTAATTACTACAAGTTTCCACTGGACAAACTGC 8715
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                GenCore version 5.1.3
        Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October 8, 2002, 23:11:25 ; Search time 10915 Seconds
                                       (without alignments)
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Title:          US-09-828-498-1
Perfect score:  9395
Sequence:       1 tgacgtggggggttgatcc.........cccaaaggccgggttctact 9395

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1797656 seqs, 1046326293 residues

Total number of hits satisfying chosen parameters:     3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    GenEmbl:*
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       31: em_htg_inv:*
       32: em_htg_other:*
       33: em_htgo_inv:*

                    SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result
 No.   Score  Match Length DB ID                          Description
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No.		Score	Length		DB ID	Pred.No.	Description
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2	9395	100.0	9395	AF121950	14	AF121950 Hepatitis
3	8106.4	86.3	9375	D87255	14	D87255 Hepatitis G
4	8100.6	86.2	9395	E14141	14	E14141 Genomic seq
5	8100.6	86.2	9395	D90600	14	D90600 Hepatitis G
6	8080.6	86.0	9373	AF081782	14	AF081782 Hepatitis
7	8018	85.3	9292	AF309966	14	AF309966 Hepatitis
8	7979	84.9	9392	AR026694	6	AR026694 Sequence
9	7979	84.9	9392	AR049120	6	AR049120 Sequence
10	7979	84.9	9392	AR065378	6	AR065378 Sequence
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12	7936.8	84.5	9351	AF031827	14	AF031827 Hepatitis
13	7936.8	84.5	9351	AF031828	14	AF031828 Hepatitis
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18	7760.6	82.6	9103	AR026828	6	AR026828 Sequence
19	7760.6	82.6	9103	AR049254	6	AR049254 Sequence
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21	7760.6	82.6	9103	HGU45966	14	U45966 Hepatitis G
22	7718.2	82.2	9367	HGU63715	14	U63715 Hepatitis G
23	7598.4	80.9	9056	AF104403	14	AF104403 Hepatitis
24	7560.8	80.5	8953	AB003289	14	AB003289 Hepatitis
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38	7398	78.7	9391	D87262	14	D87262 Hepatitis G
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                                ALIGNMENTS

RESULT 1
AX338086
LOCUS       AX338086              9395 bp    DNA        linear   PAT 09-JAN-2002
DEFINITION  Sequence 1 from Patent WO0177157.
ACCESSION   AX338086
VERSION     AX338086.1  GI:18128718
KEYWORDS    .
SOURCE      Hepatitis G virus.
  ORGANISM  Hepatitis G virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            GBV-C/HGV group.
REFERENCE   1  (sites)
  AUTHORS   Xiang,J., Wuenschmann,S., Schmidt,W. and Stapleton,J.T.
  TITLE     Full-length GB virus C (hepatitis G virus) RNA transcripts are
            infectious in primary cd4 positive T cells and methods of treating
            HIV
  JOURNAL   Patent: WO 0177157-A 1 18-OCT-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1..9395
                     /organism="Hepatitis G virus"
                     /db_xref="taxon:45255"
BASE COUNT     1707 a   2557 c   3004 g   2127 t
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ORIGIN

Query Match   100.0%;   Score 9395;   DB 6;   Length 9395;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 9395;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Db      1 TGACGTGGGGGGGTTGATCCCCCCGCCACTGGCTGCAAGCCCATAAACCGACGC 60

Qy     61 CTATCTAAGTAGACGCAATGACTCGGCGCGACTCGGCGACCGGCAAAAGTGGTGAT 120
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Db     61 CTATCTAAGTAGACGCAATGACTCGGCGCGACTCGGCGACCGGCAAAAGTGGTGAT 120

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Db    841 ACGTAGCCGGGATCCTGGGTCTGGGCGAGGTTTACTCCCGGGTCCTGGGTGTGTTG 900

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GGGAGAGGGGTGTGGGATCGAGGGAATGTCACGCTCTTGTGACTGCCCAACGGCCCCT 1320

Qy   1321 GGGTTTGGGTCCCGGCCTTTTGCCAGGCGGTTGGTGGGGGCGACCCCATCACCCATTGGA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGGTTTGGGTCCCGGCCTTTTGCCAGGCGGTTGGTGGGGGCGACCCCATCACCCATTGGA 1380

Qy   1381 GCCACGGACAAAACCAGTGCCCCCTATCATGCCCCAATATGTCTTATGGGTCTGTGTCCG 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCCACGGACAAAACCAGTGCCCCCTATCATGCCCCAATATGTCTTATGGGTCTGTGTCCG 1440

Qy   1441 TAACGTGCGTGTGGGTTCCGTCGTCTTGGTTGCCTCGACCGGCGTCGTGATTCGAAGA 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TAACGTGCGTGTGGGTTCCGTCGTCTTGGTTGCCTCGACCGGCGTCGTGATTCGAAGA 1500

Qy   1501 TCGATGTGTGGAGTTTGGTGCCGGTTGGATCTGGCCAGCTGCACCATAGCCGCTCTAGGGT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TCGATGTGTGGAGTTTGGTGCCGGTTGGATCTGGCCAGCTGCACCATAGCCGCTCTAGGGT 1560

Qy   1561 CATCGGATCGGCACACGGTGTTGAGCGTCTCCGAGTGGGAGTCCCGTCGTAACGTGTA 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CATCGGATCGGCACACGGTGTTGAGCGTCTCCGAGTGGGAGTCCCGTCGTAACGTGTA 1620

Qy   1621 TTCTGCACCGTCGGCCTGCTTCATGTGGCACCTGTGTGCGGACTGCTGGCCGCGAAACCG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TTCTGCACCGTCGGCCTGCTTCATGTGGCACCTGTGTGCGGACTGCTGGCCGCGAAACCG 1680

Qy   1681 GGTCGGTTAGATTCCCTTCCATCGGTGCGCACGGGCTTCGGCTGACAAAGGACTTGG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGTCGGTTAGATTCCCTTCCATCGGTGCGCACGGGCTTCGGCTGACAAAGGACTTGG 1740

Qy   1741 AAGCTGTGCCCTTGCTCAACAGGACAACTCCCTTCACCAGGGCCCCTGGGCAACC 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AAGCTGTGCCCTTGCTCAACAGGACAACTCCCTTCACCAGGGCCCCTGGGCAACC 1800

Qy   1801 AGGGGAGGGAGCCAACCGGTGCGGTCGCGTGCGTCCCACCGGTTTTGGGTCCTACACCAAGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AGGGGAGGGAGCCAACCGGTGCGGTCGCGTGCGTCCCACCGGTTTTGGGTCCTACACCAAGA 1860

Qy   1861 TCCGGGAATTCCCTGCATTTGGTGAAATGTCCACACACGGCCTCCGACTGGAA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TCCGGGAATTCCCTGCATTTGGTGAAATGTCCACACACGGCCTCCGACTGGAA 1920

Qy   1921 CGTTCGGTTCTTCCCCGGAGTCCCCGCCATTAACAACTCCATGCCACGGAAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CGTTCGGTTCTTCCCCGGAGTCCCCGCCATTAACAACTCCATGCCACGGAAG 1980

Qy   1981 TGTCTGAGGCATTGGGCGGAGCTGGGCTTACGGGGTTCTACGAGCCTCGGTTCGCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGTCTGAGGCATTGGGCGGAGCTGGGCTTACGGGGTTCTACGAGCCTCGGTTCGCA 2040

Qy   2041 GGTGTTCGGAGCTGATGGGACGCCCGAAATCCGGTTTGCCCCGGGGGTACGCGGCTGTCCT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GGTGTTCGGAGCTGATGGGACGCCCGAAATCCGGTTTGCCCCGGGGGTACGCGGCTGTCCT 2100
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Qy  2101 CTGGTAGACCTGACGGGTTCATACACGTTCAGGGGCACCTGCAGGGGTGGATGCGGGCA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CTGGTAGACCTGACGGGTTCATACACGTTCAGGGGCACCTGCAGGGGTGGATGCGGGCA 2160

Qy  2161 ACTTCATCCTCCTCCCACGCTGGTTGCTCTTGGATTTGTATTTGTCCTGCTCTATCTGA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 ACTTCATCCTCCTCCCACGCTGGTTGCTCTTGGATTTGTATTTGTCCTGCTCTATCTGA 2220

Qy  2221 TGAAGCTGCTGAGGCACGGTTGTCCCGTTGGTCTGCTTCGTCGTGTTGGTGTGGTGGTGA 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 TGAAGCTGCTGAGGCACGGTTGTCCCGTTGATCTGCTTCGTCGTGTTGGTGTGGTGGTGA 2280

Qy  2281 ACCAGTTGGCGGTTCTAGGACTGCCGGCGTGGACGCTGCCGTGGCGGTGAAGTTTTTG 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 ACCAGTTGGCGGTTCTAGGACTGCCGGCGTGGACGCTGCCGTGGCGGTGAAGTTTTTG 2340

Qy  2341 CGGGCCCTGCCTTGTCATGGTGTTTCGGTGGATGGGCCTTCCCACTGTCCTCGTGTGT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CGGGCCCTGCCTTGTCATGTGTTTCGGTGGATGGGCCTTCCCACTGTCCTCGTGTGT 2400

Qy  2401 CAAACCTGGTGTTGTACTTTCGGTGGAAGCACAAGGCCTGATCTATAGGACCGTGGTTGT 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 CAAACCTGGTGTTGTACTTTCGGTGGAAGCACAAGGCCTGATCTATAGGACCGTGGTTGT 2460

Qy  2461 GGAAGCTCGCTCGTGTCGCGGGCCAGTTCTGCTTCGATGTCACATTCGAGGTGACACTT 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 GGAAGCTCGCTCGTGTCGCGGGCCAGTTCTGCTTCGATGTCACATTCGAGGTGACACTT 2520

Qy  2521 GGGCCACTTCTGTCGCTGGTGGCTGGCCAGCGTGGTGGCCAGCGTGGTGCCATAGCGTC 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 GGGCCACTTCTGTCGCTGGTGGCTGGCCAGCGTGGTGGCCAGCGTGGTGCCATAGCGTC 2580

Qy  2581 CGGTGTTGGGCTGGCTGGCCAGCGTGGTGCCCATAGCGTCTCCAGCTCAA 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CGGTGTTGGGCTGGCTGGCCAGCGTGGTGCCCATAGCGTCTCCAGCTCAA 2640

Qy  2641 TGAGCGCAGGGGGTGGAAGCACCAAGGCCCTGATCTATAGGACCGTGGTCTAAAGGGTACC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 TGAGCGCAGGGGGTGGAAGCACCAAGGCCCTGATCTATAGGACCGTGGTCTAAAGGGTACC 2700

Qy  2701 AGGCCTTGTCCGCCGCCTCTGTCGCGGAGCCCCTCGGGGAGGGGCGTCCTACCAAGCTTC 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 AGGCCTTGTCCGCCGCCTCTGTCGCGGAGCCCCTCGGGGAGGGGCGTCCTACCAAGCTTC 2760

Qy  2761 TGACGTTCGGCCTGGCTGGTCCGTCATACATCTGGCCCGATGCTGTGATGAGTGGTGGTGG 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TGACGTTCGGCCTGGCTGGTCCGTCATACATCTGGCCCGATGCTGTGATGAGTGGTGGTGG 2820

Qy  2821 TGGCCTTGTCTCCTCTCGGCCGTGTTCGACGCACTGGCGCCAAGAGAGGGGCCTACCTGT 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 TGGCCTTGTCTCCTCTCGGCCGTGTTCGACGCACTGGCGCCAAGAGAGGGGCCTACCTGT 2880

Qy  2881 TGTCTCCCGGCCCTCGTTACGGCCACTGGCACGGGTCGGTGTTGTTGATGGGCGG 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TGTCTCCCGGCCCTCGTTACGGCCACTGGCACGGGTCGGTGTTGTTGATGGGCGG 2940

Qy  2941 GCGAGAAGGCCACCACCATCGGTCTCTTCTTCCGCCGCCTGGTCTCCAAGAGAGGGGCCTACCTGT 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 GCGAGAAGGCCACCACCATCGGTCTCTTCTTCCGCCGCCTGGTCTCCAAGAGAGGGGCCTACCTGT 3000

Qy  3001 TTGACCACATGGGCCTTGTTGTTGGAATGGGACGCGCGG 3060
         ||||||||||||||||||||||||||||||||||||||
Db  3001 CTTTGGAGCCCCTGTCATTGTCATCACATCAGAGATGCCGCGAGGA 3120

Qy  3061 CTTTGGAGCCCCTGTCATTGTCATCACATCAGAGATGCCGCGAGGA 3120
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 CTTTGGAGCCCCTGTCATTGTCATCACATCAGAGATGCCGCGAGGA 3120

Qy  3121 CCCTGTCCTGCCGGACAGTGCTGCGTCATGGTTACCGTGTAGCACGGGCCGGTGATGAGG 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 CCCTGTCCTGCCGGACAGTGCTGCGTCATGGTTACCGTGTAGCACGGGCCGGTGATGAGG 3180

Qy  3181 TTCTCATCGGCGTCTTTCAGGATGTGAATCATTTGCCTCCCGGGTTGTCCCGACTGCAC 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 TTCTCATCGGCGTCTTTCAGGATGTGAATCATTTGCCTCCCGGGTTGTCCCGACTGCAC 3240

Qy       CTGGTAGACCTGACGGGTTCATACACGTTCAGGGGCACCTGCAGGGGTGGATGCGGGCAC 3240

Db  3241 CAGTTGTCATCCGTCGGTGCGGAAAGGGCTTCCTGGGGTCACGAAGGCAGCCTTGACAG 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3241 CAGTTGTCATCCGTCGGTGCGGAAAGGGCTTCCTGGGGTCACGAAGGCAGCCTTGACAG 3300

Db  3301 GTAGGGATCCTGACTTACATCCAGGGAACGTCATGTGTTGGGGACGGCTACGTCACGAA 3360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3301 GTAGGGATCCTGACTTACATCCAGGGAACGTCATGTGTTGGGGACGGCTACGTCACGAA 3360

Db  3361 GCATGGGCACAATGTCTGAATGGCCTTGCTGTGTTCACAACTTCCATGGGCTTCATCCCGAA 3420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3361 GCATGGGCACAATGTCTGAATGGCCTTGCTGTGTTCACAACTTCCATGGGCTTCATCCCGAA 3420

Db  3421 CCATGCCACGCCCGTGGGGCCCTAATCCCAGGTGTGTCAGCCAGTGATGACGTCA 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3421 CCATGCCACGCCCGTGGGGCCCTAATCCCAGGTGTGTCAGCCAGTGATGACGTCA 3480

Db  3481 CGGTGTACCCGCTTCGTTGCGCACTTCGTTGCGCACTTGCCAGGCGCAGGGGACAAGG 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3481 CGGTGTACCCGCTTCCAGATGGGCAACTTCGTTGCGCACTTGCCAGGCGCAGGGGACAAGG 3540

Db  3541 CCTGTTGGGTTATTAGATCCGACGGGCGTTTGTGCCATGGCTTCGTCTCCGTCTCCGGTCCTA 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3541 CCTGTTGGGTTATTAGATCCGACGGGCGTTTGTGCCATGGCTTCGTCTCCGTCTCCGGTCCTA 3600

Db  3601 TTGAGCTGGATGTGGCCATGAGTTCGTCTCGTCTGGTCGTGTTCGTCTGGTCACCGGTCC 3660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3601 TTGAGCTGGATGTGGCCATGAGTTCGTCTCGTCTGGTCGTGTTCGTCTGGTCACCGGTCC 3660

Db  3661 TTTGCCACAAAGGGCACGCAGTAAGAATGCTCGTCGTCGTCAGTGCTCGTCTGGCGGCAGGG 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3661 TTTGCCACAAAGGGCACGCAGTAAGAATGCTCGTCGTCGTCAGTGCTCGTCTGGCGGCAGGG 3720

Db  3721 TTACTGCGGCCGGCGATTCACTTCAGTCACTGGCCCGTGGACTCAAGACTACCAACAGATGCCAAGACTACCA 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3721 TTACTGCGGCCGGCGATTCACTTCAGTCACTGGCCCGTGGACTCAAGACTACCAACAGATGCCAAGACTACCA 3780

Db  3781 CAGAACCCCCTCCGGTCGCCGGCAAAAGAGTTTCAAGGAGGCCCCCGTTGTTTATGCCTA 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3781 CAGAACCCCCTCCGGTCGCCGGCAAAAGAGTTTCAAGGAGGCCCCCGTTGTTTATGCCTA 3840

Db  3841 CGGGGCGGGAAAGAGCACCCCGCTACCCGTACCGCGTACCGGCCAACATGGGCCACAAGGTCT 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3841 CGGGGCGGGAAAGAGCACCCCGCTACCCGTACCGCGTACCGGCCAACATGGGCCACAAGGTCT 3900

Db  3901 TGATCTTGAACCCGTCGGTAGCTACCGTGAGGGCCATCACATGGGCCGGCGCTGG 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3901 TGATCTTGAACCCGTCGGTAGCTACCGTGAGGGCCATCACATGGGCCGGCGCTGG 3960

Db  3961 CGGGGAAACACCCCAGTATTACTGTGGCCATGAACACCACCACTGCTTTCACAAGGATCACTG 4020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3961 CGGGGAAACACCCCAGTATTACTGTGGCCATGAACACCACCACTGCTTTCACAAGGATCACTG 4020

Db  4021 ACTCGCCCCTTACGTATTCCACTTACGGAAGGTTTTTGGGCCAACCCTAGGCAGAGATGCTGTGA 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4021 ACTCGCCCCTTACGTATTCCACTTACGGAAGGTTTTTGGGCCAACCCTAGGCAGAGATGCTGTGA 4080

Db  4081 GGGGTGTCGGTCGGTGGTCATTTGTGACGTGGTCCAGTCAACTCGTTGTTGG 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4081 GGGGTGTCGGTCGGTGGTCATTTGTGACGTGGTCCAGTCAACTGTTGTTGG 4140

Db  4141 GCATTGGGCGTGTCAGGGAGCTGGCCGAGGATGTGAGTGCAATTGGGTGCTCTACGCCA 4200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4141 GCATTGGGCGTGTCAGGGAGCTGGCCGAGGATGTGAGTGCAATTGGGTGCTCTACGCCA 4200

Db  4201 CTGCCACCCCCCGGATCCCGATCCCCGGATCCCGATGACCCCAGCACCACCATCAATCATTGAGACAAAACTGG 4260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4201 CTGCCACCCCTCTATGGGCATGCCATCCTTCTTGAGCCGATGCGGATCGGACCGGAA 4260

Db  4261 AGTGGAGAGATCCCCTTCTATGGGCATGCCATCCTTCTTGAGCCGATGCGGATCGGACCGGAA 4320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  4261  ACGTGGGAGAGATCCCTTCTATGGGCATGGCGGATGCGGGACCGGAA  4320
          |||||||||||||||||||||||||||||||||||||||||||||||
Qy  4321  GGCATCGCTGTATTCTGCCACTCCAAGGCTGAGTGGCGGCCTGGCGGCCCAGTTTTCGG  4380
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  4381  GGCATCTCGTATTCTGCCACTCCAAGGCTGAGTGGCGGCCTGGCGGCCCAGTTTTCGG  4380

Qy  4381  CTAGGGGGTAAATGCCATCGCCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATG  4440
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4381  CTAGGGGGTAAATGCCATCGCCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATG  4440

Qy  4441  GAGACCTGGTGTGTGTGTGCCTACAGAGACGCACTATCCACTGGGTACACTGGGAACTTCGATT  4500
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4441  GAGACCTGGTGTGTGTGTGCCTACAGAGACGCACTATCCACTGGGTACACTGGGAACTTCGATT  4500

Qy  4501  CTGTCACCGATTGTGGGTTAGTCGTGGTGGTGGAGGAGTCGTCGAGGTGTGATCCCACCA  4560
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4501  CTGTCACCGATTGTGGGTTAGTCGTGGTGGTGGAGGAGTCGTCGAGGTGTGATCCCACCA  4560

Qy  4561  TTACCATCTCCCTGCGACACGTGCCCGCGTGCTGCGGCTGCGAACTGTCGATGGGGCGAGGAC  4620
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4561  TTACCATCTCCCTGCGACACGTGCCCGCGTGCTGCGGCTGCGAACTGTCGATGGGGCGAGGAC  4620

Qy  4621  GCACGGGTAGGGCAGGTCTGGGCGCTACTACGCGGGGTCGGCCAAGGCCCCTGCTG  4680
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4621  GCACGGGTAGGGCAGGTCTGGGCGCTACTACGCGGGGTCGGCCAAGGCCCCTGCTG  4680

Qy  4681  GTGTGGTGGCGCTCAGTCCTGTGCTGTGGTCGGCCGGTGTGTACCGGTGGTACGGAA  4740
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4681  GTGTGGTGGCGCTCAGTCCTGTGCTGTGGTCGGCCGGTGTGTACCGGTGGTACGGAA  4740

Qy  4741  TGGAACCTGACAGCAAAACTACTGAGACTTTACGACAACTGCCCTTACACCGCAG  4800
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4741  TGGAACCTGACAGCAAAACTACTGAGACTTTACGACAACTGCCCTTACACCGCAG  4800

Qy  4801  CCGGTCGCAGCTGACATTGGGAAGCCGCGGTGTTCTTTCGGGCGTTGCCCCGTTGAGGA  4860
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4801  CCGGTCGCAGCTGACATTGGGAAGCCGCGGTGTTCTTTCGGGCGTTGCCCCGTTGAGGA  4860

Qy  4861  TGCATCCCGATGTTAGCTGGGCCAAAAGTTCGCGGCGCTCAACTGGGGCTCCTTCCTGGGTG  4920
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4861  TGCATCCCGATGTTAGCTGGGCCAAAAGTTCGCGGCGCTCAACTGGGGCTCCTTCCTGGGTG  4920

Qy  4921  TTCAGCGGACCATGTGCCGGGAAACACTGTCTCCCGGCGATGTGGGGGGCA  4980
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4921  TTCAGCGGACCATGTGCCGGGAAACACTGTCTCCCGGCGATGTGGGGGGCA  4980

Qy  4981  CAGGTCTGAAGGCCCGAATCCGTCCACTCCTGCTGAGGTGGGCAATGATTTACCAT  5040
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4981  CAGGTCTGAAGGCCCGAATCCGTCCACTCCTGCTGAGGTGGGCAATGATTTACCAT  5040

Qy  5041  CTAAAGTGGCGCGGCCCATCACATCGTGGACGACCGGTCGGACGACCGGGGCGGAGG  5100
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5041  CTAAAGTGGCAGCCCCATCACATCGTGGACGACCGGTCGGACGACCGGGGCGGAGG  5100

Qy  5101  GTTACGTCCGCTCGCGATGCGGGGACCGGTCGGCCTCGCTATGTGCGGGGGCA  5160
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5101  GTTACGTCCGCTCGCGATGCGGGGACCGGTCGGCCTCGCTATTGCGGGGGCA  5160

Qy  5161  TGATCTATGCGTCATACACCGGTCTCTCGCACTCGTCCGGTGGTTACAGACTGGGATGTGAAGGGGTG  5220
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5161  TGATCTATGCGTCATACACCGGTCTCTCGCACTCGTCCGGTGGTTACAGACTGGGATGTGAAGGGGTG  5220

Qy  5221  GTGGCAGCGCCCCTTTATCGGCGGCATGCGGGGGAGTCGCCGGCCAACAGTGACAG  5280
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5221  GTGGCAGCGCCCCTTTATCGGCGGCATGCGGGGGAGTCGCCGGCCAACAGTGACAG  5280

Qy  5281  CCCCGGTAGACCATCGGCCGGGGGAGTCGCCGCCGCCATCGGATCGGATCGGACAG  5340
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5281  CCCCGGTAGACCATCGGCCGGGGGAGTCGCCGCCGCCATCGGATCGGATCGGACAG  5340

Qy  5341  ATGCGGTGGCCGCCATCCAGTGATTGCGGATTGGTCATGCTATGGTCGCATGACCCGTCATGACCCGTCGGGG  5400
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5341  ATGCGGTGGCCGCCATCCAGTGATTGCGGATTGGTCATGCTATGGTCGCATGACCCGTCATGACCCGTCGGGG  5400
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Qy  5401  AAGTGTGTCTTGGCCCAGGCTAAGACGGCCTACGCAGCAGTTACCACCAAGTGGC  5460
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5401  AAGTGTGTCTTGGCCCAGGCTAAGACGGCCTACGCAGCAGTTACCACCAAGTGGC  5460

Qy  5461  TTGCTGGCTGCTACACGGGCGGCGCGGGGCGGGGCCGTCCCCGCTGTTCAATTGTTGACAAGCTCT  5520
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5461  TTGCTGGCTGCTACACGGGCGGCGCGGGGCGGGGCCGTCCCCGCTGTTCAATTGTTGACAAGCTCT  5520

Qy  5521  TCGCCGGGGCGTGGGCGGCGGGGCGGTAGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGG  5580
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5521  TCGCCGGGGCGTGGGCGGCGGGGCGGTAGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGG  5580

Qy  5581  CGGCCTATGGGGCTTCTAGGAGCCCTCCATTGGCTGCTGCCGCCGTTCCTACCTCATGGGGT  5640
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5581  CGGCCTATGGGGCTTCTAGGAGCCCTCCATTGGCTGCTGCCGCCGTTCCTACCTCATGGGGGT  5640

Qy  5641  TGGGCGTCGGAGCAACGCGCAAACCCGCTTAGCCTCCGCTCCTACTAGGGGCCCGCTG  5700
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5641  TGGGCGTCGGAGCAACGCGCAAACCCGCTTAGCCTCCGCTCCTACTAGGGGCCCGCTG  5700

Qy  5701  GGACCGCTCTGGCACGCGCCTGTCGTGGGTTAACCATGGCGGCGCGTTCATGGGAAGTG  5760
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5701  GGACCGCTCTGGCACGCGCCTGTCGTGGGTTAACCATGGCGGCGCGTTCATGGGAAGTG  5760

Qy  5761  CTAGCGTCTCCCCCTCTTGGTCACCATTTTACTGGGGGCCGTGGGGGGCTGGGAGGGCG  5820
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5761  CTAGCGTCTCCCCCTCTTGGTCACCATTTTACTGGGGGCCGTGGGGGGCTGGGAGGGCG  5820

Qy  5821  TGGTGAATGCGGCTAGCGTTCTTCGGACTTTATGGCGGGGGAAACTATCATCAGAAGATC  5880
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5821  TGGTGAATGCGGCTAGCGTTCTTCGGACTTTATGGCGGGGGAAACTATCATCAGAAGATC  5880

Qy  5881  TGTGGTATGGCCATCCCAGTGCTAACCAGTCGGGGTTGCCGGGATCGCCCCTCG  5940
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5881  TGTGGTATGGCCATCCCAGTGCTAACCAGTCGGGGTTGCCGGGATCGCCCCTCG  5940

Qy  5941  GGTTGGTGTTGTACTGCAGCTAACAACTCTGGTCAGGCCGACTCTGGGACTTGTGTGGAGTTGGA  6000
          ||||||||||||||||||||||||||||||||||||||||||||
Db  5941  GGTTGGTGTTGTACTGCAGCTAACAACTCTGGTCAGGCCGACTCTGGGACTTGTGTGGAGTTGGA  6000

Qy  6001  CTACATTGCCAAGGTCTCCTGACAGTGCATCCCGACAGTTCAGCAGGCCGATTACTGTG  6060
          ||||||||||||||||||||||||||||||||||||||||||||
Db  6001  CTACATTGCCAAGGTCTCCTGACAGTGCATCCCGACAGTTCAGCAGGCCGATTACTGTG  6060

Qy  6061  ACAAGGTCAGCTGTGTCCGACGCTTGAGCCTCACTCGCGACCGTGGTTGCCCTGGTCA  6120
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Db  6061  ACAAGGTCAGCTGTGTCCGACGCTTGAGCCTCACTCGCGACCGTGGTTGCCCTGGTCA  6120

Qy  6121  ACAGGAGCCTAAGGTGGATGAGGTTCAGGTGGGTACGTCTGGGACTTGTGTGGAGTTGGA  6180
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Db  6181  TCATGCGTCAAGTGTGCCATCGCGGGGGCTCGGGGCCCTCTGCCCCGTGGTGTCAT  6240

Qy  6241  TACCCTTATGGCACTCGGGGAGGGTGGTCCGGAGAATGGTTGTTGGACGGCCATGTTG  6300
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Db  6241  TACCCTTATGGCACTCGGGGAGGGTGGTCCGGAGAATGGTTGTTGGACGGCCATGTTG  6300

Qy  6301  AGAGTCGTTGTCTTTTGGTTCGTGGTTGTGTGCGTGATCACCGGTGATGTTTTGAATGGGCAACTCAAAG  6360
          ||||||||||||||||||||||||||||||||||||||||||||
Db  6301  AGAGTCGTTGTCTTTTGGTTCGTGGTTGTGTGCGTGATGTTTTGTCGTGATTGGAATGGGCAACTCAAAG  6360

Qy  6361  ATCCAGTTTACTTCTACCAAGCTGTGACCAAGCTGTGCCAACAGTGACAGTCCCTGAACA  6420
          ||||||||||||||||||||||||||||||||||||||||||||
Db  6361  ATCCAGTTTACTTCTACCAAGCTGTGACCAAGCTGTGCCAACAGTGACAGTCCCTGAACA  6420

Qy  6421  TGCTGGGCTATGGCGAGACGTCGCCTTTGCTCCGCCCTTTGCTCCGCCCTTCAGAACACCCCGAAGGTGGTACCAT  6480
          ||||||||||||||||||||||||||||||||||||||||||||
Db  6421  TGCTGGGCTATGGCGAGACGTCGCCTTTGCTCCGCCCTTTGCTCCGCCCTTCAGAACACCCCGAAGGTGGTACCAT  6480
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Qy  6481 TCGGACGTCTGGGCTGGGTGGTGACCCTACCCACGTTGTGATCAGGCGAA 6540
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Qy  6541 CATCCGCCTACAAACTGCTCGCGCCAGCAAATCCTGTTCGGCTTGCTGTTGCTGAGCCCTATT 6600
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Db  6541 CATCCGCCTACAAACTGCTCGCGCCAGCAAATCCTGTTCGGCTTGCTGTTGCTGAGCCCTATT 6600

Qy  6601 ACGTCGACGGCATACCGGTCTCATGGACGCGGACGCGGAGCGCCTGCCATGGTCTATG 6660
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Db  6601 ACGTCGACGGCATACCGGTCTCATGGACGCGGACGCGGAGCGCCTGCCATGGTCTATG 6660

Qy  6661 GCCCTGGGCAAAGTGTCACCATTGACGGGGAACGCTACACCCTTCCGCATCAACTGCGGC 6720
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Db  6661 GCCCTGGGCAAAGTGTCACCATTGACGGGGAACGCTACACCCTTCCGCATCAACTGCGGC 6720

Qy  6721 TTAGGAATGTGGCGCCCTGAGGTGTCATCCGAGGTGTCATTGACATTGGGACGGAGA 6780
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6721 TTAGGAATGTGGCGCCCTGAGGTGTCATCCGAGGTGTCATTGACATTGGGACGGAGA 6780

Qy  6781 CTGAAGACTCAGAACTGACTGAGGCCGACCTGCCCGGCTGCCCGGCGCCGCCCTTCAGGCTA 6840
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Db  6781 CTGAAGACTCAGAACTGACTGAGGCCGACCTGCCCGGCTGCCCGGCGCCGCCCTTCAGGCTA 6840

Qy  6841 TCGAGAATGCTGCGAGAATTCTTGAACCTCACATAGATGTCATCATGGGAGAGATTGCAGTA 6900
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Db  6841 TCGAGAATGCTGCGAGAATTCTTGAACCTCACATAGATGTCATCATGGGAGAGATTGCAGTA 6900

Qy  6901 CACCCTCTCTTGTGGGAGTAGCCGGAGAGATGCCTGTGTGGGGAAGACATACCCCGCA 6960
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6901 CACCCTCTCTTGTGGGAGTAGCCGGAGAGATGCCTGTGTGGGGAAGACATACCCCGCA 6960

Qy  6961 CTCCATCGCCAGCACTTATCTCGGTTACTGAGGAGCAGCCCAGATGAGAAGAGCACCCTCGG 7020
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Db  6961 CTCCATCGCCAGCACTTATCTCGGTTACTGAGGAGCAGCCCAGATGAGAAGAGCACCCTCGG 7020

Qy  7021 TGTCTTCCTCCGCAGGAGATACCCGTCTTCAATGGAGTGTCATCCAAGAGTCCG 7080
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Db  7021 TGTCTTCCTCCGCAGGAGATACCCGTCTTCAATTCGAGTGTCATCCAAGAGTCCG 7080

Qy  7081 AGACAGCCGAAGGGGAGGAGGAAAGCGTCTTCAACGTGCTCTTTCCGTACTAAAAGCCTTGT 7140
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Db  7081 AGACAGCCGAAGGGGAGGAGGAAAGCGTCTTCAACGTGCTCTTTCCGTACTAAAAGCCTTGT 7140

Qy  7141 TTCCACAGAGCGATGCCAACGAAGAAGCTTACCGTTAAGATGTCATGCTGGTCTGTGTTGAGAAGA 7200
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Db  7141 TTCCACAGAGCGATGCCAACGAAGAAGCTTACCGTTAAGATGTCATGCTGGTCTGTGTTGAGAAGA 7200

Qy  7201 GCGTAACAGCGCTTCTTTCATTGGATTGACCGTCGGCAAGCCTGTGTGAGA 7260
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Qy  7261 TGGAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCGCCACTCCGCTTGAATTGCAGG 7320
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Db  7261 TGGAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCGCCACTCCGCTTGAATTGCAGG 7320

Qy  7321 TTGGGTGCTTGGTGGGCAATGAACTTGACCAAGTGTGACAAGGTGAGGGCTAGGCAAG 7380
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Db  7321 TTGGGTGCTTGGTGGGCAATGAACTTGACCAAGTGTGACAAGGTGAGGGCTAGGCAAG 7380

Qy  7381 AGACCTTGGCTTCCTTCTTTACATTTGGTCTGGGCTGCCACTCCGG 7440
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Qy  7441 CCAAGGCCCCTGTGGTTGAGGCCGGTGGCCTCTTGGCTCCTTGCTGGTGGCCGACCACCAAGGTGT 7500
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Db  7441 CCAAGGCCCCTGTGGTTGAGGCCGGTGGCCTCTTGGCTCCTTGCTGGTGGCCGACCACCAAGGTGT 7500

Qy  7501 ATGTCACCAACCCGACAAATGTTGGGGAGACTCCATGTCACACGTGGGTCTTGGCCGTGCCC 7560
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Qy  7561 CTAGGGTTCATGACAACAAATTCCTCGTGACTGAGGAGAGGGAGCTCAAG 7620
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Db  7561 CTAGGGTTCATGACAACAAATTCCTCGTGACTGAGGAGAGGGAGCTCAAG 7620

Qy  7621 CCTGCCTAAGCATGGTTACACTTATGAGGAGCAATAGGACTGTAAGGCGCGTAAGGCTG 7680
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Db  7621 CCTGCCTAAGCATGGTTACACTTATGAGGAGCAATAGGACTGTAAGGCGCGTAAGGCTG 7680

Qy  7681 CCATGGGCTGGGGATCTAAGGTGTCGGTCAAGGACCTCGCACCCCTGCGGGGAAGATGG 7740
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7681 CCATGGGCTGGGGATCTAAGGTGTCGGTCAAGGACCTCGCACCCCTGCGGGGAAGATGG 7740

Qy  7741 CTGTCCATGACCGGCTCCAGGAGATACTTGAAGGGACCCAGTCCCCTTTACTCTTACTG 7800
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7741 CTGTCCATGACCGGCTCCAGGAGATACTTGAAGGGACCCAGTCCCCTTTACTCTTACTG 7800

Qy  7801 TGAAAAAGGAAGTGTTCTTCAAAGACCGAAAGAGGAAGAGGACCCCCCGCCCTCATTGTGT 7860
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Db  7801 TGAAAAAGGAAGTGTTCTTCAAAGACCGAAAGAGGAAGAGGACCCCCCGCCCTCATTGTGT 7860

Qy  7861 TCCCCCCCTGGACTTCCGGATAGCTGAAAAGTTATTCTGGGACACCCCAAATCAGCGGGTAG 7920
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Db  7861 TCCCCCCCTGGACTTCCGGATAGCTGAAAAGTTATTCTGGGACACCCCAAATCAGCGGGTAG 7920

Qy  7921 CCAAGGCGGTGTTGGGGGGGCCTACGCCTTCCAGTAGTAGCACCCCAAATCAGGAATTAGGG 7980
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Db  7921 CCAAGGCGGTGTTGGGGGGGCCTACGCCTTCCAGTAGTAGCACCCCAAATCAGGAATTAGGG 7980

Qy  7981 AGATGCTCAAACTGTGGGAATCAAGAAGACACCACAGTTGCGCCATCTGTGTGGACGGCCACAT 8040
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Db  7981 AGATGCTCAAACTGTGGGAATCAAGAAGACACCACAGTTATTCTGTGTGGACGGCCACAT 8040

Qy  8041 GCTTCGACGTAGCATAACTGAAGAGAGGACGTGGCGCTGGAGAGTTTATGCCCTGG 8100
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Qy  8161 TAACCCCGAGGGGGTGCCAGTGGTATTGTAGATCCTTGACCA 8220
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Qy  8221 CCAGTGCGAGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCGCCTGTGAGAGGGTGG 8280
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Qy  8401 AGCCTTCGTATCATGCATGCTCACTGGACACGGCCCCCTGCTCCTTGCTGCTAGCTGAGT 8460
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Db  8401 AGCCTTCGTATCATGCATGCTCACTGGACACGGCCCCCTGCTCCTTGCTGCTAGCTGAGT 8460

Qy  8461 GCAATGCAGATGGGAAACGCCATTTCGGAGCGCCCCTCGCTC 8520
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Db   8641  GTGGTGGCCACCGTCTGATCCTGTGGTGCCAGGTACATGGTAATTACTACAAGTTTC  8700
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Db   8701  CACTGGACAAACTGCCTAACATCATCGTGGCCTCCACGGACCACCAGCGTTGAGGGTTA  8760

Qy   8761  CCGCAGACAACAACTAAGACAAAAATGGAGGCTGCGCAAGGTGCTGAGCGACCTCAAGCTCC  8820
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Db   9001  ATCAATTGGATTTCACAAGCCAGAGGAGTTCGCTGCGGGTCGGTTGGGTTCTTAGCCCCTC  9060

Qy   9061  TCATCGTAGCCCTCTTCGGTGAACTAAATTCATCGTGTTGCGGCAAGGTCCGGTGACTGA  9120
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Db   9061  TCATCGTAGCCCTCTTCGGTGAACTAAATTCATCGTGTTGCGGCAAGGTCCGGTGACTGA  9120

Qy   9121  TCATCACTGGAGGAGGTTCCGGGCCCTCTCCCCCAGGGGGGTCTCCCCGCTGGGTAAAAAG  9180
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Db   9121  TCATCACTGGAGGAGGTTCCGGGCCCTCTCCCCCAGGGGGGTCTCCCCGCTGGGTAAAAAG  9180

Qy   9181  GGCCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCCTGGCAGGTCAAAGCCTGATGGT  9240
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Db   9361  CCGGTAAGAGCTCCGGCCCAAAGGCCGGGTTCTACT  9395
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RESULT 2
AF121950
LOCUS       AF121950                9395 bp    RNA     linear   VRL 19-SEP-2000
DEFINITION  Hepatitis G virus strain Iowan, complete genome.
ACCESSION   AF121950
VERSION     AF121950.1  GI:4884678
KEYWORDS    .
SOURCE      Hepatitis G virus.
  ORGANISM  Hepatitis G virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            GBV-C/HGV group.
REFERENCE   1  (bases 1 to 9395)
  AUTHORS   Xiang,J., Wunschmann,S., Schmidt,W., Shao,J. and Stapleton,J.T.
  TITLE     Full-length GB virus C (Hepatitis G virus) RNA transcripts are
            infectious in primary CD4 positive T cells
  JOURNAL   J. Virol. 74 (19), 9125-9133 (2000)
  MEDLINE   20438110
   PUBMED   10982359
REFERENCE   2  (bases 1 to 9395)
  AUTHORS   Xiang,J.H., Schmidt,W.N., Labrecque,D.R. and Stapleton,J.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JAN-1999) Internal Medicine, Iowa City City Veterans
```

Administration Medical Center, The University of Iowa, SW54, GH, Iowa City, IA 52242, USA

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BASE COUNT     1707 a   2557 c   3004 g   2127 t
ORIGIN
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Qy     61 CTATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCGCGCCGACTCGGCGCCGAC  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTATCTAAGTAGACGCAATGACTCGGCGCCGACTCGGCGCGCCGACTCGGCGCCGAC  120

Qy    121 GGGTGGTGACAGGGTTGGTAGGTCGTAAATCCGGTCATCCGGTAGCCACTATAGGTGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGGTGGTGACAGGGTTGGTAGGTCGTAAATCCGGTCATCCGGTAGCCACTATAGGTGG  180

Qy    181 GTCTTAAGAGAAGGTCAAGACTCCTTGTGCCTGCGGCGAGACCCGCACGGTCCACAG  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTCTTAAGAGAAGGTCAAGACTCCTTGTGCCTGCGGCGAGACCCGCACGGTCCACAG  240

Qy    241 GTGCTGCCCTACCCGGTCGTGAATAAGGGCCCGACGTCGTCGTTAAACCGAGCCC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTGCTGCCCTACCCGGTCGTGAATAAGGGCCCGACGTCGTCGTTAAACCGAGCCC  300

Qy    301 GTCACCCACCTGGGCAAACGACGCCCACGTACGGTCCGCCCTTCAATGTCTCTCT  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTCACCCACCTGGGCAAACGACGCCCACGTACGGTCCGCCCTTCAATGTCTCTCT  360

Qy    361 TGACCAATAGGTTTATCCGGCAGTTGACAAGGACCAGTGGGCCGGCCGGGGTATGGGGA  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGACCAATAGGTTTATCCGGCAGTTGACAAGGACCAGTGGGCCGGCCGGGGTATGGGGA  420

Qy    421 AGGACCCCAAACCCTGCCCTTCCCGGTGGGCCGGAAATGCATGGGGCCACCCAGCTCCG  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGGACCCCAAACCCTGCCCTTCCCGGTGGGCCGGAAATGCATGGGGCCACCCAGCTCCG  480

Qy    481 CGGCGGCCTGCAGCCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGGCATTTCTC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGGCGGCCTGCAGCCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGGCATTTCTC  540

Qy    541 TTTTCTATACCATCAATGGCCACTCTGCTGCGGCCGGGTGGTTGAGGCCGGGGCCATTC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TTTTCTATACCATCAATGGCCACTCTGCTGCGGCCGGGTGGTTGAGGCCGGGGCCATTC  600

Qy    601 TGGCCCCGGCCACCCAGCTTGTCCCGGGAACTGGGGAGCCTGTACGGGCCCTGTCCGCTT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGGCCCCGGCCACCCAGCTTGTCCCGGGAACTGGGGAGCCTGTACGGGCCCTGTCCGCTT  660

Qy    661 CCCCGGAAGACATCGGGTTCTGGGTCTGGACGGCGGATGCCTGGTGGTCCACGG  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCCCGGAAGACATCGGGTTCTGGGTCTGGACGGCGGATGCCTGGTGGTCCACGG  720

Qy    721 TTTGCACCGACCGTTGCTGCCCACTGTATCCGACCGGGTTGGCTGGCCTGCGCCTGCAAGT  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTTGCACCGACCGTTGCTGCCCACTGTATCCGACCGGGTTGGCTGGCCTGCGCCTGCAAGT  780

Qy    781 CCGCGGCCCAGCCGGGATCGGGTGGGGAACTGGGGAGCCTGTACGGGCCCTGTCCGGCTT  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCGCGGCCCAGCCGGGATCGGGTGGGGAACTGGGGAGCCTGTACGGGCCCTGTCCGGCTT  840

Qy    841 ACGTAGCCGGGATCCGGGCGAGGTTTACTCCGGGGTCCTGACAGTTGGTGTTG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTAGCCGGGATCCGGGCGAGGTTTACTCCGGGGTCCTGACAGTTGGTGTTG  900

Qy    901 CGTTGAGGGCGCCGGGGCTCTACCTGATGCCCAACTGAAGTGTGCAGTAGAATGTGACGTTA  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CGTTGAGGGCGCCGGGGCTCTACCTGATGCCCAACTGAAGTGTGCAGTAGAATGTGACGTTA  960

Qy    961 AGTGGGGAAGTGAGTTTGGAAAGTGCCTCCAATTACTGGATTTTGG  1020
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AGTGGGGAAGTGAGTTTGGAAAGTGCCTCCAATTACTGGATTTTGG  1020

Qy   1021 AATACCTTTGCGAAAGTCCCATTTGAATTTTGGAGAGGAGTGATGAGCCTGACCCCTCTGT  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AATACCTTTGCGAAAGTCCCATTTGAATTTTGGAGAGGAGTGATGAGCCTGACCCCTCTGT  1080

Qy   1081 TGGTTTGGGTGGCCCCATTGCTCTTTTCGCTGCTGGAGCAACACGGATTGTCATGGTTTCCTGCTGG  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGGTTTGGGTGGCCCGCATTGCTCTTTTCGCTGCTGGAGCAACGGATTGTCATGGTTTCCTGCTGG  1140

Qy   1141 TGACGATGGCGGGGGATGTTGCAAGGCGCCCCGGCTCCGTTTTGGGGTCCCGCCCCTTTG  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TGACGATGGCGGGGGATGTTGCAAGGCGCCCCGGCTCCGTTTTGGGGTCCCGCCCCCTTG  1200

Qy   1201 ACTACGGGTTGAAGTGGCAGTCATGCTCGAGGGGTCAACGGGTCGGCGTCAATTCCCACTG  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ACTACGGGTTGAAGTGGCAGTCATGCTCCTGCAGGGGTCAACGGGTCGGCGTATTCCCACTG  1260

Qy   1261 GGGAGAGGGTGTGGATCGAGGGAATGTCACGCTCTTGTGTGACTGCCCCAACGGCCCCT  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GGGAGAGGGTGTGGATCGAGGGAATGTCACGCTCTTGTGTGACTGCCCCAACGGCCCCT  1320

Qy   1321 GGGTTGGGTCCCGGCCTTTGCCAGGCGGTTGGGCGGGACCCCATCACCCATTGGA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGGTTTGGGTCCCGGCCTTTGCCAGGCGGTTGGGCGGGACCCCATCACCCATTGGA  1380

Qy   1381 GCCACGGACAAAACCAGTGGCCCCTATCATGCCCCAATATGTCTATGGCTCTGTGTCCG  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCCACGGACAAAACCAGTGGCCCCTATCATGCCCCAATATGTCTATGGCTCTGTGTCCG  1440

Qy   1441 TAACGTCGTGTGGGGTTCCGTGTCTTGGTTTGCCTGTCGTTGATCGCGGTCGTGATTCGAAGA  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TAACGTCGTGTGGGGTTCCGTGTCTTGGTTTGCCTGTCGTTGATCGCGGTCGTGATTCGAAGA  1500

Qy   1501 TCGATGTGTGGAGTTTGGTGCCGGTGGATCGGCGTGCCGGCTGCACCATAGCCGCTCTAGGGT  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TCGATGTGTGGAGTTTGGTGCCGGTGGATCGGCGTGCCGGCTGCACCATAGCCGCTCTAGGGT  1560

Qy   1561 CATCGGATCGCGACACGTGGTTGAGCTGGAGTGGGCGGTCCGGTGCGTGCGTAACGTGTA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CATCGGATCGCGACACGTGGTTGAGCTGGAGTGGGCGGTCCGGTGCGTGCGTAACGTGTA  1620

Qy   1621 TTCTGGACCGTCGGCCTGCTTCATGTGCCACCTGTGTGCGGGACTGCGTGGCCCGAAACCG  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TTCTGGACCGTCGGCCTGCTTCATGTGCCACCTGTGTGCGGGACTGCGTGGCCCGAAACCG  1680

Qy   1681 GGTCGGTTAGATTCCCTTTCCATCGGTCGGTCGGGCACGGGGCCCTCCGCGGACTTGG  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGTCGGTTAGATTCCCTTTCCATCGGTCGGTCGGGCACGGGGCCCTCCGCGGACTTGG  1740

Qy   1741 AAGCTGTGCCCTCGTCAACAGGACAACTCCCTTCACCATAAGGGGGCCCCTGGGCAACC  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AAGCTGTGCCCTCGTCAACAGGACAACTCCCTTCACCATAAGGGGGCCCCTGGGCAACC  1800

Qy   1801 AGGGGAGGAGGCAACCCGGTGCGCGTGCGCGTGCCAACCGTGGGTTTGGGTCCTACCATGACCAAGA  1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AGGGGAGGAGGCAACCCGGTGCGCGTGCGCGTGCCAACCGTGGGTTTGGGTCCTACACCATGACCAAGA  1860

Qy   1861 TCCCGGATTCCCTGCATTTGGTGAAATGTCCCACACCAGCCATAGAGCCTCCGACTGAA  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 GGTGTTCCGGAGTCGATTTGGTGAAATGTCCCACACCAGCCATAGAGCCTCCGACTGAA  1920

Qy   1921 CGTTCGGGTTCTTCCCCGGAGTCCCGAGTCCATGCCGCAGGGAGGTGGATGCGGGAAG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CGTTCGGGTTCTTCCCCGGAGTCCCGAGTCCATGCCGCAGGGAGGTGGATGCGGGAAG  1980

Qy   1981 TGTCTGAGGCATTGGGCGGTGGGCTTACGGGGGGGTTCTACGAGCCTCTGGTTCGCA  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGTCTGAGGCATTGGGCGGTGGGCTTACGGGGGGGTTCTACGAGCCTCTGGTTCCCA  2040

Qy   2041 GGTGTTCGGAGCTGATGGGCTGATGGGACCGCGAAATCCGGTTTGCCCGGGGTACGGCTGTCCT  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GGTGTTCGGAGCTGATGGGCTGATGGGACCGCGAAATCCGGTTTGCCCGGGTACGGCTGTCCT  2100

Qy   2101 CTGGTAGACCTGACGGGTCATACACGTCAGGGACCTGCAGGGGCACCTGCAGGAGTGCGGGCA  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTGGTAGACCTGACGGGTCATACACGTCAGGGACCTGCAGGGGCACCTGCAGGAGTGCGGGCA  2160

Qy   2161 ACTTCATCCCTCCTCCACGCTGGTTGCTCTTGGATTTTGTATTTGTGTTTGTTGTCCTGCTATCGA  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACTTCATCCCTCCTCCACGCTGGTTGCTCTTGGATTTTGTATTTGTGTTTGTTGTCCTGCTATCTGA  2220
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Right column block:

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Qy  3301  GTAGGGATCCTGACTTACATCCAGGAGGAACGTCATGTGTTGGGACGGCTACGTCACGAA  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  GTAGGGATCCTGACTTACATCCAGGAGGAACGTCATGTGTTGGGACGGCTACGTCACGAA  3360

Qy  3361  GCATGGGCCACATGTCGAATGGCCTGCTTGCTCGTTGTCGTTCCATGGGCTTCATCCCGAA  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  GCATGGGCCACATGTCTGAATGGCCTGCTTGCTCGTTGTCGTTCCATGGGCTTCATCCCGAA  3420

Qy  3421  CCATCGCCACGCCCGTGGGGCCCTTAATCCCAGTGGTGCTGCCAGTGATGACGTCA  3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  CCATCGCCACGCCCGTGGGGCCCTTAATCCCAGTGGTGCTGCCAGTGATGACGTCA  3480

Qy  3481  CGGTGTACCCGCTTCCAGATGGGCGCAACTTCGTTGACGCCCTGCCACTTGCCAGGGGACGAGT  3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  CGGTGTACCCGCTTCCAGATGGGCGCAACTTCGTTGACGCCCTGCCACTTGCCAGGGGAGAGT  3540

Qy  3541  CCTGTTGGGTTATTAGATCCGACGGGCTTTGTGCCATGGCTTGAGCAAGGGGACAAGG  3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  CCTGTTGGGTTATTAGATCCGACGGGCTTTGTGCCATGGCTTGAGCAAGGGGACAAGG  3600

Qy  3601  TTGAGCTGGATGTGGCCATGGAGGTCTCTGACTTCCGTGGTTCGTCGTGGTTCACCGGTCC  3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  TTGAGCTGGATGTGGCCATGGAGGTCTCTGACTTCCGTGGTTCGTCGTGGTTCACCGGTCC  3660

Qy  3661  TTTGCGACAAAGGCACGCAGTAAGAATGCTCGTGTCAGTGCTCCACTCTGGCCGGCAGGG  3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  TTTGCGACAAAGGCACGCAGTAAGAATGCTCGTGTCAGTGCTCCACTCTGGCCGGCAGGG  3720

Qy  3721  TTACTGCGGCCGATTCACTAGGCCGTGACTCAAGTACCAACAGATGCCAAGACTACCA  3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  TTACTGCGGCCGATTCACTAGGCCGTGACTCAAGTACCAACAGATGCCAAGACTACCA  3780

Qy  3781  CAGAACCCCCTCCGTGCCGGCAAAAGAGTTTCAAGGAGGCCCCGTTGTTTATGCCTA  3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  CAGAACCCCCTCCGTGCCGGCAAAAGAGTTTCAAGGAGGCCCCGTTGTTTATGCCTA  3840

Qy  3841  CGGGGCGGGAAAGAGCACCCGTACCGTCGGTAGCTTGGAGTACGGCAACATGGCCCAAGGTCT  3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  CGGGGCGGGAAAGAGCACCCGTACCGTCGGTAGCTTGGAGTACGGCAACATGGCCCAAGGTCT  3900

Qy  3901  TGATCTTGAACCCGTCGGTAGTCACCGTGAGGGGCCATGGGCCCATACATGGAGCGGCTGG  3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  TGATCTTGAACCCGTCGGTAGTCACCGTGAGGGGCCATGGGCCCATACATGGAGCGGCTGG  3960

Qy  3961  CGGGGAAACACCCCAGTATTTACTGTGGCCATGACCACCACTGCTTTTCACAAGGATCACTG  4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  CGGGGAAACACCCCAGTATTTACTGTGGCCATGACCACCACTGCTTTTCACAAGGATCACTG  4020

Qy  4021  ACTCGCCCCTTACGTATTCCACTTACGGAAGGTTTTTGGCCAACCCTAGGCCAGATGCTGA  4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021  ACTCGCCCCTTACGTATTCCACTTACGGAAGGTTTTTGGCCAACCCTAGGCCAGATGCTGA  4080

Qy  4081  GGGGTGTGTCGGTGTCATTGTGACGAGTGCCACAGTCAACTGTGTTGTTGG  4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081  GGGGTGTGTCGGTGTCATTGTGACGAGTGCCACAGTCAACTGTGTTGTTGG  4140

Qy  4141  GCATGGGCGTGTCAGGGAGCTGGCGCGAGGATGTGGAGTGCAATTGGTCGTCTCACGCCA  4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141  GCATTGGGCGTGTCAGGGAGCTGGCGCGAGGATGTGGAGTGCAATTGGTCGTCTCACGCCA  4200

Qy  4201  CTGCCACCCCTCCCGATCCCCGATGACCCAGCACCCATCAATTCATTGAGACAAAACTGG  4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201  CTGCCACCCCTCCCGATCCCCGATGACCCAGCACCCATCAATTCATTGAGACAAAACTGA  4260

Qy  4261  ACGTGGAGAGATCCCTTCTATGGCATGGGATGCATACCTCTTGAGCGGAGGACCCGGAA  4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261  ACGTGGAGAGATCCCTTCTATGGCATGGGATGCATACCTCTTGAGCGGAGGACCCGGAA  4320

Qy  4321  GGCATCTCGTATTCTGCCACTCCAAGGCTGCGAGTGCGGCCCTGCCGGCGGCCAGTTTTCGG  4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4321  GGCATCTCGTATTCTGCCACTCCAAGGCTGCGAGTGCGGCCCTGCCGGCGGCCAGTTTTCGG  4380

Qy  4381  CTAGGGGGTAAATGCCATCGCCTATTACAGGGGGAAAGACAGTTCTATCATCAAAGATG  4440
          ||||||||
Db  4381
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Left column block:

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Qy  2221  TGAAGCTGGCTGAGGCACGGTTGGTCCCGTTGATCTTGCTTGCTCGTGCTGGTGGGTGA  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  TGAAGCTGGCTGAGGCACGGTTGGTCCCGTTGATCTTGCTTGCTCGTGCTGGTGGGTGA  2280

Qy  2281  ACCAGTTGGCGGTTCTAGGACTGCCCGGCTGTGACGCGTGCCGTGCGGCGGTGAAGTTTTTG  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  ACCAGTTGGCGGTTCTAGGACTGCCCGGCTGTGACGCGTGCCGTGCGGCGGTGAAGTTTTTG  2340

Qy  2341  CGGGCCCTTGCCTTGTCATGTGTTGGCCTTCCCACTGTCAGTATGATACTAGGTCTAG  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGGGCCCTTGCCTTGTCATGTGTTGGCCTTCCCACTGTCAGTATGATACTAGGTCTAG  2400

Qy  2401  CAAACCTGGTGTTGTACTTTCGGTGGATGGGCCCTCAGCGCCTCATGTTCCTCGTGTTGT  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  CAAACCTGGTGTTGTACTTTCGGTGGATGGGCCCTCAGCGCCTCATGTTCCTCGTGTTGT  2460

Qy  2461  GGAAGCTCGCTCGGGGAGCTTTCCCGCTGCACTTTGATGGGGATTTCGGCGACCCCGCG  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  GGAAGCTCGCTCGGGGAGCTTTCCCGCTGCACTTTGATGGGGATTTCGGCGACCCCGCG  2520

Qy  2521  GGCGCCACCTCTGTCGTCGGGGCCCAGTTCTGCTTCGTCGATCGTCACATTCGAGGTCGACACTT  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  GGCGCCACCTCTGTCGTCGGGGCCCAGTTCTGCTTCGTCGATCGTCACATTCGAGGTCGACACTT  2580

Qy  2581  CGGTGTTGGGCTGGGTGGTGGCCAGCGTGTGGGCCATTAGCGCTCCTGAGCGCTCAA  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CGGTGTTGGGCTGGGTGGTGGCCAGCGTGTGGGCCATTAGCGCTCCTGAGCGCTCAA  2640

Qy  2641  TGAGCGCAGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACC  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  TGAGCGCAGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACC  2700

Qy  2701  AGGCTGTGCGCCAGAGGGTGGTGCGGCAGAGGGCGTCCTACCAAGCTTC  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  AGGCTGTGCGCCAGAGGGTGGTGCGGCAGAGGGCGTCCTACCAAGCTTC  2760

Qy  2761  TGACGTTCGCCCTGCTGCTTCTTCGGACTGCTGCTCATACATCTGGCCCGATGATGATGGTGGTGG  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TGACGTTCGCCCTGCTGCTTCTTCGGACTGCTGCTCATACATCTGGCCCGATGATGATGGTGGTGG  2820

Qy  2821  TGGCCTTGGTTGCCCTCTTCGGGCTGTCTCGACTGGCCCTGGGAGGAGCTCC  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  TGGCCTTGGTTGCCCTCTTCGGGCTGTCTCGACTGGCCCTGGGAGGAGCTCC  2880

Qy  2881  TGGTCTCCCGGCCCCGGTTACGGCGACTGGCACGGGTGTGTGACTGCTGTGATGGCCGG  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TGGTCTCCCGGCCCCGGTTACGGCGACTGGCACGGGTGTGTGACTGCTGTGATGGCCGG  2940

Qy  2941  GCGAGAAGGCCACCACCATCCGACTGGTCTCCAAGAGAGGGCCTACCTGT  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  GCGAGAAGGCCACCACCATCCGACTGGTCTCCAAGAGAGGGCCTACCTGT  3000

Qy  3001  TTGACCACATGGCTCTTCTCGCGGCTGTCAAGGACTGTGTTGGAATGGGACCGCGG  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  TTGACCACATGGCTCTTCTCGCGGCTGTCAAGGACTGTGTTGGAATGGGACCGCGG  3060

Qy  3061  CTTTGGAGCCCTTGTCATTCAGTCGCATCATCACTAGGACGGTCTCGCATCAGAGATGCCGGAGGA  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CTTTGGAGCCCTTGTCATTCAGTCGCATCATCACTAGGACGGTCTCGCATCAGAGATGCCGGAGGA  3120

Qy  3121  CCCTGTCCTGCGACAGTCGCTCAGGATGTTACCCGTGTCCTCCCGGGTTTGTATGAGG  3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  CCCTGTCCTGCGACAGTCGCTCAGGATGTTACCCGTGTCCTCCCGGGTTTGTATGAGG  3180

Qy  3181  TTCTCATCGGCGTCTTTCAGGATGTGAATCATTGCCTTGCCCTGGGGTTTCCCCGACTCCAC  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  TTCTCATCGGCGTCTTTCAGGATGTGAATCATTGCCTTGCCCTGGGGTTTCCCCGACTCCAC  3240

Qy  3241  CAGTTGTCATCCGTCGGTGCGGAAAGGGCTTCCTGGGGGTCACCAAGGCAGCCTTGACAG  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  CAGTTGTCATCCGTCGGTGCGGAAAGGGCTTCCTGGGGGTCACCAAGGCAGCCTTGACAG  3300
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Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4381  CTAGGGGGTAAATGCCATGCGCTATTACAGGGGGAAAGACAGTTCATCATCAAAGATG  4440
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   4441  GAGACCTTGGTGTCGTGTCTACAGACGCACTATCCACTTGGTACACTGGGAACTTCGATT  4500
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441  GAGACCTTGGTGTCGTGTCTACAGACGCACTATCCACTTGGTACACTGGGAACTTCGATT  4500

Qy   4501  CTGTCACCGATTGTGGGTTAGTGGTGGAGGTCGTCGAGGTGACCCTTGATCCCACCA  4560
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501  CTGTCACCGATTGTGGGTTAGTGGTGGAGGTCGTCGAGGTGACCCTTGATCCCACCA  4560

Qy   4561  TTACCATCTCCCTGCGCACGTGCCCGCGTCGGCGCTCGGCGCTGTCGTGATGGCGGCGAGGAC  4620
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561  TTACCATCTCCCTGCGCACGTGCCCGCGTCGGCGCTCGGCGCTGTCGTGATGGCGGCGAGGAC  4620

Qy   4621  GCACGGGTAGGGGCAGGTCTGGGCGCTACTACGCCGGGGTCGGCGCTGTGACCTGGTACGGAA  4680
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621  GCACGGGTAGGGGCAGGTCTGGGCGCTACTACGCCGGGGTCGGCGCTGTGACCTGGTACGGAA  4680

Qy   4681  GTGTGGTGCGCTCAGGTCCTGTCTGGTCGGCGGTGGAGCCCGGTGACCTGTGACCTGGTACGGAA  4740
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681  GTGTGGTGCGCTCAGGTCCTGTCTGGTCGGCGGTGGAGCCCGGTGACCTGTGACCTGGTACGGAA  4740

Qy   4741  TGGAACCTGACCTGACAGCAGCAAACCTACTGAGACTTACGGACAACTGCCCTTACCACCGCAG  4800
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741  TGGAACCTGACCTGACAGCAGCAAACCTACTGAGACTTACGGACAACTGCCCTTACCACCGCAG  4800

Qy   4801  CCGTCGCAGCTGACATTGGGGAAGCCGCGCCGGTGTCTTTTCGGGGCTTGCCCGTTGAGGA  4860
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801  CCGTCGCAGCTGACATTGGGGAAGCCGCGCCGGTGTCTTTTCGGGGCTTGCCCGTTGAGGA  4860

Qy   4861  TGCATCCCGATGTTAGCTGGGCAAAAGTTCGGCGCGTCAACTGGCCCTTCCTTGGTGTGGGTG  4920
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861  TGCATCCCGATGTTAGCTGGGCAAAAGTTCGGCGCGTCAACTGGCCCTTCCTTGGTGTGGGTG  4920

Qy   4921  TTCCAGCGGACCATGTGCCGCGGGAAACACTGTCTCCCGGCCCATCGGATGACCCCAGTGGG  4980
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921  TTCCAGCGGACCATGTGCCGCGGGAAACACTGTCTCCCGGCCCATCGGATGACCCCAGTGGG  4980

Qy   4981  CAGGTCTGAAGGGCCCGAATCCTGTCTCCACTCCTGCTCCGTGAGGTGGGCAATGATTTACCAT  5040
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981  CAGGTCTGAAGGGCCCGAATCCTGTCTCCACTCCTGCTCCGTGAGGTGGGCAATGATTTACCAT  5040

Qy   5041  CTAAAGTGGCCGGCCCCCTTTATCGGCCATCACATCGTGGACGACCTGGTCCGTGCCGAGG  5100
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041  CTAAAGTGGCCGGCCCCCTTTATCGGCCATCACATCGTGGACGACCTGGTCCGTGCCGAGG  5100

Qy   5101  GTTACGTCCGCTGCGATGCGGACCCATCTTGATGGTGGCCTTCGCTATTGCGGGGGGCA  5160
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101  GTTACGTCCGCTGCGATGCGGACCCATCTTGATGGTGGCCTTCGCTATTGCGGGGGGCA  5160

Qy   5161  TGATCTATGCGTCATACACCGGGGTCTCTCGTGGTTACAGACTGGGATGTGAAGGGG  5220
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161  TGATCTATGCGTCATACACCGGGGTCTCTCGTGGTTACAGACTGGGATGTGAAGGGG  5220

Qy   5221  GTGGCAGCCCCCCTTTATCGGCATGGAGACACCCCAGGCCCACGCCCGGTTGTGTGCAGGTCC  5280
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221  GTGGCAGCCCCCCTTTATCGGCATGGAGACACCCCAGGCCCACGCCCGGTTGTGTGCAGGTCC  5280

Qy   5281  CCCCGGTAGAGACCATCGGCCGGGGGAGAGTCTGCGCCATCGGATGCCAACACAGTGACAG  5340
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281  CCCCGGTAGAGACCATCGGCCGGGGGAGAGTCTGCGCCATCGGATGCCAACACAGTGACAG  5340

Qy   5341  ATGCGGTGCGGCCATCCAGTGGATTGCGATTGCGATTGTCAGTCATGCACCCGTCGATCGGGG  5400
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341  ATGCGGTGCGGCCATCCAGTGGATTGCGATTGCGATTGTCAGTCATGCACCCGTCGATCGGGG  5400

Qy   5401  AAGTGCTGTCCTTGGCCTACGGCTAAGCACGGCCGAGCGCCTACGACCCTACCACCAAGTGGC  5460
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401  AAGTGCTGTCCTTGGCCTACGGCTAAGCACGGCCGAGCGCCTACGACCCTACCACCAAGTGGC  5460

Qy   5461  TTGCTGGCTGCTACACGGACGCGGGCGGCCGTCCCACTGTTTCAAGCTCT  5520
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   5461  TTGCTGGCTGCTACACGGACGCGGGCGGCCGTCCCACTGTTTCAATTGTTGACAAGCTCT  5520
Qy   5521  TCGGCCGGGGGCTGGACGTGGGCGGCGGTGGTAGGCCCCATTGCCACAGTGTAATAGCTCGCGGCAGTGG  5580
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521  TCGGCCGGGGGCTGGACGTGGGCGGCGGTGGTAGGCCCCATTGCCACAGTGTAATAGCTCGCGGCAGTGG  5580

Qy   5581  CGGCCTATGGGGCTTCTAGGAGCCCTCCATTGGCTGCTGCGCTTCCTACCTCATCGGGGT  5640
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581  CGGCCTATGGGGCTTCTAGGAGCCCTCCATTGGCTGCTGCGCTTCCTACCTCATCGGGGT  5640

Qy   5641  TGGGGTCGGAGGCAAACGCGCAAACCCGCTTCCGCCTCCCTACGCGGCCGCTG  5700
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641  TGGGGTCGGAGGCAACGCGCAAACCCGCTTCCGCCTCCCTACTAGGGGCCGCTG  5700

Qy   5701  GGACCCCTCTGGCCACGCCTGTCGTGGGGTTAACCATGGCGGCCGTTCATGGAAGTG  5760
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701  GGACCCCTCTGGCCACGCCTGTCGTGGGGTTAACCATGGCGGCCGTTCATGGAAGTG  5760

Qy   5761  CTAGCGTCTCCCCCCTTCCTTGTCACCATTTTACTGGGGCCGTGGGGGCTGGGAGGGCG  5820
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761  CTAGCGTCTCCCCCCTTCCTTGTCACCATTTTACTGGGGCCGTGGGGGCTGGGAGGGCG  5820

Qy   5821  TGGTGAATGCGGCTAGCCTTGTCTTCGACTTTATGCGGGGAAAACTATCATCAGAAGATC  5880
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821  TGGTGAATGCGGCTAGCCTTGTCTTCGACTTTATGCGGGGAAAACTATCATCAGAAGATC  5880

Qy   5881  TGTGGTATGCCATCCCAGTGCTAACCAGTCCGGGGCTTGCCGGATCGCCCTCG  5940
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881  TGTGGTATGCCATCCCAGTGCTAACCAGTCCGGGGCAGACTTGCCGGATCGCCCTCG  5940

Qy   5941  GGTTGTGTTGTACTCAGCTAACAACTGGTTGAACCGTCTGCTGA  6000
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5941  GGTTGTGTTGTACTCAGCTAACAACTGGTTGAACCGTCTGCTGA  6000

Qy   6001  CTACATTGCCAAGGTCCTCATGCATCCCTGACACAGTTACTTTCAGCAGGCCGATTACTGTG  6060
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6001  CTACATTGCCAAGGTCCTCATGCATCCCTGACACAGTTACTTTCAGCAGGCCGATTACTGTG  6060

Qy   6061  ACAAGTCTCAGCTGTCTCCACTCCTGAGCCTCCGCACCGTGGTTGCCCGTGGTCA  6120
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6061  ACAAGTCTCAGCTGTCTCCACTCCTGAGCCTCCGCACCGTGGTTGCCCGTGGTCA  6120

Qy   6121  ACAGGGAGCCAAGGTGGATGGAGGTTCAGGTGGGTACGTCTGGGAGTGGA  6180
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6121  ACAGGGAGCCAAGGTGGATGGAGGTTCAGGTGGGTACGTCTGGGAGTGGA  6180

Qy   6181  GGTTGGTGTTGTTACTCAGCTGCCATGTGATGCCAGACTTCGGGACCTCTCGCCCCGGTGGTCAT  6240
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6181  GGTTGGTGTTGTTACTCAGCTGCCATGTGATGCCAGACTTCGGGACCTCTCGCCCCGGTGGTCAT  6240

Qy   6241  TACCCTTATGCACTCGCGGGAGGGGTTGGTCCGGGAGAATGTGTTGGACGGCCATGTTG  6300
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6241  TACCCTTATGCACTCGCGGGAGGGGTTGGTCCGGGAGAATGTGTTGGACGGCCATGTTG  6300

Qy   6301  AGAGTCGTTGTCTTTTGCGTGGTGGTGATCACCGGTGATGTTTGAATGGGCAACTCAAAAG  6360
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6301  AGAGTCGTTGTCTTTTGCGTGGTGGTGATCACCGGTGATGTTTGAATGGGCAACTCAAAAG  6360

Qy   6361  ATCCAGTTTACTCTACCAAGCTGTGCAGGCATTATTGGATGGGACCAGTCCCTGTGAACA  6420
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6361  ATCCAGTTTACTCTACCAAGCTGTGCAGGCATTATTGGATGGGACCAGTCCCTGTGAACA  6420

Qy   6421  TGCTGGCTATGGCACTCGCGCCCTTTGCTCGCGCCTGTCAGAGACACCCCGAAGTGGTACCAT  6480
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6421  TGCTGGCTATGGCACTCGCGCCCTTTGCTCGCGCCTGTCAGACACCCCGAAGTGGTACCAT  6480

Qy   6481  TCGGGACGTCTCGGGTGGCTGAGGTGGTTGACCCCTACCACCAAGTGGC  6540
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6481  TCGGGACGTCTCGGGTGGCTGAGGTGGTTGACCCCTACCACCAAGTGGC  6540

Qy   6541  CATCCGCCTACAAAACTGCTCGCGCCAGCAAATCCTGTGTTGCTGGCTCGTGTTGCTGAGCCCTATT  6600
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6541  CATCCCCTACAAAACTGCTCGCGCCAGCAAATCCTGTGTTGCTGGCTCGTGTTGCTGAGCCCTATT  6600
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Left column:

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Qy  6601 ACGTCGACGGCATACCGGTCTTCATGGACGCGGACGCGCGAGCGCGCCTGCCATGGTCTATG 6660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6601 ACGTCGACGGCATACCGGTCTTCATGGACGCGGACGCGCGAGCGCGCCTGCCATGGTCTATG 6660

Qy  6661 GCCCTGGGCAAAGTGTCACCATTGACGGGGAACGCTACACCCTTCCGCATCAACTCAACTG 6720
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Db  6661 GCCCTGGGCAAAGTGTCACCATTGACGGGGAACGCTACACCCTTCCGCATCAACTCAACTG 6720

Qy  6721 TTAGGAATGTGCGCCCTCGAGGTGTCATTGACATTGGACGGAGA 6780
         ||||||||||||||||||||||||||||||||||||||||||||
Db  6721 TTAGGAATGTGCGCCCTCGAGGTGTCATTGACATTGGACGGAGA 6780

Qy  6781 CTGAAGACTCAGAACTGACTGAGGCCGACCCTGCCCGCCGGCCCTTCAGGCTA 6840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6781 CTGAAGACTCAGAACTGACTGAGGCCGACCCTGCCCGCCGGCCCTTCAGGCTA 6840

Qy  6841 TCGAGAATGCTGCGAGAATTCTTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTA 6900
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Db  6841 TCGAGAATGCTGCGAGAATTCTTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTA 6900

Qy  6901 CACCCTTCTCTTGTTGGGAGTAGCCGAGAGATGCCTGTGTGGGAGAAGACATACCCCGCA 6960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6901 CACCCTTCTCTTGTTGGGAGTAGCCGAGAGATGCCTGTGTGGGAGAAGACATACCCCGCA 6960

Qy  6961 CTCCATCGCCAGCACTTATCTCGGTTACTCGGTTAAGATGTCATGCTGTGTTGAGAAGA 7020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6961 CTCCATCGCCAGCACTTATCTCGGTTACTCGGTTAAGATGTCATGCTGTGTTGAGAAGA 7020

Qy  7021 TGTCTTCCTCCAGGAGGATACCCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCG 7080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7021 TGTCTTCCTCCAGGAGGATACCCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCG 7080

Qy  7081 AGACAGCCGAAGGGGAGGGAGGAAAGCGTCTTCAACGTGCTCTTCCGTACTAAAAGCCTTGT 7140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7081 AGACAGCCGAAGGGGAGGGAGGAAAGCGTCTTCAACGTGCTCTTCCGTACTAAAAGCCTTGT 7140

Qy  7141 TTCCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGATGTCATGCTGTGTTGAGAAGA 7200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7141 TTCCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGATGTCATGCTGTGTTGAGAAGA 7200

Qy  7201 GCGTAACACGCTTCTTTTCATTGGATTGACGGTCCGTCGCTGACGTGCCGACGCTGTGTGAGA 7260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7201 GCGTAACACGCTTCTTTTCATTGGATTGACGGTCCGTCGCTGACGTGCCGACGCTGTGTGAGA 7260

Qy  7261 TGGAAATCCAGAACCATACAGCCTATTGTGACAAGTTGACAAGTTGACAAGTTACCTTGCAGG 7320
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Db  7261 TGGAAATCCAGAACCATACAGCCTATTGTGACAAGTTGACAAGTTGACAAGTTACCTTGCAGG 7320

Qy  7321 TTGGGTGCTTGGTGGTGGGCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAG 7380
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Db  7321 TTGGGTGCTTGGTGGTGGGCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAG 7380

Qy  7381 AGACCCTGGCTTCCTTCTCTACATTGGTCTGGGGTGCGGGGTGCCACTGACGAGGGCCACTCCGG 7440
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Db  7381 AGACCCTGGCTTCCTTCTCTACATTGGTCTGGGGTGCGGGGTGCCACTGACGAGGGCCACTCCGG 7440

Qy  7441 CCAAGCCCCCTGTGGTGAGGGAGCCCGGTTGGCTCCTTGCTGTGGCGCCGACACCACCAAGGTGT 7500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7441 CCAAGCCCCCTGTGGTGAGGGAGCCCGGTTGGCTCCTTGCTGTGGCGCCGACACCACCAAGGTGT 7500

Qy  7501 ATGTCACCACCGGACAGCAATGTGTTCCCGTGGCACTCCGTCCTGAAGAGAAGTTGACCTTTCTGGCGTGCCC 7560
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Db  7501 ATGTCACCACCGGACAGCAATGTGTTCCCGTGGCACTCCGTCCTGAAGAGAAGTTGACCTTTCTGGCGTGCCC 7560

Qy  7561 CTAGGGTTCATGACAAATTCCTCGTGACTCGTGTGTGCCATAGAGCGCGTCAAGAGGCGCTCAAG 7620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7561 ATGTCACCAACCCGACAAATTCCTCGTGACTCGTGTGTGCCATAGAGCGCGTCAAGAGGCGCTCAAG 7620

Qy  7621 CCTGCCTAAGCATGGGTTACACTTCATGGAGGCAATAAGGACTGTAAGGCCACCATGCTG 7680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7621 CCTGCCTAAGCATGGGTTACACTTCATGGAGGCAATAAGGACTGTAAGGCCACCATGCTG 7680
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Right column:

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Qy  7681 CCATGGGCTGGGGATCTAAGGTGTCGGTCAAGGACCTTCGCCACCCCTGCGGGGAAGAGATGG 7740
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Db  7681 CCATGGGCTGGGGATCTAAGGTGTCGGTCAAGGACCTTCGCCACCCCTGCGGGGAAGAGATGG 7740

Qy  7741 CTGTCCATGACCGGCTCCAGGAGATACTTGAACGGGACGGCCAGTCCCCTTTACTCTTACTG 7800
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Db  7741 CTGTCCATGACCGGCTCCAGGAGATACTTGAACGGGACGGCCAGTCCCCTTTACTCTTACTG 7800

Qy  7801 TGAAAAAGGAAGTGTCTTCAAAGACCGAAAGAAGAAGAAGGCCCCCGCCCTTCATTGTGT 7860
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Db  7801 TGAAAAAGGAAGTGTCTTCAAAGACCGAAAGAAGAAGAAGGCCCCCGCCCTTCATTGTGT 7860

Qy  7861 TCCCCCCTGGACTTCCGGATAGCTGAAAAGCTTATTCTGGACACCCCAAATCAGCGAATTAGGG 7920
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Qy  7921 CCAAGGGCGGTGTTGGGGGGGGCCTACGCCTTCCAGTACACCCCAATCAGCGGACGCCACAT 7980
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Db  7921 CCAAGGGCGGTGTTGGGGGGGGCCTACGCCTTCCAGTACACCCCAATCAGCGGACGCCACAT 7980

Qy  7981 AGATGCTCAAACTGTGGAATCAAAGAAGACACCATGCGCCATCTGTGTGGACAGCTTTATGCCCTGG 8040
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Qy  8041 GCTTCGACAGTAGCATAACTGAAGAGGACGTGCGCGCTGGACGTGGCTGGACAGAGCTTATGCCCTGG 8100
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Db  8041 GCTTCGACAGTAGCATAACTGAAGAGGACGTGCGCGCTGGACGTGGCTGGACAGAGCTTATGCCCTGG 8100

Qy  8101 CTTCAGACCATCCAGATGGTGCGTGCCCTGGGGAAATACTATGCCTCTGGCACAATGG 8160
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Db  8101 CTTCAGACCATCCAGATGGTGCGTGCCCTGGGGAAATACTATGCCTCTGGCACAATGG 8160

Qy  8161 TAACCCCGAGGGGGTGCCAGTGGTGAGAGGTATTGTAGATCCTCAGGGGTCTTGACCA 8220
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Db  8161 TAACCCCGAGGGGGTGCCAGTGGTGAGAGGTATTGTAGATCCTCAGGGGTCTTGACCA 8220

Qy  8221 CCAGTGCCAGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCGCCGCCCTGTGAGAGGTGG 8280
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Db  8221 CCAGTGCCAGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCGCCGCCCTGTGAGAGGTGG 8280

Qy  8281 GGCTGAAAAATGTCTCGCTCCTCCATCGGCCGATGACTGTTTGATCATATGCGAACGC 8340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8281 GGCTGAAAAATGTCTCGCTCCTCCATCGGCCGATGACTGTTTGATCATATGCGAACGC 8340

Qy  8341 CTGTGTGCGATCCTAGGCGACGCGTTTGGGCGAGCCCTGGCGAGCTACGGGTACGCATGCG 8400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8341 CTGTGTGCGATCCTAGGCGACGCGTTTGGGCGAGCCCTGGCGAGCTACGGGTACGCATGCG 8400

Qy  8401 AGCCTTCGTATCATGCAACTTTGAATGCGACACGGCCCCCTTCTTCGACACCGGCTAGCTGAGT 8460
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Db  8401 AGCCTTCGTATCATGCAACTTTGAATGCGACACGGCCCCCTTCTTCGACACCGGCTAGCTGAGT 8460

Qy  8461 GCAATGCAGATGGGAAACGCCATTTCTTCCTGACCACCGGCCACTTCGGAGGCCCCTCGCTC 8520
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Db  8461 GCAATGCAGATGGGAAACGCCATTTCTTCCTGACCACCGGCCACTTCGGAGGCCCCTCGCTC 8520

Qy  8521 GCATGTCGAGCGAGTACAGTGACCCAATGCTTCGGCCATCGGTTACATCCTCCTATACC 8580
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Db  8521 GCATGTCGAGCGAGTACAGTGACCCAATGCTTCGGCCATCGGTTACATCCTCCTATACC 8580

Qy  8581 CTTGGCATCCTATCACACGGTGGTCATCATCCTCCACGTGCTCACCTGCGCGTTTAGGG 8640
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Db  8581 CTTGGCATCCTATCACACGGTGGTCATCATCCTCCACGTGCTCACCTGCGCGTTTAGGG 8640

Qy  8641 GTGTGGCACACCGTCTGATCCTGTGTCGTGCAGGTACAATGTGAATTACTACACAAGTTTC 8700
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Qy  8701 CACTGGACAAACTGCCTAACATCGTGCCCCACCGACCAGCAGCCGGTTGAGGGGTTA 8760
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Db  8701 CACTGGACAAACTGCCTAACATCGTGCCCCACCGACCAGCAGCCGGTTGAGGGGTTA 8760

Qy  8761 CCGCAGACAACAACTAAGACAAAAATGGAGGGCTGGCAAGGTGCTGGCAGACCTCAAGCTCC 8820
Db  ...
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Db  8761 CCGCAGACACAACTAAGACACAAAAATGAGGAGCTGGCAAGGTGCTGAGCGACCTCAAGCTCC 8820
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Qy  8821 CTGGCCTAGCAGTCCACCGGGAACGAAGGCCGGGCATTGCGAACGCGTATGCTCCGGTCGC 8880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8821 CTGGCCTAGCAGTCCACCGGGAACGAAGGCCGGGCATTGCGAACGCGTATGCTCCGGTCGC 8880
Qy  8881 GCGGTTGGCGTGAGTTGGCTAGGGGGCTGTTGTGGGCGTCACCGCCTGCGGCTTCCCCTC 8940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8881 GCGGTTGGCCTGAGTTGGCTAGGGGGCTGTTGTGGGCGTCACCGCCTGCGGCTTCCCCTC 8940
Qy  8941 CGGAGATGTCGTGTATCCCGGGGGGTTTCCCCCCTTTCCCCCCCTATAGGGGTGTGGTTC 9000
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Db  8941 CGGAGATTGCTGGTATCCCGGGGGGTTTCCCCCCTTTCCCCCCCTATATGGGGGTGTGGTTC 9000
Qy  9001 ATCAATTGGATTCACAAGCCAGAGGAGTCGCTCGGCCGGTGGGTTCTTAGCCCCTGG 9060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9001 ATCAATTGGATTCACAAGCCAGAGGAGTCGCTCGGCCGGTGGGTTCTTAGCCCCTGG 9060
Qy  9061 TCATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGCGCAAGGTCCGGTGACTGA 9120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9061 TCATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGCGCAAGGTCCGGTGACTGA 9120
Qy  9121 TCATCACTGGAGGAGGTTCCCGCCCTCCCCGGGGTCTCCCCGCTGGGTAAAAAG 9180
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Db  9121 TCATCACTGGAGGAGGTTCCCGCCCTCCCCGGGGTCTCCCCGCTGGGTAAAAAG 9180
Qy  9181 GGCCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCCTGGCAGGTCAAAGCCTGATGGT 9240
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Qy  9241 GCTAATGCACTGCCACTTCGGTGGCGGGTCGCTACCTTATAGCGTAATCCGTGACTACGG 9300
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Qy  9301 GCTGCTCGCAGAGCCCCGCCCCGGATGGGCACAGTGCCACTGTGATCTGAAGGGGTGCACC 9360
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Qy  9361 CCGGTAAGAGCTCGGCCCCAAAGGCCGGGTTCTACT 9395
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COMMENT   updated (05-Nov-1996) by Li Shao.
FEATURES   Location/Qualifiers
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          /note="GBV-C/HGV group"
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          /db_xref="GI:1731800"
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          RIVMFLLVTMAGMSQGAPASVLGSRPFDRGLTWQSCSCRANGSRIPTGEKVWDRGNV
          TLLCDCPNGPWVLPAFCQAIGWGDPITHWSHGQNGWPLSCPQEFVYGSVSTCVWGSA
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RESULT 3
D87255
LOCUS   D87255   9375 bp   RNA   linear   VRL 07-FEB-1999
DEFINITION Hepatitis G virus RNA for polyprotein, complete cds.
ACCESSION   D87255
VERSION   D87255.1 GI:1731799
KEYWORDS   polyprotein.
SOURCE   Hepatitis G virus (isolate:HGV-Iw) cDNA to genomic RNA.
ORGANISM   Hepatitis G virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            GBV-C/HGV group.

REFERENCE   1 (bases 1 to 9375)
AUTHORS   Shao,L.
TITLE   Direct Submission
JOURNAL   Submitted (20-AUG-1996) Li Shao, Yamagata University School of
            Medicine, 2nd Department of Internal Medicine; Iida-nishi 2-2-2,
            Yamagata, Yamagata 990-23, Japan
            (E-mail:shori@med.id.yamagata-u.ac.jp, Tel:0236-28-5309,
            Fax:0236-28-5311)
REFERENCE   2 (bases 1 to 9375)
AUTHORS   Shao,L., Shinzawa,H., Zhang,X. and Takahashi,T.
TITLE   Complete nucleotide sequence of hepatitis G virus isolated from a
            Japanese patient with non-A,non-B,non-C, and non-E hepatitis
JOURNAL   Unpublished (1997)
REFERENCE   3 (sites)
AUTHORS   Shao,L., Shinzawa,H., Ishikawa,H., Ishikawa,K., Zhang,X., Ishibashi,M.,
            Misawa,H., Yamada.N., Togashi.H. and Takahashi,T.
TITLE   Sequence of hepatitis G virus genome isolated from a Japanese
            patient with non-A-E-hepatitis: amplification and cloning by long

BASE COUNT   1674 a   2556 c   2994 g   2151 t
ORIGIN

Query Match   86.3%;   Score 8106.4; DB 14; Length 9375;
Best Local Similarity   91.6%;   Pred. No. 0;
Matches 8589; Conservative 0; Mismatches 0; Indels 786; Gaps 1;

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Db   1080  GCTGCTGCTTGAGCAACGGATTGTCATGGTCTTCCTCGTTGGTGACAATGGCGGGGATGTC  1139
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Qy   1280  AGGGAATGTCACGCTCTTGTGTGACTGCCCAACGGCCCCTGGGTTTGGGTCCCGGCCTT  1339
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Qy   1940  AGTCCCGCCCATTAACAACTGCATGCCGGCAACCTGCTAGGCACGGAAGTGTCTGAGGCGG  1999
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Db   1920  GACGCCGCCCCTTAACAACTGTATGCGTGTGGGCACGAAGTGTCCCAGGCACTCGGCGCG  1979

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Qy   2120  CATACACGTCCAGGGCACCTGCACCGGCCACTTGCTGGCAACTTCATCCCTCCTCCACG  2179
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Qy     80  GACTCGGCCGCCGACTCGGCCGCCGGCCAAAAGGTGGTGGATGGCGGTGTGACAGGGTTGGT  139
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Qy    380  GCGAGTTGACAAGGACCAGTGGGGGCCCGGGGTTATGGGAAGGACCCCAAACCCTGCCC  439
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Db    361  GCGAGTTGACAAGGACCAGTGGGGGCCCGGGGGCT-TGGGAGGGGACTCCAAGCCCTGCCC  419

Qy    440  TTCCCGGTGGGCGGGAAATGCATGGGCGCCACCCAGCTCCGCGGCGCCTGCAGCGCGGGG  499
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Db    420  TTCCCGGTGGGCGGGAAATGCATGGGCGCCACCCAGCTCCGCGGCGCCTGCAGCGCGGGG  479

Qy    500  TAGCCCAAGAATCCTTCGGGTGAGGCGTTGGCATTTCTCTTTTCTATACCATCATGGC  559
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Db    480  TAGCCCAAGAATCCTTCGGGTGAGGCGTTAGCCTTAGGGTGCACGATTTGCACTGACCGATGGC  539

Qy    560  AGTCCTTCTGCTCCTCGTGGTTGAGGCCGGCCATTCTGGCCCCCGGCCACCCACGC  619
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Qy    620  TTGTCCAGCGAATGGGCAATATTCCTCACAAAATTGCTGTCGGGTGCACCGACCGGGGTT  679
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Qy    680  CTGCCTGGAAGGCGATGCCTGGTCGGCCACCGGTTGCACCGGCCGCCGTTGCTG  739
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Db    660  CTGCCTGGAAGGTGGATGCCTGGTAGCCGTTAGGCCTTAGGGTGCACTGACCGATGCTG  719

Qy    740  GCCACTGTATCAGGCGGGTTTGGCTGCGTGTGCGCTGGCAAGTCCCGCGCCCAGCTCGTTGG  799
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Db    720  GCCACTGTATCAGGCGGGTTTGGCGTGTGCGCCTGCAAGTCCCCAAACTGTTGGG  779

Qy    800  GGAACTGGGAGCCGTGTACGGGCCCTGTCTCGGCTTCGGCTCGGTTCTCGGGGATCCTGGG  859
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Db    780  GGAGCTGGGAGCCGTTTACGGGCCCTGTCTCGGGATCTGGGATCTTGGG  839

Qy    860  TCTGGGCGAGGTTTACTCGGGTTTGCTGTGTTGCGTTGAGGCGCCGGGGTCTA  919
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Db    840  CCTGGGAGGAGTGTACTCGGGGTGTGGATGAGCTTGACCGCCGGGGTCATT  899

Qy    920  CCTGATGCCCAACCTGAAGTGTGCAGTAGAAATGTGACGTTAAGTGGGAAGTGAGTTTTG  979
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Qy   1040  ATTTGAATTTTGGAGAGGAGTTGATGAGCCTTGACCCCTCTGTTGGTTTGGGTGGCCGCATT  1099
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Qy  2240  GTTGGTGTCCGTTGATCTTGCTTCTGCGTGGTGTGGGTGAACCAGTTGGCGGTTCTAGG  2299
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Db  2220  GTTGGTCCCGCCTGATCTTGCTATTGCTATTGCTATGTGGCGGTGGTGAACCAGCTGGCCAGTTTTAGG  2279

Qy  2300  ACTGCCGGCTGTGGACGCTGCGTGGCGGTGAAGTTTTGCGGGCCCTGCCTTGTCATG  2359
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Db  2520  GGCCGAGTTCTGCTTCGATGCTACATTCGAGGTGGACACTTCGGTGCTGGGTGGGT  2579

Qy  2600  GGCAGCGTGGTGGCTGGGCCATAGCGCTCTGAGCTCAATGAGCGGCAGGGGGGTGGAA  2659
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Qy  2660  GCACAAGGCCGTGACTCTATAGGACGTGGTGTAAAGGTACCAGGTGTGCCGCCAGAGGGT  2719
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Qy  2720  GGTGCGGAGCCCCCTCGGGAGGGGGCCTCCTACCCAAGCTTCGACGTTCGCGTTGGTCTT  2779
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Db  2700  GGTGAGGAGCCCCCTCGGGAGGGGCCTGTGTGTGCCCAAACCCTGAGCGTTCGCGTTGGTGCTT  2759

Qy  2780  GGCCTCATACATCTGGCCGGATCTGCGCAAGAGGGCCTTGGTGGTTCCTCCTCTCTT  2839
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Db  2760  GGCCTTCGTGTGCCAAGATGTGCCGGGAGGGACGCCCTATTTGTTCGATCATATGGTTCCTT  2819

Qy  2840  CGGCCTGTTCGACGACTGGACTGGGCCCGGGAGGAGCCTCGTTGCCCCCGCCCTCGTT  2899
          ||  | ||  ||||||||||||||    |||||||| | || |||||||||||||| ||
Db  2820  TGGTCTGTTCGACGACGTTCCGACTGGGCCCGGAGGAGCCATGGTATCCCGGGCCCCTCGTT  2879

Qy  2900  ACGGCGACTGGCACGGGTCGGTTGAGTCGTTGATCGCGGGGCGAGAAGGCCACCACCAT  2959
          || ||||||||| |||| |||   || ||||||||| |||||||||||||||||| |||
Db  2880  GCGGCGTCTCGGCGATCGAGTCGGTGTCATCATACGGAGACGGAGAAGGCGAGAAGGCCACAGGT  2939

Qy  2960  CCGACTGGTCTCCAAGATGTCGCAAGAGGGCCTACCTGTTGACCACATGGCTCTTT  3019
          ||  | |||||||||||| || || ||  ||||||| || |||||||||||| |||
Db  2940  CCGGTTCGTCTCCAAGATGTGCGAGGGCGACGCCTATTTGTTCGATCATATGGTTCCTT  2999

Qy  3020  CTCGGCGCGTCGTGTCAAGGAGCCGTGTTGGAATGGGACGCGGCCCTTTGTCATT  3079
          ||||||||||||||||||| |||||   |||| ||| |||||||||||||||||||
Db  3000  CTCGGCGCGTTAAGGAGCCGTGTGAGTGGAGACTGGCATGTGGCACGCGGCCCTTTGAGCCTTGTCATT  3059

Qy  3080  CACTAGGACGGACTGTCGCATCATCAGAGATCGCGGGCGAGAAGGCCCGTCTCTGCGGACAGTG  3139
          |||||||||||||||  |||||| ||||| ||||||| |||||| | ||||||||||||||||
Db  3060  CACTAGGACGGACTGTCGCATCATACGGAGACGCCGCGCGCCGAGAAGGCGAGAAGGTCCTCGGGCGAGTG  3119

Qy  3140  CGTACTGGTCTCCAAGATGTCGTAGCACGGGCGGGGTTTCTCATCGGCGTCTTTCA  3199
          ||| | ||||||||||||||||||||| ||| | || ||||||||||||| ||||
Db  3120  CGTCATCGGCTTCCAAGATGTGCCTCCGGTTGTGCCTCCCCGTGATGAGGTTCATCGGCGTTTTCCA  3179

Qy  3200  GGATGTGAATCATTTGCCTCCTGGGGTTTGTCCGGACGGCGTAGCACAGGTCTCATCCGCGGTG  3259
          |||||||||||||||||||  || ||| |||||||| || || ||||||||||||||||||||
Db  3180  AGATGTGAACCATTTGCCTCCTGGGGTTTCATCATTGCCTCCTGGGGTTACATGTTCATCGGGATCCTGACTTGTG  3239

Qy  3260  CGGAAAGGGCTTCCTGGGGGTTGGTTCACGAAGCCTCGTTCATCCGCGGTG  3319
          ||||||||||||||||||||||||  ||||||| |||||||||||||||||
Db  3240  CGGAAAGGGCTTCCTGGGGGTTGGTCACGAAGGGTCGGCGGGATCCTGACTTGTGACTTACA  3299
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Qy  3320  TCCAGGGAACGTCATGGTGTTGGGACGGCTACGTCACGAAGCATGGCACATGTCTGAA  3379
          |||||||||||||||||||||||||||||||  | |||||||||||||||||||||||
Db  3300  TCCAGGGAACGTCATGGTGTTGGGACGGCTACGTCACGTCGCGAAGCATGGGAACATGTCTTGAA  3359

Qy  3380  TGGCCTGCTGTTCACAACTTCCATGGGCGCTTCATCCCGAACCATGCCACGCCCGTGGG  3439
          ||| | ||  | |||||| |||| ||| | ||||||||||   |||| || |||||||
Db  3360  CGGCTTGCTTCGTTCGCGACTTTCCATGGGCCTTCATCCCGAACCATGCCACGCCCGTGGG  3419

Qy  3440  GGCCCTTAATCCCAGGTGTGGTCAGCGTGATGACGACCGTCACGGTGTACCCGGCTTCCAGA  3499
          |||||||||  | |||||| ||  |||   || ||| ||| ||||||||||| |||||||||
Db  3420  GGCCCTTAATCCTGAGGTGTGGTCAGCCAGTGTCAGGCGTGTCAGCCAGCTGGTGTTGTTTGTACTT  3479

Qy  3500  TGGGGCAACTTCGTTGACGCCCTGCACTTGCCAGGCGGACAAGGGGGACAAGGTTGGCCAT  3559
          |||| ||||||||||| ||| || || ||||| || ||||| |||| |  | |||||||||
Db  3480  TGGGGCAACTTCGTTGACGCCCTGCACTTGCCAGGCTGTGTTGTTTGGTCATCAGATC  3539

Qy  3560  CGACGGGGCTTTGTTGCCATGGCTTGAGCAGGGGGACAAGGTTGAGCTGGATGTGGCCAT  3619
          |||||||| ||  |||||| ||| |||  || |||| |||| || |||||||||||||||
Db  3540  CGACGGGGCTTTGTTGCCATGGCTTGAGCAGGGGGACAAGGTGAGCTGGATGTGGCCAT  3599

Qy  3620  GGAGGTCTCGACTTCCGTGGTTCGTCGCCACTTCGGCGGCGCAGGGTTACTGCGCGCGATTCAC  3679
          |||||||||||||||||  ||| || ||| ||| |||| || ||||| |||||||||||||||
Db  3600  GGAGGTCTCGACTTCCGTGGTCCGTCGCCACTTCGGCGGGGTAGGGTTACCCGCGGTCGGTTCAC  3659

Qy  3680  AGTAAGAATGCTCGTCAGTGTCCACTCTGGCGGCCAGGGTTACTGCGGCGCCGATTCAC  3739
          ||  ||||||||||| ||||  |||||| |||| ||||| |||||| ||||||| ||||
Db  3660  GGTAGGAATGCTCGTCCGTCCGTGGTAGGGTTAGGTTACCCGGGTAGGGTTAGGTTCAC  3719

Qy  3740  TAGGCCGTGGACTCAAGTACCAACAGATGCCAAGACTACCACAGAACCCCTCCGGTGCC  3799
          || |||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  3720  TAGGCCGTGGGACTCAAGTACCAACAGATGCCAAGACTACCACAGACCCCTCCGGTGCC  3779

Qy  3800  GGCAAAAGGAGTTTCAAGGAGGCCCGTGTTGTTATGCCGGGGGGCGGGAAAGAGCAC  3859
          |||||||||||||||||||||||||| | | ||||| |||||||||||||||||||
Db  3780  GGCAAAAGGAGTTTCAAAGAGGCCCGTGTTGTTTATGCCTACGGAGGGCGGGAAAGAGCAC  3839

Qy  3860  CCCGGTACCGTTGGAGTACGGCAACATGGGCCACAAGGTCTTGATCTTGATCTTCGGT  3919
          ||||| || |||| ||||||||||||||||| |||||| |||||||||||||||||||
Db  3840  CCCGGTCCCGTTGGAGTACGGCAACATGGGCCACAAGGTCTTAATCCTGGTTAATCTCCGGT  3899

Qy  3920  AGTACCGTGAGGGCCATGGGCCCATACATGGAGCACGTCAACACCCCAGTAT  3979
          |   || |||| |||||| |||||| |||||||| || ||||||||||||||
Db  3900  GGCCACTGTGAGAGCCATGGGCCATTACATGGAGCACGTGGTGTGTGTGAGGTCAACCAAGCAT  3959

Qy  3980  TTACTGTGCCATGACACCACTGCTTCACAAGGATCAACTTGGTGCAATTGGTTAGTATTC  4039
          || ||||| |||||||||||||  |||||| |||| ||||||||   || ||||| |||
Db  3960  ATACTGTGGCCATGACACCACTGCTTTCACGAGGATCACTTGGTGTCCCCGCCTACTCTGACATACTC  4019

Qy  4040  CACTTACGGAAGGTTTTGGCCAACCCCAGGGCCAGTGATGCTGAGGGGTGTCGGTGGTCAT  4099
          |||||||||||||||| |||||||||||||  |||| | | ||||||||| || ||||||
Db  4020  AACCTACGGAAGGTTTCTCGCCAACCCCAGGGCCAGTGATGCTCATTGAGAGGTGGGTCGGTGGTCAT  4079

Qy  4100  TTGTGACAGTGCCACAGTCATGACTCAACGTGTTGTTGGGCGTGTCAGGGA  4159
          |||||||||||||||||||||||||||||||||||| |||| || ||||||
Db  4080  TTGTGATGAATGCCACAGTCATGACTCAACGTGTGTGTTGGGCATTGGCCACCGGGA  4139

Qy  4160  GCTGGCGCGAGATGTGGAGTGCAATTGGTGCTCGTCTACCCCCACTGACTCGTATTC  4219
          ||||| | || ||||  |||| ||||||| ||| | ||| |||| ||| || |||||
Db  4140  GCTGGCACGTGGGGTGCGAGTGCAACTTGTGCTCTCTACGGTACTGCCGGCTCCTCCGGGCTC  4199

Qy  4220  CCCGATGACCCAGCACCCCATCAATCATTGAGACAAAACTGGAGATCCCCTT  4279
          ||| | |||||  || ||| ||||  |||||||||| | ||||| ||||| ||
Db  4200  CCCATGACCAGCACACACCCATCTATCATTGAGACTAAGCTGGATGTGGGAGAGATCCCCTT  4259

Qy  4280  CTATGGGACCATGGCTGGTTTGTCCCGACGTCTCATCGGCGTATTCTGCCA  4339
          |||| |||||| |  ||| || || || || ||||||||||  | ||||||
Db  4260  TTATGGGGCATGGCATAGCTTGTCCGGCCGTTTCTCGCTCCGTATTTTGCCA  4319

Qy  4340  CTCCAAGCTGAGTGCGAGCGGTAGCAGGTAGGGATGGGGGGTAAATGCCAT  4399
          ||| ||||| ||||||| ||||||||| |||| ||||||||||||| ||||
Db  4320  TTCCAAGCTGAGTGCGAGCGGTAGCAGGTAGAGGGGCCGCCAGTTTCTGCGCCTATTTTGCCA  4379

Qy  4400  CGCCTATTACAGCGGGGGAAAGACACAGTTCTATCATCAAAGATGGAGACCTGGTGGTGTGC  4459
          ||||||||||||||||||||||||| | || ||||||||||| ||||| ||||||||||||
Db  4380  CGCCTATTACAGCGGGGGAAAGACAGTTCTATCATCAAAGATGGAACGCGTGGTGGTGTGC  4459
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Db  4380  ||||||||| |||||| |||||||||| ||||||||||| |||||||| || |||||| ||
          TGCCTATTATAGGGCAAAGACAGTTCATCATCAAGGACGAGACTTAGTGTGTGTCGCC   4439

Qy  4460  TACAGACGCACTATCCACTGGGTACACTGGTACACTCGATTCGTCTCACCGATTGTGGGTT   4519
          ||||||||||||||||||||| |||||||||||||| |||||| ||  ||||||
Db  4440  TACAGACGCACTATCCACTGGGTACACTGGTACACTTCGATTCGTCTCACCGACTGCGGGTT   4499

Qy  4520  AGTGGTGGAGGAGGTCGTCGAGGTGAGGTGACCCTGATCCCACCATTACCATCTCCCTGCCAC   4579
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  4500  AGTGGTGGAGGAGGTCGTCGAGGTGACCCTTGATCCCACCATTACCACCTCCCTGCGAC   4559

Qy  4580  GGTGCCCGCGTCGGCTGAACTGTCGATCAGCCGGACCGGACGCCACGGGGGCAGGTC   4639
          |||| || ||||||||||||||| ||| ||||||||||||| |||||||||||||||
Db  4560  AGTGCCTGCTTCGGCTGAATTGTCGATCAGCAGACGACGACCACGGGTAGGGGCAGGTC   4619

Qy  4640  TGGGGCGCTACTACTACGCCGGGGTCGGCAAGGCCCTGCTTGTGTGTCGCCTTCAGTCC   4699
          |||||||||||||||||||||||||||||||||||||| ||  |||||||||||||||
Db  4620  TGGGGCCTACTACTACGCCGGGGTGGGCAAAGCTCCCGCTGTGTGTTCGCTCGGGTCC   4679

Qy  4700  TGTCTGGTCGGCGGTGGAAGCCCGGTGACCTGTACGGAATGGAACCTGACCTGACAGC   4759
          |||||||||||||||||| |||||||||||||||||||||||||| |||||||||||
Db  4680  TGTCTGGTCGGCGGTGGAAGCCCGAGTGACCTGTATGGAATGGAACCTGACTTGACAGC   4739

Qy  4760  AAACCTACTGAGACTTTACGACACAACTGCCCTTACCGCAGCCGTCGCCAGCTGACATTGG   4819
          |||||||||||||||| ||| ||||||| |||||||| |||||||||||||||||||| |
Db  4740  TAACCTACTGAGACTTTACGACACTGCCCTTACCGCAGCCGTCGCCAGCTGACATCCG   4799

Qy  4820  GGAAGCCGCGGTGTCTTTTCGGGGCTTCGCCCGTGAGGATGCATCCCGATGTTAGCTG   4879
          ||| ||||||||||| ||||||  || ||||||||||||||||| |||||||||||||
Db  4800  AGAAGCCGCGGTGTCTTTCTCTGGGCTCGCCCCATTGAGGATGCACCCCACGTTAGCTG   4859

Qy  4880  GGCAAAAGTTCGCGCGTCAACTGGCCCTTCGTGTTGGTGTTCAGCCGGACCATGTGCCG   4939
          |||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||
Db  4860  GGCAAAAGTTCGCGCGTCAACTGGCCCTTCGTGTTCAGCCGGACCATGTGCCG   4919

Qy  4940  GGAAACACTGTCTCCCGCCCATCGGATGACCCCCAGTGGCAGTCTGAAGGGCCCGAA   4999
          ||||||||||||||||||||||||||||||| ||||||||||||| |||||||||| |
Db  4920  GGAAACACTGTCTCCCGGTCTCCATCGGATGACCCCCAATGGCAGTCTGAAGGGCCCAAA   4979

Qy  5000  TCCTGTCCCACTCCTGCTGAGGTGGGCCAATGATTACCATCTAAAGTGGCCGGCCATCA   5059
          |||||||||||||||||||||||||||| ||||| |||||| |||||||||||||||||
Db  4980  TCCTGTCCCACTCCTGCTGAGGTGGGCCAACGATTACCATCTAAAGTGGCCGGCCATCA   5039

Qy  5060  CATCGTGGACGACCTGGTCCGTAGGCTCGGAGGGTTACGTCCGCTGCGATGC   5119
          ||||| |||||||||||||| || |||| || |||||||||||||||||||||
Db  5040  CATAGTGGACGACCTGGTCCGAGGCTCCGGAGGGTTATGTCCGCTGCGACGC   5099

Qy  5120  GGGACCCATCTGATGGTGGCCTATTGCGGGGGGCATGAGATCTATGCGTCATACAC   5179
          || |||||||||||||||||||||| ||||||| ||||||| ||||||||||||||||
Db  5100  TGGCCCATCTTAATGTGGTGGTCTCGCTATCGCGGGGGGCATGATGTCTCACTACGTCTTACAC   5159

Qy  5180  CGGGTCTCTCGTGGTGGTTACAGACTGGGATGTGAAGGGGGTGCAGCCCCTTTATCG   5239
          |||| - ||||||||||||||||||||||||||||||| |||| ||||||||||||||
Db  5160  CGGGTCAATAGTGGGTGGTGACAGACTGGGATGTGAAGGGGTGGCCGCCCCCCTTTATAG   5219

Qy  5240  GCATGGAGACGGCCAGCCACGCCCAGCCCCGGTTGTCCCCCGGTAGACCATCGGCC   5299
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  5220  GCATGGAGACGGCCAGCCACGCCCACAACCGGTTGTCCCCCGGTAGACCATCGGCC   5279

Qy  5300  GGGGGAGAGTCTGCCGCCATCGGATGTGGGGGGTGCCAACACAGATGCCGGCGGCCATCCA   5359
          ||||||||| |||||||||||||||||||||||| ||||||||| |||||||||||||||
Db  5280  GGGGGGAGAGTCTGCCGCCATCGGATGTGGGGGGTGCCAACACAGATGCCGGCGGCCATTCA   5339

Qy  5360  GGTGGATTGCGATTGGTCAGTCATGACCCGTCGATCGGGGAAGTGCTGTCCTTCGGCCCCA   5419
          ||||| |||||||||||| |||||||||||||||||| |||||||||||||||||||||||
Db  5340  GGTGGATTGCGATTGGTCAGTCATGACCCGTCGATCGGAGAAGTGCTGTCCTTGGCTCA   5399

Qy  5420  GGCTAAGACGGCCGAGGGCTACGCAGCTTACCACCAAGTGCTTGGCTTGCTGCTACACGGG   5479
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  5400  GGCTAAGACGGCCGAGGGCTACACAGCGACGACCACACAGCTTGGCTTGCTGCTACACGGG   5459

Qy  5480  GACGCGGGCCGTCCCCACTGTTCAATTGTTGACAAGCTCTTCGGGGGCGGGGCGGC   5539
          ||||| |||||||||||||||||||| || ||||| ||||||||||||||||||||
Db  5460  GACGCGGGCCGTTCCCACTGTTCAATTGTTGACAAGCTCTTCGCCGGAGGGTGGGCGGC   5519

Qy  5540  GGTGGTAGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGCGGCGGCCTATGGGCGTTCTAG   5599
          ||| ||||| ||||||| |||| ||||  || ||||||||||| |||||| |||||||||
Db  5520  TGTCGGTAGGCCATTGTCACAGCGTGATCGCGTGCGGCAGTGCAGCCTACGGGGTTCAAG   5579

Qy  5600  GAGCCCTCCATTGGCTGCTGCCGCTTCCTACCTCATGGGGCGTTGGGCGTCGGAGGCAACGC   5659
          ||||||||  || ||| |||||||||||||||||||| |||||| |||||||||||||||||
Db  5580  GAGCCCTCCGTTGGCAGCTGCCGCTTCTTACCTGATGGGGCGTTGGGGGTGGGGGCAACGC   5639

Qy  5660  GCAAACCCGCTTAGCCTCCGCTCCTACTAGGGCCGTTGGGACGCCTCTTGGGACCACGCC   5719
          |||| ||| ||||||| |||||||||| ||||||||||||||||| ||||||||||||||
Db  5640  TCAAACGCGTCTGGCATCCGCTCCTATTGGGGCTGTTGGGGACCGCCCTGGGCCACTCC   5699

Qy  5720  TGTCTGGGTTAACCATGCGGGGCGTTCATGGGAAGTGCTAGCGTCTCCCCCCTT   5779
          ||||| |||||| |||||||||||||||||||||||||||||||||||||||||
Db  5700  TGTCGTGGGTTTAACCATGCGGGGCGTTTATGGGAGGTGCTAGCGTCTCCCTCCTT   5759

Qy  5780  GGTCACCATTTACTGGGGGCCCGTGGGGGGCTGGTGAATGCGCGGGCTAGCCT   5839
          |||||||||||||| ||||| ||  |||||||||||||||||||||||||||||
Db  5760  GGTCACCATTTACTGGGGGCTGTGTAAGAAGTGGGAAGGCGTCGTCAACGGCGGCGAGCCT   5819

Qy  5840  TGTCTTCGACTTTATGCGGCGGGAAACTATCATCAGAGATCTGTGTATGCCATCCCAGT   5899
          |||||| ||||||||||||||| || ||||||||||||||||| ||||||||||||||||
Db  5820  TGTCTTTGACTTCATGGCGGGGGAAACTTTCATCAGAGATCTGTGTATGCTATCCCAGT   5879

Qy  5900  GCTAACCAGTCCGGGGCAGGACTTGCGGGATCCGCCTCGGGTTGGTGTTGTACTCAGC   5959
          ||| || |||||||||  |||| ||||||||||||||  ||||||| ||| |||||||||
Db  5880  GCTGACTAGTCCGGGGATCCGGGATCCGCCTCGGGTTGGTTGTTTGTACTCAGC   5939

Qy  5960  TAACAACTCTGGCACTACCACTTGGTTGAACCGTCTGCTGACTACATTGCCAAGGTCCTC   6019
          |||||||||||| || |||| |||||||||||||||||||||||| ||||||||||||| |
Db  5940  TAACAACTCTGGCACTACCACTTGGTTGAACCGTCTGCTGACTACATTACCTAGGTCTTC   5999

Qy  6020  ATGCATCCCTGACAGTTACTTTCAGCAGGCCGATTACTGTGACAAGTCTTCAGCTGTGCT   6079
          ||||||||||||||||||||||||||| |||||| ||||||| |||||||| |||||||||
Db  6000  ATGCATCCCTGACAGTTATTCCAGGCAGCGCTGACTATTGTGACAAAAGTCTCAGCTGTGCT   6059

Qy  6080  CCGAGCCTTGAGCCTCGACCTGCACCGTGGTTGCCCGTGGCTCAACAGGAGGCCTAAGGTGGA   6139
          ||| ||||||||||||  |||||||| ||||| |||| ||||||||||||||||||||||||
Db  6060  CCGGCCGTTGAGCCTTACCCGCACTGTGGTTGCCTTGGCTCAACAGGAGGCCTAAGGTGGA   6119

Qy  6140  TGAGGTTCAGGTGGGTACGTCTCGGGACTTGTGGGAGTGGATCATGCGTCAAGTGCGCAT   6199
          |||||||||||||||| ||| ||||||  |||||||||||||||||||||||||||||||
Db  6120  CGAGGTTCAGGTGGGTACGTCTCGGGACCTGTGGGAGTGGATCATGCGTCAAGTGCGCAT   6179

Qy  6200  GGTGATGGCCAGACTTCGGGGCCTTCGGGCGTCGTCATTACCCTTATGCCACTGCGG   6259
          || |||||| |||||||| |||||||||| |||||| |||||| | |||||||||||||
Db  6180  GGTCATGGCTAGACTCAGGGCCCTCGGGCGTGTCACTACCTTTGTGGCACTGTGG   6239

Qy  6260  GGAGGGGTGGTCCGGAGAATGTGTTGTTGGACGGGCCATGTTGTTGGACGTCGTTGTTGTGG   6319
          |||||| ||||||||||||||| |||||||||||| ||||||||||| |||||||||||||
Db  6240  GGAGGGGTGGTCCGGAGAATGTTGGACAGTCCCGTGAACATGCTGGGTTACGGTGAAAC   6299

Qy  6320  TTGCGTGATCACCGGTGATGTTTGAATGGGCAACTCAAAGATCCAGTTACTCTACCAA   6379
          |||||||||||||||||||| || |||||||||||||||||  ||||||||||||||||
Db  6300  GTGTGTGATCACCGGTGATGTTCTAAATGGGCAACTCAAAGAACCAGTTTACTCTACCAA   6359

Qy  6380  GCTGTGCAGGCATTATTGGATGGGGACAGTCCTGTGAACATGCTGGCTATGGCCGAGAC   6439
          ||||||||||||||  ||||||| |||||||||||||||||||||| |||||||| |||
Db  6360  GCTGTGCCGGCACTATTGGATGGGGACAGTCCCTGTGAACATGCTGGTTACGGTGAAAC   6419

Qy  6440  GTCGCCTTTGCTCGCCTCAGACCTCAGAGAGGTGGTTACCATTCGGGACGTCTGGGTGGGC   6499
          ||||| |  |||  ||||| ||||| ||||||||| ||||||||| ||||||||||||||
Db  6420  ATCGCCCCCTGGCCTCTGACACCCGAAGTTGTTACCCTTCGGGGCGGTCTGGGGGGC   6479

Qy  6500  TGAGGTGGTGGTGACCCTGATGTTTGAATGGGCAACTCAAAGATCCAGTTGTGCT   6559
          ||||| ||||| ||||||| | |||||||||||| ||||| |||||||||||||||
Db  6480  TGAGGTGGTGGTGACCCCCACCCAGTGAGTGACCAGTTGCTGCT   6539

Qy  6560  GCGCCAGCAAATCCTGTCGGCTGCTGTGTGGCCCTTATTACGTGCGACGGGCATACCGGT   6619
          |||||||||| |||||||||||||||||| |||||||||  ||||||||| ||||||||
Db  6540  GCGCCAGCAAATCCTATCGGCTGCTGTGAGCTGAGCCCGTCGGTACGTGCGACGGCATTCCGGT   6599
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Qy   6620 CTCATGGGACGCCGGACGCGCGAGCGCGCTGCCATGGTCTATGGCCGGCTCAC 6679
          |||||||| || ||||   |||||||||||||||||||||||||||||||||
Db   6600 CTCGTGGGACGGGGACGCGCGGCGCGCCATGGTCTATGGCCGGCAAAGTGTTAC 6659

Qy   6680 CATTGACGGGGAACGCTACACCCTTCCGCATCAACTGCGGCTTAGGAATGTGGCGCCCTC 6739
          |||||||||||||||||||||||||   |||||||||| |||| |||||||||||||||
Db   6660 CATTGACGGGGAGCGCTACACCCTCCATCAACTGCGGCTCAGGAATGTGGCACCCCTC 6719

Qy   6740 TGAGGTGTCATCCGAGTGTCATTGACATTGGACCGGAGACTGAAGACTCAGAACTGAC 6799
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6720 TGAGGTTTCATCCGAGTGTCATTGACATTGGACCGGAGACTGAAGACTCAGAACTGAC 6779

Qy   6800 TGAGGCCGACCTGCCCGCCGGCGGCCGCTGCAGCCTCATCGAGAATGCTGCGAGAAT 6859
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6780 TGAGGCCGACTTGCCCGCCGGCGGCCGCTGCAGCCTCATCCAAGCGATCGAGAATGCTGCGAGGAT 6839

Qy   6860 TCTTGAACCTCACATAGTGCTCATCATGGAAGATTGCAGTACACCCTCTTGTGGGAG 6919
          |||||||   |||||||| |||||||||||||||||||||||||||||||||||||
Db   6840 TCTTGAACCGCATATATTGATGTCATCATGGAAGATTGCAGTACACCCTCTTGTGGTAG 6899

Qy   6920 TAGCCGAGAGATGCCTGTGTGGGGAGAAGACATACCCCGCACTTCCATCGCCAGCACTTAT 6979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6900 TAGCCGAGAGATGCCCTGTGTGGGGAGAAGACATCCCCGCACTTCCATCGCCAGCACTTAT 6959

Qy   6980 CTCGGTTACTGAGAGCAGCCCAGATGAGAAGACCCCGTCGGTGTCTTTCCTGCGAGGAGGA 7039
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6960 CTCGGTTACTGAGAGCAGCTCAGATGAGAAGACCCCGTCGGTGTCTTTCCTGCGAGGAGGA 7019

Qy   7040 TACCCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCAAGACAGCCGAGAGGGGAGGA 7099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7020 TACCCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCGAGACAGCCGAGAGGGGAGGA 7079

Qy   7100 AAGCGTCTTCAACGTGGCTCTTTCCGTACTAAAAGCCTTGTTTCCGAGCGATGCCAC 7159
          ||  |||||||||||||||||||||||||||||||||||| |||||||||||||
Db   7080 AAGTGTCTTCAACGTGGCTCTTTCCGTACTAAAAGCCTTGAATTTCCGAGCGATGCCAC 7139

Qy   7160 AAGAAAGCTTACCGTTAAGATGTCATGCGTGTGTTGAGAAGAGCGTAACACGCTTCTTTTC 7219
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   7140 CCGGAAGCTTACCGTCAAGATGTCATCGTGTGTTGAGAAGAGCGCACACGTTTCTTTTC 7199

Qy   7220 ATTGGGATTGACGGTGCTGCTGACGTGGCCAAGCCTGTGTGAGATGGAAATCCAGAACCATAC 7279
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db   7200 GCTGGGATTGACGGTGCTGCTGACGTGGCCAAGCCTGTGTGAGATGGAAATCCAGAACCATAC 7259

Qy   7280 AGCCTATTGTGACAAGGTGCGCACTCCGCTTGAATTGCAGGTTGGGCGTTGGTGGTGGCAA 7339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7260 AGCCTATTGTGACAAGGTGCGCACTCCGCTTGAATTGCAGGTTGGGCGTTGGTGGTGGCAA 7319

Qy   7340 TGAACTTACCTTGAATGCAAGAGTTGACAAGGTTAGGCAAGAGACCTTGGCTTCCTTTCTC 7399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7320 TGAACTTACCTTGAATGCAAGAGTTGACAAGGTCAGGCAAGAAACCTTGGCCTCCTTCTC 7379

Qy   7400 TTACATTTGGTCTGGGGTTGCCACTAGGAGAGGCCACTCCGGCCAAGCCCCCTGTGGTGAG 7459
          ||||||||||||||||||||||||||||||| ||||||| ||||||||||||
Db   7380 CTACATTTGGTCTGGGCGTGCCACTGACTGGCTACTCCGGCCAAGCCCCCTGTGGTAAG 7439

Qy   7460 GCCGGTTGGTCCTTGCTGGTTGTGCTTGTATGTCACCACCAAGGTGTCACCCGGACAA 7519
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   7440 GCCGGTTGGTCCTTGCTGGTTGTGGCAGCACCACCAAGGTGTTCCAACCCAGACAA 7499

Qy   7520 TGTTTGGGAAGAAGTTGACAAGGTTGACCTTCTGCGGTGTCCCCTAGGGTTCATGTGACAAATT 7579
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   7500 TGTGGGGAAGAAGTTGACAAGGTTGACCTTCTGCGGTCTCCGAGGGTTCATGACAAATA 7559

Qy   7580 CCTCGTGGACTCCATGAGCCGCGCTAAGGCGCTGAAGCCTAGCTGCCTAAGCCATGGGTTA 7639
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Db   7560 CCTCGTGGACTCGATCGAGCCGCGCTAAGGAGGCGCTCAAGGCCTGCCTGAGCCATGGGTTA 7619

Qy   7640 CACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCCATGGGGATCTAA 7699
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Qy   7700 GGTGTCGGTCAAGGACCTCCCACCCTGCGGGGAGATGCTGTCCATGACCGGCTCCA 7759
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Db   7680 GGTGTCAGTCAAGGATCTTCCACCCTGCGGGGAAGATGCTGGCCATGACCGGCTCCA 7739

Qy   7760 GGAGATACTTGAAGGGACGGCCAGTCCCCTTTACTCTTACTGTAGTGAAAAAGGAAGTGTTCTT 7819
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Qy   7820 CAAAGACCGAAAGGAGAAGGAAGGCCCCCCGCCTCATTGTGTTCCCCCCTGGACTTCCG 7879
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Qy   7880 GATAGCTGAAAAGCTTATTCTGGAGACCCCCAAATCAGCGAATTAGGGAGAGTGCTGCGAGAAT 7939
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Qy   7940 GGCCTACGGCCTTCCAGTACACCCCAAATCAGCGAATTAGGGAGAGTGCTCAAACTGTGGGA 7999
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Qy   8000 ATCAAAGAGACACCATGGCCATCTGTGTGGACGCCACATGCTTCGACGAGTAGCATAAC 8059
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Qy   8180 AGTGGTGAGAGGTATTGTAGATCCTCAGGGGTCTTGACCCAGTGCGAGCAACTGCTT 8239
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Qy   8240 GACTTGCTATATCAAGGTGAAAGCCGCTGTGAGAGGGTGGGCTGAAAAATGTCTGCT 8299
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Qy   8300 CCTCATCGCTGGCGATGACTGTTTGATCATATGGACACGGCCTGTGTGCGATCCTAGCGGA 8359
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Qy   8420 ACTGGACACGGCCCCCTCTCCACTTGGCTAGCTGAGTGCAATGCAGATGGGAAACG 8479
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Qy   8480 CCATTTCTTCCTGACCACCGACTTTCGGAGGCCCCTCGCTCGAGCGTACCAGTACAG 8539
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Qy   8540 TGACCCCAATGGCTTCGGCGTTACATCCCTGGCATCCTATACCCTTGGCATCATCACACG 8599
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Qy   8600 GTGGGTCATCATCCCTGCTCACCGTCTGACGTTAGGGTGTGGCACACCGTCTGA 8659
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Qy   8720 CATCATCGGTGCCCTCCACAGGGCCAATAAGGACTGTGAAGCTGCCACAGCAGGTTACCGAGACCAACTAAGAC 8779
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                      /organism="unidentified"
                      /db_xref="taxon:32644"
     BASE COUNT      1692 a   2554 c   2995 g   2154 t
ORIGIN

Query Match          86.2%;    Score 8100.6;   DB 6;   Length 9395;
Best Local Similarity 91.4%;    Pred. No. 0;
Matches 8586;   Mismatches 809;   Conservative 0;   Indels 0;   Gaps 0:

Qy      1 TGACGTGGGGGGTTGATCCCCCCGGCACTGGGTGCAAGCCCATAAACCGACGC 60
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Qy     61 CTATCTAAGTAGACGCAATGACTCGGCGCGACTCGGCGCGACTGGTGGTGGTGGAT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    181 GTCTTAAGAGAAGGTCAAGACTCCTCTTGTGCTGCGGGAGACTCGTCGTGTTAAACCGAGCCC 240
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Qy    301 GTCACCCACCTGGGCAAACGACGCCACGTACGGTCGCCCTTCAATGTCTCTCT 360
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Qy    361 TGACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAGTGGGGGCCCGGGGGTTATGGGGA 420
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Qy    541 TTTTCTATACCATCATGGCCACTGTATCGGGGTTGCGTGTCGGGTTCGGCTCTCGGCTT 600
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Db    541 TTTTGTACTGACCAGCTGCCACTGTATCAGGCGAGCTTGACGGGGCCCCGGCAAGTT 600

Qy    601 TGGCCCCGGCCACCACGCTTGGGAATGGCGAATGGGCAATATTTCCTCACAAATTGTCTGTG 660
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Qy    721 TTTGCACGACCGTTGCTGGCCACTGTATCAGGCGGAAGT 780
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Qy   8840 GAAGAAGGCCCGGGCCATTGGCCAACGCGTATGCTCCGGTGCGCGGCTGGGGTTGGGCTGAGTTGGC 8899
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Qy   9080 GTGAACTAAATTCATCTGTTGCGGCAAGGTCCGGTGACTGATCATCACTGGAGGAGGTTC 9139
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KEYWORDS    JP 1997276000-A/2.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 9395)
  AUTHORS   Okamoto,H.
  TITLE     HEPATITIS NON-A NON-B NON-C VIRAL GENE NUCLEOTIDE AND DETECTION
  JOURNAL   Patent: JP 1997276000-A 2 28-OCT-1997;
            NIATSUKU:KK
COMMENT     OS   GBV-C/HGV
            PN   JP 1997276000-A/2
            PD   28-OCT-1997
            PF   18-APR-1996 JP 1996134117
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Qy   3241 CAGTTGTCATCCGTCGGTGCGGAAAGGGCTTCCTGGGGTCACGAAGGCAGCCTTGACAG 3300
          | |||||||||||||| |||||||| |||||||||||||||||||| ||||||||||||
Db   3241 CCGTTGTCATCCGGCGGTGCGGAAGGGGTTCCTGGGGTCACTAAGGCTGCCTTGACAG 3300

Qy   3301 GTAGGGATCCTGACTTACATCCAGGGAACGTCATGGTTGTTGGGGACGGCTACGTCACGAA 3360
          || |||||||||||||| ||||||||||||||||||||||||||||||||||||||| ||
Db   3301 GTCGGGGATCCTGACTTGCATCCAGGGAACGTCATGGTTGGGGGACTGCCACGTCGCGGAA 3360

Qy   3361 GCATGGGCACACGTCTGAATGGCCTGCGTCGTTCACAACTTTCCATGGGCTTCATCCCGAA 3420
          |||| || || ||| || |||| |||||| |||||||||||||||||||||||||||||||
Db   3361 GCATGGGAACGTGTTTGAACGGCTGCGTCGTTCACAACTTTCCATGGGCTTCATCCCGAA 3420

Qy   3421 CCATGCCACGCCCGTGGGGGCCCTTAATCCCAGGTGGTTGTCAGCCAGTGATGACGTCA 3480
          |||||||||||||||| ||||||||||||||||||||| ||||||| || |||||| ||
Db   3421 CCATGCCACCCTGTGGGGGCCCTAAATCCCAGGTGGTCGGCAAGTGATGATGATGTCA 3480

Qy   3481 CGGTGTACCCGCTTCCAGATGGGCAACTTCGTTGCGTCCCTGCACTTGCCAGGCGGAGT 3540
          ||||||||| || |||||||||| |||||| ||||||||||||| |||||||||||||
Db   3481 CGGTGTACCCCTCCCCCGGATGGGCAACCTCGTTAACACCCGCTGCACCCTGCCAGGCTGAGT 3540

Qy   3541 CCTGTTGGGTTATTAGAGTCCGACGGGGCGTTTGTGCGCTTCAGTGCTGTCCACCTTGGCGCCAGGG 3600
          | ||||||||||| ||| |||||| || ||| | ||||||||||||||||||| ||||||||||
Db   3541 CCTGTTGGGTCATCCGATCAGACGGGGAATGGCTTTATGCCATGGCTTTGAGCGTCCAGGGGGACAAGG 3600

Qy   3601 TTGAGCTGGATGTGGCCCATGGGCGTCTCTGACTTCGTTGTTCGTGTTCCGTTCACCGGTCC 3660
          | |||||||||| |||||||||||||||||| |||| ||||||||| ||||||||||| ||
Db   3601 TAGAGCTGGATGTGGCCCATGGGCGTCTCTGATTTCGATTTCCGTTCCTGTTCACCGTGTCT 3660

Qy   3661 TTTGCGACAAAGGGCACGCAGTAAGAATGCTCGTTCGTGTCAGTGCTCCACCTGCCCGGCCAGGG 3720
          || | |||||||||||||||||||| | ||||| | ||||||||||||||| ||||||||||||
Db   3661 TGTGTGACGAGGGACACGCAGTAGGAATGCTCGTTCGTGTCAGTGCTCCATCCGGCTGTGTCGGG 3720

Qy   3721 TTACTGCGGCCGAGTTCACTGAGGTCCTGACTCAAGCTCAAGGAGATGCCAAGACTACCA 3780
          ||| | |||| |||||||||| | |||||||||||||||| |||||||||||||||||
Db   3721 TCACCCGGCCTGATTCACTGAGGTCCTGACTCAAGCTCAAGGAGATGCCAAAACTACCA 3780

Qy   3781 CAGAACCCCTCCGGTGCCGCTACCCGTCCAGGAGTTTGGAGTACGGCCCACATGGGCCCTA 3840
          ||||||||||| ||||||||||||||| ||||||||||||||||| ||| ||||||||||
Db   3781 CTGAACCCCTCCGGTGCCAGCCGTCCGGTTCCAAAGAGTTTGGAGTACGGCCCCGTTTTATGCCTA 3840

Qy   3841 CGGGGGCCGGAAAGAGCACCCGCGTCCGCGGTACCGTCCGCAACATGGGCCCGCACAAGGTCT 3900
          ||||||||||||||||||||| |||||| |||||||| ||| ||||| ||||||||||||||
Db   3841 CGGGGGCCGGAAAGAGCACCGCGTCCGCGGTACCGTCCGCAACATGGGCCGCACAAGGTCT 3900

Qy   3901 TGATCTTGAACCCGTCGGTAGCTACCGTGCTACTGGCCATGAGAGCGTCCATACATGGAGCGGCTGG 3960
          || | | ||||||||||||| || |||||||||||| |||||||||||||||| | ||||||||
Db   3901 TAATCCTAAACCCCTCAGTGGCTACTGGCCATGAGAGCGTCCATGGCCCTTACATGGAGCGACTGG 3960

Qy   3961 CGGGGAAACACCCCAGTATTACTGTGGCCATGACCACTGCTTTCACAAGGATCACTG 4020
          |||| |||| ||| || | || ||||||| ||||||| ||||||||||||| ||||
Db   3961 CGGGCAAACATCCAGTGGTGGTCTTCACCGGGATTACTGTGGCCATCATGACTGCTTTCACGAGGATTACTG 4020

Qy   4021 ACTCCGCCCTTACGTATTCCACTTACGGAAGGTTTTTGGCCAACCCTAGGCCAGATGCTGA 4080
          || || | |||||| | |||||||||||||||||||||||||||||||||||||||
Db   4021 ACTCCGCCCTTACGTATTCTACCTATGGGAAGGTTTCTGGCCAACCCTAGGCCAGAGTGCTCC 4080

Qy   4081 GGGGTGTGCCGTTCGGTGGCTGGTCATCGTGACGAGTGCCACAGTCAACTGTCAACTGTGTTACTGG 4140
          |||| |||| |||||||| || ||||| |||| |||||||||||| || |||||||||||
Db   4081 GGGGTTGCGCCGTTCGGTTTCGGTGGCTCATCGTGACGAGTCAGCTGTCAGCTTGTGCTCTACGGCA 4140

Qy   4141 GCATTGGGCGTGTCAGGAGCTGGCGCGAGGATGCGGCAATTGGTGCTTACGCTCTACCGCCA 4200
          |||| |||||||| ||  |||||||||||||||||||||||||||||| |||||||||||||
Db   4141 GCATCCGGCGGCGAGCTACGGCAGCGTGGTGCCTGCCGCGCTGTGGCTGAGTGCAGCTTGTCTCTACGCCA 4200
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Qy   4201 CTGCCACCCTCCCGGATCCCGGTGACCCAGCACCATCAATCATTGAGACAAAACTGG 4260
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   4201 CTGCCACACTCCCGGGTCCCCGGTCCCCTATGACCCAGCACCATCAATTATTGAGACCAAACTGG 4260

Qy   4261 ACGTGGGAGAGATCCCCTTCTATGGCATGGCATACTCCTTGAGCGGATCGGACCGGAA 4320
          | ||||||||| ||||||||||||||||||| |||||||||||||||||| ||||| |
Db   4261 ATGTGGGAGAGATCCCCTTCTATGGCATGGCATACCCTCGAGCCCTCGAGCGGCAATGCGAACCGGTA 4320

Qy   4321 GGCATCTCGTATTCTGCCACTCCAAGGCTGCGAGCGGCGCCTGCGCGGCCAGTTTTCGG 4380
          |||||||||||||||||||||| |||||||||||||||||| |||||||||| ||||||
Db   4321 GGCATCTTGTATTCTGCCATTCCAAGGCGGCGAGTGTGACCCGGTGAGCCGGCCAGTTTTCCG 4380

Qy   4381 CTAGGGGGTAAATGCCATCGCCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATG 4440
          | |||| ||||| |||||| |||||| |||||||| ||||||||||||||||||||
Db   4381 CGAGGGGGTCAACGCCATCGCCTATTATAGGGGAAAGGACCAGTTCTATCATCAAGGACG 4440

Qy   4441 GAGACCTGGTGGTGTGCTACAGACGCCACTATCCACTGGGAACTTCGATT 4500
          |||||||||||| |||||| |||||||||||| |||||||||||||||||
Db   4441 GTGACCTGGTGGTGTGTGTGCCACAGACGCCACTATCCACGGGGAACTTCGATT 4500

Qy   4501 CTGTCACCGATTGTGGGTTAGTAGTGGTGGAGGTCGTCGAGGTGACCCTTGATCCCACCA 4560
          |||||||||||||| || ||||||||||||||||| ||||||||||||||||||| ||||
Db   4501 CTGTCACTGATTGTGGGTTAGTGGTGGTGGAGGTCGTTGAGGTGACCCCTTGATCCCACCA 4560

Qy   4561 TTACCATCTCCCCTGCCACGGTGCCCCGTCGCGTCGAACTGTCGATGCGCGGCGGAGGAC 4620
          ||||||||||||||||||||| |||||||| || |||||| ||||||||||||||||||
Db   4561 TTACCATCTCCCCTGCCACGGTCCGTCGGTCCGGTCCGCAGAATTGTCGATGCAACGGCGGAGGAC 4620

Qy   4621 GCACGGGTAGGGCAGGTCTGGCCGCTACTACGGCGGGTCGCAAGGCCCCTGCTG 4680
          ||||||||||| ||||| ||||| ||||||||| |||||||||||||| ||||
Db   4621 GCACGGGTAGAGGCAGTGCGGCCGCTACTACGGCTGGGTCGCAAAGCCCCTGCGG 4680

Qy   4681 GTGTGTCGCAGTGACATTGGGCAGGCCGCGGTGTTCTTTTCGGGGCTTGACCGGTACGGAA 4740
          || |||| |||||| ||||||||| || |||| ||||||| | || |||||||||||| |
Db   4681 GTGTGTGCCGCTGTCAGGTCCTGTCTCGGTGGTCAGCGCTGGAAGCCGGAGTGACCTGGTACGGAA 4740

Qy   4741 TGGAACCTGACCTGACAGCACAAACTACTGAGACTTTACGACAACTGCCCTTACACCGCAG 4800
          ||||||||||||||||||||||||| |||||||||||| |||| ||| | || ||||||||
Db   4741 TGGAACCTGACCTGACAGCACAAACTACTGAGACTTTACGACGACTGCGCCTGCTTACACCGCAG 4800

Qy   4801 CCGTGCAGCTGACATTGGGACGTGTCTTCTTTCGGGGCTTGCCCGTTGAGGA 4860
          |||| |||||||||| ||||| ||| ||| ||||| ||||||||||||||||
Db   4801 CCGTGCAGCTGACTGGGACGTGTCTTCTCGTGTTTCTCCGGGCTGCCCGTTGAGGA 4860

Qy   4861 TGCATCCGATGTTAGCTGGCAAAGTTCGGCGGCGCAAAGTTCGGGCCCTTCCTGGTGTGGTG 4920
          ||| |||| ||| ||||||||| ||| | ||||||||| |||||||||||||| |||||||
Db   4861 TGCACCCGATGTTAGCTGGCAAAGTGCCGCGGCGTCAATTGGCGACCCTCGTTGGTGGGTG 4920

Qy   4921 TTCAGCGACCATGTGCGGGACCCCATCGGATGACCCCAGTGGG 4980
          ||||||||||| ||||| ||||||||| ||||||||||||||||
Db   4921 TTCAGCGACCAGTGTGCCGGGAAACACTGTCCCATCGGGACGACCCCCAATGGG 4980

Qy   4981 CAGGTCTGAAGGGCCCGAATCCTGTCCCACTCGCTGGAGTGGGCCAATGATTACCAT 5040
          ||||||||||||||||| ||| || |||| ||||||| ||||||| ||||||||||
Db   4981 CAGGTCTGAAGGGCCCAAATCCTGTTCCACTACTGCTGGAGTGGGCCAATGATTACCAT 5040

Qy   5041 CTAAAGTGGCCGGCCATCACATCGTGCGACCTGGTCGTGGACGACTCACTG 5100
          ||| ||||||||||||||| |||| ||||||| | ||||||||||||||||
Db   5041 CTAAGTGGCCGGCCACCACATTGTTGACGACGTGGTCGTAGGCCTCGTGTGGCGGAGG 5100

Qy   5101 GTTACGTCCGGCTGCGATGCGGGACCCATCTTGATGGTGGGCCTCGTATTGCGGGGGGCA 5160
          |||||| |||||||||||||| ||||| ||||||||||||||||| | ||||||||||||
Db   5101 GTTACGTCCGGCTGCGACGCGGGACCCCATCTTGATGGTGTGGGCCTTGCCATAGCAGGGGCA 5160

Qy   5161 TGATCTATGCGTCATCACCGGGTCAACTGTGTTGTTGG 5220
          ||||||| ||| || ||||||||||||||||| |||||
Db   5161 TGATCTACGCGTCTTACACCGGGTCATTGGTGTGTGACTGTGAAGGGTGAGTGTCAGTGG 5220

Qy   5221 GTGGCAGCCCCTTTATCGGCAGGATGGCAATTGGTGCTTGTGCAGTCC 5280
          |||| ||||||| |||||||||| |||||||||||| ||||||||||||
Db   5221 GTGGCAGCCCCCTTTATCGGCAGGAGGAGACAGGACCCAGCCCGTTGTCAGTGG 5280

Qy   5281 CCCCGGTAGACCATCGGCCGCCGGGGGAGAGTCTGCGCGCCATCGATGCCAACACAGTGACACAG 5340
          ||||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||
Db   5281 GCATCCGGCAGTAACGGCCGCGGCTGGCGGCTGTGTCCCCTGTGTCTGTCTACGCCA 5340
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Db  6361 AACCAGTTACTCTACCAAGCTGTGCAGGCACTATTGGATGGGACCGTTCCTGTGAACA 6420

Db  6361                                                            6420
Qy  6421 TGCTGGGTATGGGTGAGGACGAGT-G|-|||||-||-|||TTGCTCTGCTCGGCTCGCCT 6480
Db  6421 TGCTGGGTTACGGCGAAACATCCCCTGTCCGACACTCCAAAGGTGGTTCCTT 6480

Qy  6481 TCGGGACGTCTGGGTGGGCTGAGGTGGTGGTGACCCGTTGTGATCAGGCGAA 6540
Db  6481 TTGGGACGTCGGGCTGGGCTGAGGTGGTGACCCCGTACCCAGCTGGTGATCAGGAGGA 6540

Qy  6541 CATCCGCCTACAAACTGCTGCGCCAGCAAATCCTTGTCGGCTGCTGTTGCTGAGCCCTATT 6600
Db  6541 CCTCTTCCTACAAGTTGCTGCGCCAGCAAATCCTATCAGCTGCTGTTGCTGAGCCCTATT 6600

Qy  6601 ACGTCGACGGCATACCGGTCTCATGGACGCGGAGCGGCCTGCCATGGTCTATG 6660
Db  6601 ATGTTGATGGCATACCGGTCTCATGGACGCAGATGCTGTGCACTGCTATGGTTTATG 6660

Qy  6661 GCCCTGGCAAAGTGTCACCATTGACGGGGAACGCTACACCCTTCCGATCAACTGCGGC 6720
Db  6661 GCCCTGGCAAAGTGTTACCATTGACGGGGAGCCGTACACCCTTCCGATCAACTGCGGC 6720

Qy  6721 TTTAGGAATGTGGCGCCCTGAGGTGTCATCCGAGGTGTCATTGACATTGGGACGGAGA 6780
Db  6721 TTTAGGAATGTGGCGCCCTGAGGTTCATCCGAGGTGTCATAGACATTGGGACGGAGA 6780

Qy  6781 CTGAAGACTCAGAACTGACTGAGGCCCTGCCGCCCGGCTGCAGCGTATCAACTGCGGC 6840
Db  6781 CTGAAGACTCAGAACTGACTGAGGCCCTGCCGCCGGCTGCTGCCTGCTGTCTCCAAGCGA 6840

Qy  6841 TCGAGAATGCTGCGAGAATTCTTGAACCTGCTCCATGATGTCATCATGGAAGATTGCAGTA 6900
Db  6841 TCGAGAATGCTGCGAGGATTCTTGAACCGCCACATTGATGTCATCATGGAAGATTGCAGTA 6900

Qy  6901 CACCCTCTCTTTGTGGGAGTAGCCGAGAGATGCCTGTGTGTGGGAGAAGACATACCCCGCA 6960
Db  6901 CACCCTCTCTTTGTGGGAGTAGCCGAGAGATGCCTGTGTGTGGGAGAAGAGTGCCCCCGCA 6960

Qy  6961 CTCCATCGCCAGCACTTATCTCGGTTACTGAGAGCCAGATGAGAAGACCCGTCGG 7020
Db  6961 CTCCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCTCAGATGAAGAGACCCGTCGG 7020

Qy  7021 TGTCTTCCTCGCAGGAGATACCCGTCTTCGACTCATTGGAGTCATCCAAGAGTCCG 7080
Db  7021 TGTCCTCTTCCTCGCAGGAGATACCCGTCTTCGACTTCGAGTCATCCAAGAGTCCG 7080

Qy  7081 AGACAGCCGAAGGGGAGGAAGGTGTCTTCAACGTTGCCTCTTTCCGTACTACTAAAAGCCTTGT 7140
Db  7081 AGACAGCTGAAGGGGAGGAAGAGTGTCTTCAACGTTGCTTCTTTCCGTATTAAAAGCCTTGT 7140

Qy  7141 TTCCACAGAGCGATGCCAACAGAAAGCTTACCGTTAAGATGTCATGCGTGTGTTGAGAAGA 7200
Db  7141 TTCCACAGAGCGATGCCAACAGAAAGCTTACCGTCAAGAATGTCATGCGTGTGTTGAGAAGA 7200

Qy  7201 GCGTAACACGCTTCTTTCATTGGAGATTGGACGGTCGCAAGCCGTGTGAGA 7260
Db  7201 GCGTCACACGCTTCTTTCGTTAGGTTGGACGGTCGGCTAGCCGTGTGTGTGAAA 7260

Qy  7261 TGAAATCAGAACCATACAGCCTATTGTGACAAGGTGCCACTCCGCTTGAATTGCAGG 7320
Db  7261 TGAAATCAGAACCATACAGCCTATTGTGACAAGGTGCCACTCCGCTTGAATTGCAGG 7320

Qy  7321 TTGGGTGCTTGGTGGTCGGGCAATGAACTTACCTTGAATGAGGCTAGGCAAG 7380
Db  7321 TTGGGTGCTTGGTGGTCGGGCAATGAACTTACCTTGAATGAGGCCAGGCAAG 7380

Qy  7381 AGAGTCGTTGTCTTTGGTGCTGATCACCGGTGATGTTTTGAATGGGCAACTCAAAG 7440
Db  7381 AGACCTTGCTTGTCTTCTCCTACATCTGTTCCTACTGGGCAACTCAAAG 7440

Qy  7441 CCAAGCCCCTGTGGTGAGGCGTTCCCGTGGGGGTCCCGTTTAGTGTGGCTGACACCAAGGTGT 7500
Db  7441 CTAAACCACTGTGGTGAGGCCTGTGAGGCGTGGGGGTCCCGTTTAGTGGTGCTGACACTAAAGTGT 7500
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Db  5281                                                            5340
Qy  5281 CCCCGGTAGACCATCGCCGGGGCGGGGGGAATCTTGCGCCCATCGATGCCGATGCCAAGACAGTGACAG 5340

Qy  5341 ATGCGGTGGCGCCATCCAGTGGATTGCGATTGGTCAGTCGATCGGGG 5400
Db  5341 ATGCGGTGGCGCCATCCAGTGGATTGCGATTGGTCAGTTATGACCCTGTCGATCGGGG 5400

Qy  5401 AAGTGTGTCCTTGGGCACTGAGGCCTAAGACGGCCGAGGCCTACGCCAGCTACCACCAAGTGGC 5460
Db  5401 AAGTACTGTCCTTAGCTCAGGCTAAGACGGCCGAGGCCTACCACCAGCTGGATGACGCCAAGTGGC 5460

Qy  5461 TTGCTGCTGGTCACAGGGGACGCGGCGGCCGTCCCACTGTTTCAATTGTTGACAAGCTCT 5520
Db  5461 TCGCTGCTGGTCACAGGGGACGCGGGGCCGTCCCTACTGTTTCAATTGTTGACAAGCTCT 5520

Qy  5521 TCGCCCGGGGGGCTGGGGCGGCCGTGGTAGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGG 5580
Db  5521 TTGCGACCGAGGTGGCCGTCCCGTGGTGGCCCATTGCCACAGTCGTATGATGGGCCGTGG 5580

Qy  5581 CGGCCTATGGGGCTTCTTAGGAGGGGTTTCATTGGCTGCTGCCGCTTCCTACCTCATGTGGGT 5640
Db  5581 CGGCCTACGGGGCTTCCAGAGAGCCCGCGCCCCGCGCGTTCCTACCTCATGTGGGAT 5640

Qy  5641 TGGGCGTCGGAGGCAACGCGCAAACCGCTTAGCCTCCGGCTTCCTACTAGGGGCCCTG 5700
Db  5641 TGGGCGTCGGAGGCGAACGCGCAGACCGCGGCTCCTCTGGATCCGGCTTCCTATTGGGGGCTGCTG 5700

Qy  5701 GGACCGGCTCTGGGCACCCGTCTGTGGGGTTAACCAGTGCGGGCGCGTTCATGGGAAGTG 5760
Db  5701 GTACCGCCCCTGGGCACGTCGTTCGTGGGACTAACCAGTGCGTTCATGGGGGTG 5760

Qy  5761 CTAGGGCGTCTCCCCCTTCCTTGGTCACCATTTTACTGGGGGGCCGTGGGGGCGTGGGGACGGGCG 5820
Db  5761 CCAGGGCGTCTCCCCCTCCTTGGCACTATTCTACTCTACTGCCGGAGGTTGGGAGGGCG 5820

Qy  5821 TGGTGAATGCGGCTAGCCTTGTTCTTCTGACTTTATGCGGGGGAAACTTATCATCAGAAGATC 5880
Db  5821 TTGTCAACGCGCAAGCCTTGTCTTCGACTTTATGCGGGGAAGCTTTCATCAGAAGATC 5880

Qy  5881 TGTGGTATGCCATCCAGTGCTAACCAGTCCGGGGATCGCCCTCG 5940
Db  5881 TGTGGTATGCCATCCAGTGCTAACCAGTCCGGGGATCGCGCTCTTG 5940

Qy  5941 GGTTGGTGTTTGTACTCAGCTAAGAGGTTGGATGAGGTTCAGGTTGAACCGTCTGCTGA 6000
Db  5941 GTCTGGTTTTGTACTCAGCTGGATGAGGTCGCAGGTTCGGATCTCTGGGAGTGA 6000

Qy  6001 CTACAATTGCCAAGGTCAGTGATGAGTGTCCATGCATGCGTGACTTTCAGCAGGCCGATTACTGTG 6060
Db  6001 CTACGTTGCCGAGGTCCTCAGCGTCATGCCATGTCGTGACTTTCAGCAGGCCGACTACTGCG 6060

Qy  6061 ACAAGGTCTCAGCTGCTGCGTGTCCCGTCGTTGGCTCCGAGAATGGTTGTTGCCCTGGTCA 6120
Db  6061 ACAAGGTTCGGAGTGCAGTTCGCCGTCGTTGGTTGCGGAATGGCTGCACCCGCCGCCTGGTCA 6120

Qy  6121 ACAGGGAGCCTAAGGTAGGTTCAGGTTGGATGAGGTCGCAGGTCTCGGGAGTGGA 6180
Db  6121 ACAGGGAACCCAAGGTGGGATGAGGTCGCAGGTCTCGGGGGATCTCTGGGAGTGGA 6180

Qy  6181 TCATGGTCAAGTGACAGTGCCGATGCGATGGTCATGGCCATGTCGTGGTGTGTCAT 6240
Db  6181 TCATGGCGACAGGTTCCGAGGTCATGGCCATGGTCAGGTGACTTTTGAATGGCAACTCAAAG 6240

Qy  6241 TACCCTTATGGCACTGCGGGGAGGGGTTGGTTGTTGTTGCCATGTTG 6300
Db  6241 TCCCCGTTGTTGGCCATTGCGGGGAATGGCGTTGGACGGTCATGTGG 6300

Qy  6301 AGAGTCGTTGTCTTTGGTGTTGCGTGATCACCGGTGATGTTTTGAATGGGCAACTCAAAG 6360
Db  6301 AGACGCCCTGTCTTTGTGTTTGTGGATGTGTGACCGTTTTGAATGGGCAACTCAAAG 6360

Qy  6361 ATCCAGTTACTCTACCAAGCTGTGCAGGCACTATTGGATGGGGACCGTCCCTGTGAACA 6420
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Qy  7501 ATGTCACCAACCCGGACAATGTTGGGAGAGAGTTGACAAGGTTACCTTCTGGCGTGCCC 7560
         ||||| |||||| ||  ||||||||||||||||||||||||||||||||||||||||||
Db  7501 AGTGTTACCAACCAGACAATGTGGGGGAGGAGGGTAGACAAGGTGACCTTCTGGCCGCTC 7560

Qy  7561 CTAGGGTTCATGACAAAATTCCTGTGGACTCCATAGAGGGCCGGCTTAAGAGGGCAGCTCAAG 7620
         |||||||  ||||||||  ||||| ||||||||||||| ||| ||||||||||||||||||||
Db  7561 CTAGGGTTCATGACAAAATTCCTGTGGACTCGAGCGTGCTGCAGCTCGAGCGGCCGCTCAAG 7620

Qy  7621 CCTGCCTAAGCATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTG 7680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7621 CCTGCCTAAGCATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTG 7680

Qy  7681 CCATGGGCTGGGGATCTGGGTGTCGGTCAAGGACCTCGGCACCCCTGCGGGGAAGGATGG 7740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7681 CCATGGGCTGGGGATCTGGGTGTCGGTCAAGGACTTGGCACCCCTGCGGGGAAGGATGG 7740

Qy  7741 CGTTCCATGCAACCGGCTCCAGGAGATACTTGAAAGGACGGCCAGTCCCCTTTACTCTTACTG 7800
         | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7741 CGGTTCACGACCCGGCTCCAGGAGATACTTGAAGGACGCCAGTCCCCTTTACTCTTACTG 7800

Qy  7801 TGAAAAGGAAGTGTTCTTCAAAGACCGAAAGAAGAAGAGGCCCCCACCTCCATTGTGT 7860
         |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db  7801 TGAAAAGGAGGTGTTCTTCAAAGACCGTAAGGACGGAGAGGCCCCCACCTCCATTGTGT 7860

Qy  7861 TCCCCCCCTGGACTTCCGATAGCTGAAAAGCTTATTCTTGGAGACCCTGGACGGGTAG 7920
         |||||||||||||||||||||||| ||||||| ||  ||  |||||||||||||||||
Db  7861 TCCCCCCCTGGACTTCCGATAGCTGAAAAGCTTATCTTTGGAGATCCTGGACGTGTGT 7920

Qy  7921 CCAAGGCGGTGTTGGGGGGGCCTTACGCCTTCCAGTACACCCCAAATCAGCGAATTAGGG 7980
         ||||||||||||||||||||||||||| |||||||||||||||||||||||||| |||||
Db  7921 CCAAGGCGGTGTTGGGGGGGCTTATGCCTTCCAGTACACCCCACCCCAGGGGTGGTTAGGG 7980

Qy  7981 AGATGCTCAAACTGTGGGAATCAAAGAAGACACCATCGCCTCTGTGTGACGCCCACAT 8040
         ||||||||||||||||||||||||||||||| ||||| ||||||| |||||||||| |
Db  7981 AGATGCTCAAACTGTGGGAATCAAAGAAGAAACACCTTGCGCCTGTGTGTGATGCCACGT 8040

Qy  8041 GCTTCGACAGTAGCATAATAACTGAAGAGGACGTGGCCGCTGGGAGACAGCTTTATGCCCTGG 8100
         ||||||||||||||| | |||||||| || ||| ||||||| |||| ||||| | |||||||
Db  8041 GCTTCGACAGTAGCATAATAACTGAAGAGGACGTGGCCGCTGGGAGACAGCTTTATGCCCTGG 8100

Qy  8101 CTTCAGACATCCAGAATGGGTGCGTGCCCTGGGGAAAATACTATCGCCTTCGGCACAATGG 8160
         |||||||||||||||| ||  |||||| || |||||||||||||| ||||| ||||||||
Db  8101 CTTCCGACCATCCAGATTGGGTGCGTGCCGGCAGCGTTGGGGAAATACTACTGGCACCATGG 8160

Qy  8161 TAACCCCGAGGGGTGCGTGCCAGTGGGCTGAGAGGTATTGTAGATCCTCAGGGGTCTTGACCA 8220
         |  ||||||||||||||| || |||||||||||||||| ||| ||||| |||||||||||||
Db  8161 TCACCCCGAGGGGTGCCCGCCAGTGGGCTGAGAGGTATTGTAGATCCTCCGGGCTCTTGACCA 8220

Qy  8221 CAGTGCGAGCAACTGCTTGACTTGGGTGCGGTCCAGCGTTGGGGAAAGCCCGCTTGTGGAGGGGTGG 8280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8221 CTAGTGCGAGCAACTGCTTGACTTGGGTGCGGTCCAGCGTTGGGGAAATACTAAGGTGAGAGGGGTGG 8280

Qy  8281 GGCTGAAAAATGTCTCGCTCCCAATGCGTCGCGACGACTGTTTGATCATATGCGAACGGC 8340
         |||| ||||||| ||| |||||||||||| | |||||||||| |||||||||||||||||
Db  8281 GGCTGAAGAACGTCTCGCTCCTCACTCCTATAGCCGCGATGACTGTTTGATCATATGCGAACGGC 8340

Qy  8341 CTGTGTGCGATCCTAGCGACGCGTTTGGGCCAGAGCCCTGGCGAGCTACGGCTACCCATCGC 8400
         |||||| | |||||||| | |||| ||||||||||| || ||||||||||| ||||||| |
Db  8341 CGATGTGTGATCCTAGTGAGTGCGTTGGGTAGAGCCCTTGGCCTAGTGGGTACGCCGTGCG 8400

Qy  8401 AGCCTTCGTATCATGCATCATCATGGCGTTTCGCTCCTTGGCTTGCCGAGT 8460
         ||||||||| |||||| | | ||| || |||| ||||||| ||| || |||
Db  8401 AGCCTTCGTATCATCGATCATCATTGGACACGGCCCCCTTCGCTCCACTCGGCCTTGGCCGAGT 8460

Qy  8461 GCAATGCAGATGGGAAACGCCCATTTCTTCCTGACCACGGACTTTCGGAGGCCCCTCGCTC 8520
         |||||||||||||||||  |||||||||| |||||||||||||||||||||| ||||||||
Db  8461 GCAATGCAGATGGGAAGCGCCCATTTCTTCCTGACCACGGACTTTCGGAGGCCCCTCGCTC 8520

Qy  8521 GCATGTCGAGCGAGTCAGTGACCGAGTCTTCGGCCATCGGTTACATCCTCCTCTATACC 8580
         ||||| |||||||||||| |||| ||| ||||||| |||||||| |||||||||||
Db  8521 GCAATGTCGAGCGAGTCAGTGACCGAGTGCGTTCGGCCATTGGTTTACATCCTCCTCTATATC 8580
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Qy  8581 CTTGGGGATCCTCATACACGGTGGTCATCATCCTCCACGTGCTCACCTGCGCGTTCTCACGG 8640
         | |||| | ||| | |||||||||||||||||||||||||||| |||| || | || ||||
Db  8581 CCTGGCCACCCCCATCACACGGTGGGTCATCATCCTCCATGTGCTTACTTGCTGTTTTTTAGGG 8640

Qy  8641 GTGGTGGCACACCGTCTGATCCTGTGGGTGGTGGCCAGTACACATTGTAATTACTACAAGTTTC 8700
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Qy  8701 CACTGACAAACTGCCTAACATCATCTGTGGCCCTGCGCCTCCACGGACCAGCAGCCGTTGAGGGTTA 8760
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Qy  8821 CTGGCCTAGCAGTCACCGGGAAGAAGGCCGGGGACCATTGCGAACGCGTATGCTCCGGTCGC 8880
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Qy  8881 GCGGTTGGCTGAGTTGCGGTAGGGGGTCGTGTTTGTGCCCCTTTTCCCCTCATATGGGGGTGTTC 8940
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Db  8881 GCGGTTGGGCTGAGTTGCGGTAGGGGGTGCGGGTTGTGCGGATCCAGCCTTTCCCGGCTCCCCCTC 8940

Qy  8941 CGGAGATTGCTGGTATCCCCGGGGGTTCCCCCTTTCCCCCCTATATGGGGGTGTGTTC 9000
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Qy  9001 ATCAATTGGATTCACAAGCCAGAGAGTCGCTGGGTGAACTAAATTCATCTGTTGCGCAGGCCACAT 9060
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Db  9001 ATCAATTGGATTCACAAGCCAGAGAGTCGCTGGGTGAACTAAATTCATCTGTTGCGCAGGCCACGA 9060

Qy  9061 TCATCGTAGCCCTCTTCGGGTGCGTTCCCGGTCCCGGTGAACTGA 9120
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Qy  9121 TCATCACTGGAGGAGGTTCCCCGCCCTTGGGAGGAGGCATGGTGGTTACTAACCCCTGGCGATGGT 9180
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Qy  9181 GGCCCGGCCTTGGAGGAGGTTGCGGTCATGTGGGAGGTCAAAGCCTGATGGT 9240
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Qy  9241 GCTAATGCACTGCCACTTCGGTGGCCGGGTCGCTCCACTTTATACCGTAATCCGTGACTACGG 9300
         ||||||||||||||||||| |||| |||||||||||||||||||| ||||||||||||||||||
Db  9241 GCTAATGCACTGCCACTACGGTGGCCGGGTCGCTCCACTTTATACCGTAATCCGTGACTACACGG 9300

Qy  9301 GCTGCTCGCAGAGCCCTCCCCGGATGGGCACAGTGCACTGTGATCTGAACTGAAGGGGTGCACC 9360
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Db  9301 GCTGCTCGCAGAGCCCTCCCCGGATGGGCACAGTGCACTGTGATCTGAGTCAAGGGGTGCACC 9360

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Db  9361 CCGGTAAGAGCTCGGCCCAAAGGCCGGGTTCTACT 9395
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RESULT 5
D90600
LOCUS       D90600                  9395 bp    RNA     linear   VRL 07-FEB-1999
DEFINITION  Hepatitis GB virus C genomic RNA for polyprotein isolate GT110,
            complete cds.
ACCESSION   D90600
VERSION     D90600.1  GI:1944460
KEYWORDS    complete genome; polyprotein.
SOURCE      Hepatitis GB virus C (isolate:T110) cDNA to genomic RNA.
ORGANISM    Hepatitis GB virus C
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            GBV-C/HGV group.
REFERENCE   1  (bases 1 to 9395)
AUTHORS     Okamoto,H.
TITLE       Direct Submission
JOURNAL     Submitted (14-MAR-1996) Hiroaki Okamoto, Jichi Medical School,
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  CTATCTAAGTAGAGCAATGACTCGGCCGCCGACTCGGCGACCGGCCAAAAGGTGGTGGAT  120

Qy   121  GGGTGGTGACAGGGTTGGTAGGTCGTAAATCCGGTCATCCTGGCGGAGACCGCACGGTGG  180
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   181  GTCTTAAGAGAAGGTCAAGACTCCTTCTGTGCTCGCGGAGACCGCGGTCGTTAAACCGACCAG  240
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Db   301  GTTACCCGCCTGGCAAAGACGACGCCCACGTACGGTCCACGTTCGCCCCTTCAATGTCTCTCT  360

Qy   361  TGACCAATAGTTTATCCGGCAGTGACAAGGACCAGTGGGGGCCGGGGGTTATGGGGA  420
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Db   361  TGACCAATAGTTTATCCGGCAGTGACAAGGACCAGTGGGGGCCGGGGGTATGGGGA  420

Qy   421  AGGACCCCAAACCTGCCCTGCCCCGGCGGGCCCGGGAAATGCATGGGGGCCACCCAGCTCCG  480
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Qy   481  CGGGCGGCCTGCAGCGGGTAGCCAAGAATCCTTCGGGTGGAGGGCGGTGGCATTTCTC  540
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Qy   541  TTTCTATACCATCATGGCAGTCGTTGCCGTTCCTCCTTCGTGGGGCCGGGGCCATTC  600
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Qy   601  TGGCCCCGGCCACCCAGCGCTTGTCGAGCGAATGGCAATATTCCTCACAAATTGCTGTG  660
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Qy   661  CCCCGAAGACATCGGGTCTGCCTGGAAGGCCGATGCCTGGTGGCCCTGGGTGCCACGG  720
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Db   661  CCCCAGAAGACATTGGGTTCTGCCTGGAAGGTGATGCCTAGTGGCGTTGGGTGCCACGG  720

Qy   721  TTTGACCGACCGTTGCTGGCCACTGTATCAGGCCGGGTTTGGCTGCGTGGCCAAGT  780
          |||| || |||||||||||||||||||||||||||||||||||| ||||||||||||
Db   721  TTTGTACTGACCGATGCTGGCCACTGTATCAGGCCGGGTTTGGCTGCGTGGCCAAGT  780
```

           Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
           329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
           Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)

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REFERENCE   2 (sites)
  AUTHORS   Okamoto,H.
  JOURNAL   Unpublished (1996)
REFERENCE   3 (sites)
  AUTHORS   Okamoto,H., Nakao,H., Inoue,T., Fukuda,M., Kishimoto,J., Iizuka,H.,
            Tsuda,F., Miyakawa,Y. and Mayumi,M.
  TITLE     The entire nucleotide sequences of two GB virus C/hepatitis G virus
            isolates of distinct genotypes from Japan
  JOURNAL   J. Gen. Virol. 78 (Pt 4), 737-745 (1997)
  MEDLINE   97275884
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Qy   841 ACGTAGCCGGGATCCTGGGCTCGGGCGGAGGTTACTCCGGGTCCTGACAGTTGGTGTTG    900
         |||| |||||||||  ||||||||||||  |  ||| || ||||   | ||||||||||||
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Qy   901 CGTTGAGGCGCCGGGTCTACCTGATGCCCAACTGAAGTGTGCAGTAGAATGTGACGTTA   960
         |||||||| | |||  ||| |||| |||||||| | ||  | ||||||| | |  |  |
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Qy   961 AGTGGGAAGTCAGTTTTGGAGATGGACTGAGCAGTTGGCCTCCAATTACTGGATTTTGG  1020
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Qy  1201 ACTACGGGTTGAAGTGGCAGTCATGCTCCTGCAGGGCTAACGGGTCGCGTATTCCCACTG  1260
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Qy  1441 TAACGTGCGTGGGTTCCGTGTCTTGGTTTGCCTCGACCGGCGTCGTGATTCGAAGA     1500
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Qy  1501 TCGATGTGTGGAGTTTCGTGCCGGTTCGATCCGCCAGCTGCACCATAGCCGCTCTAGGGT  1560
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Qy  1561 CATCGGATCGCGACACGGTGTTGAGCTCTCCAGTTGGGGAGTCCCGTGCCTAACGTGTA  1620
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         ||||| |||| ||||||||  || | |||| | |||||  | | || |||||||||||||
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Qy  2041 GGTGTTCGGAGCTGATGGACGCCGAAATCCGTTGCCCGGGTACGCATGGCCATGCTGTCCT  2100
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         ||| | ||| |||||| | || | | || ||||| | || |||||| || || |||| |
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Qy  2161 ACTTCATCCCTCCCCACGCTGGTCTTCTTGGATTTTGTATTTGTCCTGCTCTATCTGA  2220
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Qy  2221 TGAAGCTGGTGAGGCACGGTTCTAGGACTGCCGGCTGTGTGGTGTGGTGTGGGTGA  2280
         |||||||||||| || || |||| |||| |  |||| || || |||||||||| ||
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         | |||||| | |  |  ||| |||| |||| ||||||| ||||| || | || |||||||||||
Db  2341 TGGGCCCCGCCTTTGTGTACTTTCCGGGAGCTTCCCGGGGGCGCTTCCGATGGGGGATTCGGCACGT  2400

Qy  2401 CAAAACCTGGTGTGTACTTTCGGTGGATGGGCGGCCACCCCCATTGGA  2460
         |||||| |||| || ||| |||| || |||| | | |||||||| ||||
Db  2401 CAAAACCTGTGTCGTTGTACTTTCCGTGATGGGCCGGCCATCATTAGCCGCTCGA  2460

Qy  2461 GGAAGCTCGCTCCGGGAGCTTCCCGGGATTTTGATGGGGATTCGGCGACCCCCG  2520
         |||||||||| || || |||||||| | | |||||| || | |||| |||||||
Db  2461 GGAAGCTCGCTCCGGGGGCTTCCCGGGGATCGGGTTCTCGATGCTGTTCGGCCGGATCCGCG  2520

Qy  2521 GGGCCACCTCTGTCCTCGGGGCCCGAGTTCGTCGTTCGATGTGCATTGCACACTTGAGGTTGGACACTT  2580
         ||| ||  ||||| ||||||| |||| || |  | || || ||| || ||| | ||| |||| |||||
Db  2521 GGGCACCCTCCGTCCGTCGGGGGCCGAGTTCGTTCGTTCGATGTCCGATCTGCATTGCACACGTGGTGCGGTGGCACGT  2580

Qy  2581 CGGTGTTGGGCGTGGGTGGCCAGCGGTGGCCATAGCCGCTCCTGAGCTCAA  2640
         ||| ||| |||||  |||| ||||||||| || |  || ||  |||| ||
Db  2581 CGGTGCTGGGCGTGGGTGGCTGGCCAGTGTGGTTGAGCCTCCATTGCGGTGCCATTGCCTGAGCTCGA  2640

Qy  2641 TGAGGCGGCACAGGGGTGGAAGCGCCGTGGATCTCATAGGACGTGTGTAAAGGGTACC  2700
         ||||| || | ||| || ||||| ||||  | |  | ||| ||||| | |||||||||
Db  2641 TGAGGCGCCGCAGGTTGGAGCGGAAGCACAAGAGGCCCGTGGTCTGGTGTCGTTCGTTGTGTAAAGGGTACC  2700

Qy  2701 AGGCTGTGCCGCAGAGGGTGGTGCGACAGGCCGTCCTCCGGGAGGGCGTCCTACCAAGCTTC  2760
         ||||| ||||| || |||| |||| |  || |   | ||||| ||||| ||||||| | ||
Db  2701 AGGCTATTCGCCAAAGGTGGTGAGGTCCCATACCGGGGAGGCGGCGCAACCAAACCCCG  2760

Qy  2761 TGACGTTCGCGTCCTGGTGTGTCCGCCGATCGTGATGATGCTGTGGTGG  2820
         ||| |  | | | |||||| |  || ||  ||  |||||||| ||| |||
Db  2761 TGACGTTTGCCTTGGCCTCATCACTCGGCCTCATCATCTGGCCCAGATGCTGTATGATGTTGGTGGTGG  2820

Qy  2821 TGGCCTTGGTCTCCTCCTCCGGCCACTGCACCTCGAGGAGGTCC  2880
         ||| | | | | | | | |  ||||| |||| | ||| ||||| |
Db  2821 TTGCCTTGGTTTCGTGTTCTGGCCACCGGTTGCGTTCGGCCACTGCACCTCGTGGAGGAGTCT  2880

Qy  2881 TGGTCTCCCGGCCCTCGTTACGGCGACTGGCACGGGTGGTTGGTGTGTCGTGATGGCGG  2940
         |||| | | || |||  | || | | ||||| | ||| | |||| | | |||||||||||
Db  2881 TGGTTTCCGTTGCCCGTTGTTGCCGTTCGACCGGTTTGGCGCGGGTGGTGTTGGTATGGCGG  2940

Qy  2941 GCGAGAAGGCCACCACCATCCGACTGGTGTCTCCAAGATGTGCCGCAAGAGGGGCCTACCTGT  3000
         | ||||||||||||||||||||||||| |||| | |  |  ||| ||| ||| ||  |||||
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Db   2941 GTGAGAAGGCCACAACTGTCCGACTGGTTCCAAGATGCGCGAGAGGGGCTACTTGT 3000

Qy   3001 TTGACCACATGGGCTCTTCTCCGCGCGCTTGTTGGAATGGGACGCGG 3060
          ||| |||||||||| | |||||||||||||   |||||||||||||||||| ||||
Db   3001 TCGACCAATATGGGCTCTTCTCCGCGCGCTCAAGGAGCGCGTTGTTGGAATGGGACGGCGG 3060

Qy   3061 CTTTGGAGCCCTTGTCATTCACTAGGACGACTGTCGCATCATCAGAGATGCCGCGAGGA 3120
          |||||| || |||||| ||||||||||||||||||||||||| || ||||||||||||
Db   3061 CTTTGGAACCACTGTCATTCACTAGGACGACTGTCGCATCATCAGAGAGATGCCGCGAGAA 3120

Qy   3121 CCCTGTCCTCGGGACAGTGCGTCATGGGTTACCCGTGTAGCACGGCGCGTGATGAGG 3180
          ||| |||| ||| |||||||||||| ||||||||||| ||||||| ||||||||||||
Db   3121 CCCTGTCTCGCGACAGTGCCGTCACGGGGTCCCGTGTAGCGGCGCGTGATGAGG 3180

Qy   3181 TTCTCATCGGCTGCTTTCAGGATGGTGAATCATTTGCCTCCCCGGTTGTCCGACTGCAC 3240
          |||||||| ||||||||||||||||||| ||| ||||||||| |||||||||||||
Db   3181 TGCTCATCGGGTCTTTCAGGATGTGAATCATTTGCCTCCCCGGTTCGTCCGACCGCGC 3240

Qy   3241 CAGTTGTCATCCTCGGTGCCGAAAGGCGCTTCCTGGGGTCACGAAGGCAGCCTTGACAG 3300
          ||| |||||||||| || |||||| ||||||||||| ||||||| |||||||||||||
Db   3241 CCGTTGTCATCCGGCGGTGCCGAAAGGCGCTTCCTGGGGGTCACTAAGGCTGCCTTGACAG 3300

Qy   3301 GTAGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTTGGGGACGGCTACGTCACGAA 3360
          ||||||||||| ||| |||||||||||||| |||||||| |||||||| |||||||||||
Db   3301 GTCGGGATCCTGACTTGCATCCAGGGGACGTGTTGGTGTTGGGGACTCGCGACTCGGCGAA 3360

Qy   3361 GCATGGCACATGTCGAATGGCCTGCTGTCTGCACAACTTCATGGGCTTCATCCCGAA 3420
          |||||||| || ||||| |||||||||||||||||||||||||||| ||||||||||
Db   3361 GCATGGAACGTGTTGAACGGCTTGCTGTCTGCACAACTTCATGGGCTTCATCCCGAA 3420

Qy   3421 CCATGGCCACGCCGTGGGGCCCTTAATCCCAGTGTGTCAGCCAGTGATGACGTCA 3480
          ||||| |||||| || ||||||||||| |||||| |||||||||||||||||||||||
Db   3421 CCATGTGTCACCTGTACCACCTGTGTGGGGGCCCTAAATCCCAGGTGTGTCGGCAAGTGATGATGTCA 3480

Qy   3481 CGGTGTACCCGCTTCAGATGGGGCAACTTCGTTGCACGCCCTGCACTTGCCAGGCCGGAGT 3540
          ||||||||||||| |||| ||||||||||| |||| ||||||||||||||||||||||
Db   3481 CGGTGTACCCTTCCCCGACGGGGCAACTCGTTAAACCCTGCCACTTGCCAGGCTGAGT 3540

Qy   3541 CCTGTTGGGTTATTAGATAGGGACGGCTTTGTGCCATGGCTTGTGACCAAGGGGACAAGG 3600
          |||||||||| | |||| ||||||| ||||||||||||||||||||||||||||||||||
Db   3541 CCTGTTGGGTCATCCGATCAGACGGGGCTTTATGCCATGGCTTGTGACCAAGGGGACAAGG 3600

Qy   3601 TTGAGCTCGATGTGGCCATGGCCATGAGGAGTTTCAAGGAGGCCCCGGTCC 3660
          ||| |||| ||||| |||||||||||||| |||||||||| ||||||||||
Db   3601 TAGAGCTCGATGTGGCCATGGCCATGAGGAGTTTCAAGGAGGCCCCGGTCC 3660

Qy   3661 TTTGCGACAAAGGGCAGCACGCAGTAAGAATGCTCGTGTCAGTGCCACTCTGCCGGCAGGG 3720
          | |||||||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db   3661 TGTGTGACAAAGGGCAGCACGCAGTAGGAATGCTCGTGTCCGTGCCACTTGCCGGCTCGG 3720

Qy   3721 TTACTGCGGCCGATTCCACTAGGCCGTGCTTGTGGACTCAAGTTCCAACAGAGCCAAGACTACCA 3780
          |  | ||| |||| |||||||||||||||||||||||| ||||||||||||| ||||||||||
Db   3721 TAATCCTAAACCCCTCAGTGGCTACTGTGAGACGCCCTTACATGGGCCCTTACATGGAGCGCACTACCA 3780

Qy   3781 CAGAACACCCCGGTTCCGGTGCCGGCAAAAGGAGTTTTCAAGGAGGCCCCGGTTGTTTATGCCTA 3840
          ||| ||||| ||| |||||| ||||||||||| |||||||||||| |||||| || ||||||||
Db   3781 CTGAACCCCGGTTCCGGTGCCGGCAAAACATGTTGTTGTTTTTCAACGAGGATTACTG 3840

Qy   3841 CGGGGGCAAAAGAGCACCCCGGTGCAGTGGTACGGCAACATGGGCCACAAGGTCT 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   3841 CGGGGCCGGAAAAGAGCACGCCCGGTGCAGTGGTACGGCAACATGGGCCACAAGGTCT 3900

Qy   3901 TGATCTTGAACCCGTCGGTAGCTCAACCCTGAGGGCCCATGAGCATGGAGCCGGCTGG 3960
          || | ||||||||||||||||||||||||||||||||||||||| ||||| ||||| ||
Db   3901 TAATCCTAAACCCCTCAGTGGTACTGTTCCACTGGTAGCCCTTACATGGAGCGCACTGTGG 3960

Qy   3961 CGGGGAAAACACCCCCAGTATTTACTGTGTCCATGCCCCACTGCTTTCACAAGGATCACTG 4020
          ||||||||||||||||||||| || ||||||||||| ||||||||||||||||||||||
Db   3961 CGGGCAAACAATCCAAGCATATACTGTCGACCACCACTGCTTTCACGAGGATTACTG 4020

Qy   4021 ACTCGCCCCTACGTATTCCACTTACGGCAAGGTTTTTGGCCAACCCTAGGCAGATGCTGA 4080
          ||||||||| ||||||||||||| |||||| |||||| ||||||||||||||||||||
Db   4021 ACTCCCCCGACGTATTCTACCTATGGGAGGTTTCTGCCAACCCCTAGGCAGATGCTCC 4080
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Qy   4081 GGGTGTGTCGGTGGTCATTTGTGACGAGTGCCCAGTCATGACTCAACTGTGTTGTTGG 4140
          |||||||||||||| |||||||||||||||||||||||||||||||||||||| | | ||
Db   4081 GGGGGGTTTCGGTTGTCATCTGTGACGAGTGCCCAGCCATGACCGAACCAACTGTGTTACTGG 4140

Qy   4141 GCATTGGGCGTGTCAGGGAGCTGGCGCGAGGATGTGGAGTGCAATTGGTCGTCTCACGCCA 4200
          |||| |||| ||||||| ||||||||||| || ||||||||| |||| |||||||| |||||
Db   4141 GCATCGGGCAGTACGGAGCTGGCGCGCGGCTGTGGAGTGCAGCTGGTCAGCTTGCTCTCTACGCCA 4200

Qy   4201 CTGCCACCCTCCCGATCCCGATGAGACCCAGCACCATCAATCATTGAGACAAAAACTGG 4260
          ||||| |||||||||||||||||||| | |||||| || ||| || ||||| |||||
Db   4201 CTGCCACAACCTCCGGGTCCCCTATGACCCACGCACCATCAATTATTGAGACCAAAACTGG 4260

Qy   4261 ACGTGGGAGAGATCCCCTTCTATGGCATGCATGGCGGATGCCGGACCGGAA 4320
          |||||||||||| |||||| |||||||| ||||| |||| |||||| |||||
Db   4261 ATGTGGGAGAGATCCCCTTCTATGGGCTCTATCATCATCAAGGACG 4320

Qy   4321 GGCATCTCGTATTCTGCCACTACGACTGAGTGCGAGCCCTGCGGGCCCAGTTTTCGG 4380
          |||||||| ||| ||| ||||||||||| ||||||||| ||||||||||||||||| |
Db   4321 GGCATCTTGTATTCTGCCATTACGACTGAGTGTGAGCCCTGCCGTCCCAGTTTTCCG 4380

Qy   4381 CTAGGGGGTAAATGCAATGGGGAAAGACAGTTCTATCATCAAAGATG 4440
          ||||||| ||||| |||| |||| || ||||||||||||||| ||| |||
Db   4381 CGAGGGGGTCAAGCCATCCGCCCTATTATAGGGAAAGGACAGTTCTATCATCAAGGACG 4440

Qy   4441 GAGACCTGGTGGTCTGTCTGCTACGACGCAATCCCACTGGTACACTTCGATT 4500
          |||||||||||| || ||||| |||| || ||||||| |||||| ||||||||
Db   4441 GTGACCTGGTGGTCTGTGCTGCCACTATCCACCGGGTACACTTCGATT 4500

Qy   4501 CTGTCACCGATTGTGGGTTAGTGGTGGAGGAGTCGTCGAGGTGACCGTCA 4560
          |||||||| ||||| |||||| ||||||| |||||||| |||||||||||||
Db   4501 CTGTCACTGATTGTGGGTTAGTGGTGGAGGAGTCGTCAGCGGTGGACTCCACCA 4560

Qy   4561 TTACCATCTCCTGCGCTGTCGGCACGGTGCCCGCGTCGAACTGTCAGCGGCGAGGAC 4620
          ||||||||||||||| ||||| |||||||| |||| ||| |||||| ||||||||||
Db   4561 TTACCATCTCCCTGCGTCGTCGGCAGCGTGCCGCTTACGACTGTTGTCAACGGGCGAGGAC 4620

Qy   4621 GCACGGGTAGGGACGCAGGCTCGGCGCTACTACGCGGGGGTCGGCAAGGCCCCTGCTG 4680
          ||||||||| ||||| ||||||||| || ||||||||||| ||||||||| |||||||
Db   4621 GCACGGGTAGGGACGCAGGTCGGCGCTCTACTACGCGGGGTGGCAAAGCCCCGCGG 4680

Qy   4681 GTGTGGCTGCGTCCAGGTCGCCGTGGGCAAAAGTTCGACCTGGTGACCTGTACGGAA 4740
          ||||| ||||||| ||||||||||||| ||||||| ||||||| ||||||| ||||||
Db   4681 GTGTGGTGCCGCTCCAGGTCCTGGTGGCAAAAGTGCGCGGCGCGTCAATTGGCCTCGGTTACGGAA 4740

Qy   4741 TGGAACCTGACCTGACAGCAGCAAACCTACTACGACTTCGCCCTTACACCGCAG 4800
          |||||||||||||||||| ||||||||||| ||||||| ||||||||||||||||
Db   4741 TGGAACCTGACCTTGACAGCAGCAAACCTTACGACTTTTTACGACTTACACCGCAG 4800

Qy   4801 CCGTCGCAGCTGACATTGGGGAAGCCCGGTGTTCTTTTCGGGGCTTCGGGGGGTG 4860
          ||||| ||||||||||| ||||||||||||| || ||||| || ||||| ||||||
Db   4801 CCGTCGCGCGACTGACATGCGGAGCGGCGCGTGTTTTTCTCGCGGCTTGCCGGGGTG 4860

Qy   4861 TGCATCCCGATGTTAGCTGGGCAAAAGTCGCGGCGGCGTCAATTGGCCCATGCCTA 4920
          ||||||||||||| |||| ||||||||| | |||| ||| |||||| ||||||||||
Db   4861 TGCACCCGATGTTAGCTGGGCAAAAGTGCGGCGCGCGTTGTTGCTTCGTTGGTGGGGTG 4920

Qy   4921 TTCAGCGGACCATGTGCCGGACCCAGTGGGG 4980
          ||||||||||||||||||||||||| ||| ||
Db   4921 TTCAGCGGACCATGTGCCGGAAACACTGCTCTCCGGTCCCATCGGACGACGACCCCCAATGGG 4980

Qy   4981 CAGGTCTGAAGGGCCCGAATCCTGCCCACTCCTGCTGAGGTGGGGCAATGATTTACCAT 5040
          ||||||||||| ||||||| ||| | || |||||| ||||||||||||||| ||||||||
Db   4981 CAGTCTGAAGGCCCCAAATCCTGTTCCACTCCTGAGTGGGGCAATGATTTACCAT 5040

Qy   5041 CTAAAGTGCGGCCGGCCATCACATCGGACGACCTTCGGCGGTCGGGGGTGCGGGAGG 5100
          || |||||||||||||||||||||||||| |||| |||||| ||||| ||||||||||
Db   5041 CTAAGGTGCGGCCGCCACCACATTGTTGACGACCTTGGTCGTCTAGGCGTGTGCGGGAGG 5100

Qy   5101 GTTACGTCCCGTGCGACGGGGACCATCTTGATGGTGGCGGGGGCA 5160
          |||||||||| |||||||||||||| |||||| |||||||||| |
Db   5101 GTTACGTCCGGTCGCGACGGGGACCCATCTTGATGGTGGCGGGGGGCA 5160
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Qy   5161  TGATCTATGCGTCATACACCGGGTCTCTCGTGGTTACAGACTGGGATGTGAAGGGGG  5220
                ||||| ||| |||||| |||||||||||| ||  ||||| |||||||||||||||||
Db   5161  TGATCTCACGCGTCTTACACCGGGTCATTGGTGGTGGTGACAGACTGGGATGTGAAGGGGG  5220

Qy   5221  GTGGCAGCCCCCTTTATCGGCATGGAGACCAGGCCACGCCCCAGCCAGCGGGGTTGTGCAGGTCC  5280
           |||||||||||||  |||||||||||||| |||||| ||||||||||||||||||||| |||||||
Db   5221  GTGGCAGCAGCCCCTTTATCGGCATGGAGACCAGGCCACGCCCCAGCCAGCGGGGTTGTGCAGGTCC  5280

Qy   5281  CCCCGTAGACCATGGCGGCCGGGGGGAGAGTCTGCCGATGGCCAACACAGTGACAG  5340
           |||||||||||||||  ||||||||||| ||||||||| |||||||||||||||||
Db   5281  CCCCGTAGACCATCGGCGGCCGGGGGGGAATCGGCGATGCCAAGCAGTGACAG  5340

Qy   5341  ATGCGGTGGCGGCCATCCAGTGGATTGCGATTGCCGATTGTCAGTCATGACCCTGTCGGGG  5400
           |||||||||||||||||||||| ||||| |||||||||||||||||||||||| ||||||
Db   5341  ATGCGGTGGCGGCCATCCAGTGGATTGCCGATTGTCAGTTATGACCCCTGTCGGGG  5400

Qy   5401  AAGTGTGTCCTTGGCCACGGAGCCTACGCAGCCTACCACCAAGTGGC  5460
           |||||||||| |||||||| |||||||||| |||||| |||||||||
Db   5401  AAGTACTGTCCTTAGCTCAGGGAGACGGCCGGGCCTACACACCGCCAACCGCCAAGTGGC  5460

Qy   5461  TTGCTGGCTGCTACACGGGAGACGCGGCCCGTCCCACTGTTCAATTGTTGACAAGCTCT  5520
           | ||||||||||||||| |||| |||||||||||||| |||||||||||||||||||||
Db   5461  TCGCTGGCTGCTCTACACGGGGAGACGCGGCCCGTCCCCTACTGTTTCAATTGTTGACAAGCTCT  5520

Qy   5521  TCGCCCGGGGGGCTGGGGCCGGTGGTTAGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGG  5580
           |  ||||||||| |||||||| |||| |||||| |||  ||||||| |||||||||||||
Db   5521  TTGCCCGGAGGTGGGCCTGCCGTGGTTGCCAGGCCGTCACAGCTGCAGTGG  5580

Qy   5581  CGGCCTATGGGGCTTCTAGGAGCCCTCCATTGGCTGCTGCCGGCCGTCCTACCTCATGGGGT  5640
           |||||||||||| ||||||||||| |||||| |||||||| ||||| |||||||||||| ||
Db   5581  CGGCCTACGGGGCTTCCAGGAGCCCGTTGGCCGCCGCCGTTGGGGGAGGTTGGGAGGGCG  5640

Qy   5641  TGGGGCTCGGAGGCAACGGCAAACCCGTCTAGGCCTCCGCTCCTCTACTAGGGCCGCTG  5700
           || ||||| ||||| ||||| || ||||||  ||| |||||||||||||||| ||||||
Db   5641  TGGGGCTCGGAGGTAACGCGGCAGACGCCTTGTCTTTGCATCCGCGCTTGGCATCCCTATTGGGGCTGCTG  5700

Qy   5701  GGACCCCTGCCATCCGGTGGGGTTAACCAGTCCGGGGCCGTTCAGGGAAGTG  5760
           |||||| |||||||||| ||||| |||||||| |||||||| |||| |||||
Db   5701  GTACCCCCTGCCATCCGGGTTGTCGTGGGACTAACCAGTCCAGAGGTGCCGTTCAGGGGGGTG  5760

Qy   5761  CTAGGCTCTCCCCCTTCCTTGGTCACCATTTTACTTGGGGGCCGTGGGGGCG  5820
           |  |||||||||||||| |||||||||||| ||||| ||||| ||||||| |
Db   5761  CCAGGCTCTCCCCCTTCCTTGCTCACTATTCTACTAGGGGCGGTGGGAGGGCG  5820

Qy   5821  TGGTGAATGGCGGCTAGCCTTTATGCGAGCTTGACTTTATGCGGGGAAACTATCATCAGAAGATC  5880
           | || |||||||||||| |||| |||||||  |||||| |||||| |||||||||||||||||||
Db   5821  TTGTCAACGCGGAGCAGCCTTGTCTTTCGACTTTATGCGGGGAAGCTTTCATCAGAAGATC  5880

Qy   5881  TGTGGTATGCCATCCAGTGCTAACCAGTCCGGGGCACTTGCGGGATCGCCCTCG  5940
           |||||||||||||||||||||| || |||||||||||||||||| |||||||| |
Db   5881  TGTGGTATGCCATCCAGTGCTAACCAGTCCGGGGCACTTGCGGGATCGCCTCTTG  5940

Qy   5941  GGTTGTGTTGTACTTGTACTCAGCTAACAACTCTGGCACTACCACTTGGTTGAACGGTCTGCTGA  6000
           |  |||||| |||||| ||||||||||||||||| |||||||||||||||||||||||||||||
Db   5941  GTCTGGTTTGTTTACTCAGCTAACAACTCTGGCACTACCACTTGGCTGAACCGTCTGCTGA  6000

Qy   6001  CTACATTGCCAAGGTGCCATGCATGCAGCCCTGACAGGCCGGATTACTGCG  6060
           ||| ||||||||| ||||||||||||| |||||||||  ||||| |||||||
Db   6001  CTACGTTGCCAAGGTCCTGCCAGCTCCTGCGCATTCCTGCAGCAGGCTGACTTACTGCG  6060

Qy   6061  ACAAGGTTCGCCCCGTGTTGCTCAGCCTTGAGCCTTCCACCGGGTTGCCCCTGGTCA  6120
           |||||| |||||||||||||||||| |||||||| ||||| |||||||| ||||||||
Db   6061  ACAAGGTTCGCCCCGTGTTGCTCAGCCTTGAGCCTTCCACCGGGTTGCCCCTGGTCA  6120

Qy   6121  ACAGGGAGCCTAAGGTGCTGATGGTCATGGGTTGGGCTACGGTTGGGGAGTGGA  6180
           |||| |||||||||| ||| ||||||| ||||||||||| |||||| |||||||
Db   6121  ACAAGGTTTCGGTGATGAGTGGATGCAGTGCTGGGTTGGGATCTGGGGATCTCGGGGGAGTGGA  6180

Qy   6181  TCATGCGTCAAGTGCGCATGGATGGTGTCATGGCTCTCCGCCCGGTGTGTCAT  6240
           |||||| ||||||| |||||||||| ||||||||||| ||||||||||||||||
Db   6181  TCATGCGTCAAGTTGCGCATGGTGTCATGGTCATGGTGTCAC  6240

Qy   6241  TACCCTTATGCGCACTGCGCGGGAGGGGTGTTCCGGAGAAATGGTTGTTGTTGGACGGCCATGTTG  6300
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   6241  TCCCGTTGTGTGCATTGCCGGGGAGGGGTTGGTGGCTGTGTCCGGGATGGTGTTGGACGGTCGTGTGG  6300

Qy   6301  AGAGTCGTTGTCTTTGTTCGTGATCACCGGTGTGCGTGATCACCGGTGATGTTTGAATGGGCAACTCAAAG  6360
           |||| ||||| |||| |||| |||||||||| ||||||| ||||||||||||||||||||||||||||||
Db   6301  AGAGCCCGTCGTCTTTGTTCGTGATGTGATAACCGGTGACGTTTGAATGGGCAACTCAAAG  6360

Qy   6361  ATCCAGTTACTCTACCAAGCTGTGCAGGCATTATTGGATGGGACAGTCCCTGTGAACA  6420
           |  ||||| ||||||||||||| |||||||||||||||||| ||||||||||||||||
Db   6361  AACCAGTTACTCTACCAAGCTGTGCAGGCACTATTGGATGGGACCGTTCCTGTGAACA  6420

Qy   6421  TGCTGGCTATGGCGAGACGTCGCCTTGCTGCCGCCCAGACACCCGAAGGTGGTACCAT  6480
           ||||| |||| |  || | || || ||||| |||| | ||||| |||| |||||||| |
Db   6421  TGCTGGGTTACGGCGAAACATCCCCTCTCCTGGCTTCCGACACTCCAAAAGTGGTTCCTT  6480

Qy   6481  TCGGGACGTCTGGGTGGCTGAGGTGTGTGCTGAGGTGTGTCACCCCAGTTGTGATCAGGCGAA  6540
           ||||||| ||||| |||||| |||||||||| |||||||||||||||||||||||||||||||
Db   6481  TTGGGACGTCGGGGCTGCTGAGGTGTGTGACCCCACCCCAGTTGTGATCAGGAGGA  6540

Qy   6541  CATCCGCCTACAAAACTGCTCGCCGCCGACAAATCCTGTCGGCTGCTGTTGCTGACGCCCTATT  6600
           ||  || ||  |||||| |||| ||||| ||||| | |||||| |||| ||||||| ||||||||
Db   6541  CCTCTTCCTACAAGTTGCTCGCCGCCAATCCTATCAGCTGCTGTTGCTGTCGCTGCCGTGCCCTATT  6600

Qy   6601  ACGTCGACGCCATACCGGTCTCATGGACGCGGAGCGGCCGCTGCCCAGGGTCGTCTATG  6660
           ||  |||||||||||||||||||  ||||| |||||| ||||| |||||||  |||||||
Db   6601  ATGTTGATGCCATACCGGTCTCATGGGACACCCGACCTCGTGCACCTGCTCATGGTTTATG  6660

Qy   6661  GCCCTGGCAAAGTGTCACCATTGACGGGGAACGCTACACCCCTTCCGCCATCAACTGCGGC  6720
           |||| |||||||||   |||  ||||||| |||||||||||| |||| |||||||  ||||
Db   6661  GCCCTGGCAAAGTGTACCATTGACGGGGAGCGCTACACACCCTGCCGCCGCACCAGTTGCGGC  6720

Qy   6721  TTAGGAAATGTGGCGCCCTCTGAGGTGTCATCCGAGGTGTCATTGGGGACGAGA  6780
           ||||||||||||||||||| |||||||| ||||||||||| ||||||||||||||
Db   6721  TTAGGAATGTGGCGCCCTCTGAGGTGTCATCCGAGGTGTCATAGACCGGGAGA  6780

Qy   6781  CTGAAGACTCAGAACTGACTGAGGCGCGGCCGGCCCCTGCCCAGGGCTA  6840
           |||||||||||| |||||||||||| | ||||| ||||| ||||||||||
Db   6781  CTGAAGACTCAGAACTGACTGAGGCGCACCTGCTGCTGCCCACCAGCGA  6840

Qy   6841  TCGAGAATGCGCAGAATTCTTGAACCTTCACAGATGATGTCATCATGGGGGAAGATTGCAGTA  6900
           ||||||||| ||||||| ||| |||| |  |||||| ||||| ||||||||||||| |||||||
Db   6841  TCGGAGAATGCTGCAGAGATTCTTGAACCGCACAATCGATGTCATTGTTGGGGAGACTGCCAGTA  6900

Qy   6901  CACCCTCTCTTTGTGGAGTAGCCGAGAGATGCCTGTGTGTGGGAGAAGACATACCCCGCA  6960
           |||| || |||| |||| ||| ||||| |||||| ||||| |||||||||||  |||||||
Db   6901  CACCCTCTCTTCGTGGAGTAGCCGAGGATCCTGTGTGTGGGAGAAGACGTCCCCCA  6960

Qy   6961  CTCCACTGCCGCCACACTTATCTCGGTTACTGAGAGCAGCCCAGAGAAGAGAAGACCCTCGG  7020
           |||| |||||||| |||||||||| |||||| ||||||||| |||| ||||||| ||||||||
Db   6961  CTCCATCGCCAGCGATGCTTATCTCTTACCGGTTACCGGAGAGCAGCAGCTCAGATGAAGCAGCTTGCGAGACCCCGTCGG  7020

Qy   7021  TGTCTTCCTCCGGAGGATACCCCTTCTCATTCGAGGTCATCCAGGTCGTGTGTGGA  7080
           |||| |||||||||||| |||||| ||||| ||||||||||||||| ||||||| ||
Db   7021  TGTCCCTTCCTCCGGAGGATACCCCTCCTCAGGACTCATTCGAGGTCATCCAGGTCATCATTGTGTGAAA  7080

Qy   7081  AGACAGCCGAGGGAGGGAGGAGGGAAAGCGTCTTCCGGTCGGCCTTTTCCGTACTAAAAGCCTTGT  7140
           |||||||||| | |||| ||||||||||||||| ||||| |||| ||| ||||| |||||||| |||
Db   7081  AGACAGCTGAAGGGGGAAGGGGAGGGAAAGCGTCTCTTCCGGCTGGCCTTTTCCGTATTAAAAGCCTTGT  7140

Qy   7141  TTCCACAGGCGATGCCACAGAAAGCTTACCGTTGTTGTGAGAAGA  7200
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Qy   7201  GCGTAACACGCTTCTTTTCATTGGGATTGACGGTCGCCTGCGTGGCAAGCCTGTGTGAGA  7260
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Db   7201  GCGTCACAGCGCTTCTTCTTCCTTCGTTAGGGTTAGGGTTAGCGGCCGCACTCGGCCACTCGGCTAGCTGTCCTTGTGAAA  7260

Qy   7261  ACAGGGAACCCAAGGTGGATGAGGTGCAGCCTATTGTGAACCATACAGCCTTT  7320
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Db   7261  TGGAAATCCAGAACCATACAGCCTATTGTGACAAGTGCGCAACTGCTCCGCTTGAATTGCAGG  7320

Qy   7321  TTGGGTGCTTGGTGGGCAATGAACTTACCTTTGAATGTGACAAGTGCAGGTAGGCCAAG  7380
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Qy  7441 CCAAGCCCCGTGGTGAGGCGGTTGGCTTCTCGTGGCCGACACCAAGGTGT 7500
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Db  7441 CTAAACCACCTGGTGTGAGGCCGGTGGGGTCCCGTTAGTGGCTGACACTACTAAAGTGT 7500

Qy  7501 ATGTCACCAACCGGACAATGTTGGGGAGAGAGTTGACAAGGTTACCTTCTGGCGTGCCC 7560
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Db  7501 ATGTTACCAACCCGGACAATGTGGGGGAGAGGTAGACAAGGTGCAACAGGTGACCTTCTGGCGCGCCTC 7560

Qy  7561 CTAGGGTTCATGACAAAATTCCTCGTGGACTTCGTGGAGAGCCGCGTAAGAGGCAGCTCAAG 7620
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Qy  7621 CCTGCCTAAGCATGGTTACACTTATGAGGAGCAATAAGGCCAATGCCACATGCTG 7680
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Qy  7681 CCATGGGCTGGGATCTGTCGGTCAAGGACTCGGCCACCCCTGCGGGGGAAGATGG 7740
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Qy  7801 TGAAAAAGGAAGTGTTCTTCAAAGACCGAAAGGAAGAGAAGAGTCATTGTGT 7860
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Qy  7861 TCCCCCCCTGGACTTCCGGATAGCTGAAAAGCTTATTCTTGGGACCCCTGGACCCCTGGACGGGTAG 7920
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Qy  7921 CCAAGGCGGTGTTGGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGGAATTAGGG 7980
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Qy  7981 AGATGCTCAAACTGTGGGGAATCAAAGAGAGACACCACATGCGCTGTGTGGACGCGCCACAT 8040
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Qy  8041 GCTTCACGACAGTAGCATAACTGAAGAGGACGTTGGCCGCTGAGACAGAGCTTTATGCCCTGG 8100
         |||||||| ||| |  | |  |||| ||||| |||||||||  ||||||| |||||||||||||
Db  8041 GCTTCACGACAGTAGTATTACTGAAGAGGACGTTGGCCGCGGAGACAGAGGTTTATGGCTATCTCTGG 8100

Qy  8101 CTTCAGACCATCCAGAATGGTGCGTGCCGTGGGGAAATACTATGCCTTGGCCACAATGG 8160
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Db  8101 CTTCCGACCATCCAGATTGGTGCCGAGCGGTGCCAGCGTTGGGGAAATACTATGCCTCCAGGCACCATGG 8160

Qy  8161 TAACCCCGAGGGGTGCCACTGGGTGAGAGGTGCCAGTGGGGTCTTGACCA 8220
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Qy  8221 CCAGTGCGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCCCGCCTTGTGAGAGGGTGG 8280
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Qy  8461 GCAATGCAGATGGGAAACGCCATTTCTTCCTGACCACGACGACTTGCGAGGCCCCTCGCTC 8520
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Qy  8881 GCGGTTGGGCTGAGTTGGCTAGGGGGCCTCCCCCTCCCCCCCTC 8940
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Qy  9061 TCATCGTAGCCCTTCTTCGGGTGAACTAAATTCATCTGTTGCGCGCAAGGTCCGTGACTGA 9120
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BASE COUNT     1679 a     2558 c     2992 g     2144 t
ORIGIN

Query Match           86.0%;     Score 8080.6;     DB 14;     Length 9373;
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Matches 8579;        Mismatches 794;     Conservative 0;     Indels 2;     Gaps 2;

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Qy    381  CGAGTTGACAAGGACCAGTGGGGGGTTATGGGGCAGGGAAGGACCCCAAAACCCTGCCCT  440
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Qy    801  GAACTGGGAGCCGTGTACGGCCCCTTGTCGTCCGGGGATCCCACGCGGGATCGGG  860
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SOURCE   Hepatitis G virus.
ORGANISM Hepatitis G virus
          Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
          GBV-C/HGV group.
REFERENCE 1 (bases 1 to 9373)
AUTHORS   Zhu,F.L., Qi,Z.T., Shao,L., Ren,H. and Song,Y.B.
TITLE   Splicing and cloning of the full-length genomic cDNA of GB virus
          C/hepatitis G virus
JOURNAL   Ti Erh Chun i Ta Hsueh Hsueh Pao 19, 301-306 (1998)
REFERENCE 2 (bases 1 to 9373)
AUTHORS   Zhu,F.L., Qi,Z.T., Shao,L., Ren,H. and Song,Y.B.
TITLE   Direct Submission
JOURNAL   Submitted (31-JUL-1998) Department of Microbiology, Second Military
          Medical University, 800 Xiang Ying Road, Shang Hai 200433, China
REFERENCE 3 (bases 1 to 9373)
AUTHORS   Zhu,F.L., Qi,Z.T., Shao,L., Ren,H. and Song,Y.B.
TITLE   Direct Submission
JOURNAL   Submitted (04-JAN-1999) Department of Microbiology, Second Military
          Medical University, 800 Xiang Ying Road, Shang Hai 200433, China
REMARK   Sequence update by submitter
COMMENT   On Jan 5, 1999 this sequence version replaced gi:3421387.
FEATURES   Location/Qualifiers
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                RIVMVFLLVTMAGMSQGAPASVLGSRPFDRGLTWQSCSCRANGSRIPTGEKVMDRGNA
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         |||||||||||||||| ||| ||||| ||||||||||||||||||||||||||||||||||
Db   959 AGATGGACTGAGCAGCTGGCCTTCCAATTACTGGATCTTGGAATACCTTTGGAAAGTCCCG 1018

Qy  1041 TTTGAATTTGGAGAGGAGTGATGAGCCTGACCCCTCGTTGGTTTGGTTGGCCGCATTG 1100
         |||| |||  ||||  |||||||||||||||||||| | ||||| ||||||||||||||
Db  1019 TTTGATTTCTGAGGGGGTGTGATGAGCTTGACCCCGTTGGTTTTGCGTGGCCGCATTG 1078

Qy  1101 CTTTTGCTGGAGCAACGGATTGTCATGGTTTCTCGTGGTGACGATGGCGGGGATGTTG 1160
         |||| |||||||||||||||||||| |||||| ||||||||||| |||||||||||||
Db  1079 CTGCTGCTTGACCAACGCAGTTGCATCGTCTTCCTGTTGGTGACAATGGCGGGGATGTCG 1138

Qy  1161 CAAGGCCGCCCCCCGCCTTCGGGGTCCCCGCCCTTTGACTACGGGTTGAAGTGGCAG 1220
         ||||||||||||| | |||| |||||||||||||||||||| ||||||||||||||||
Db  1139 CAAGGCCGCTCCGCGCCCTCTGGGTCTCGCCCCCTTTGACCGTGGGTTGAACAGTTTAGGA 1198

Qy  1221 TCATGGTCCTGCAGGGTAACGGTCGCGTATTCCCACTGGGGAGAGGTGTGGGATCGA 1280
         ||||||||||||||| ||||||||||||| ||||||||||||||||||||  |||||||
Db  1199 TCTTGGTCCTTGTGTAGGGCTAACGGTCTGCGTATTCCGACCGGGAGAGAGGTGTGGGATCGA 1258

Qy  1281 GGGAATGTCACGCTCTTGTGTGACTCGCGTCGTGATTGCGCCCAACGGCCCCGGGTTTCCGGCCTTT 1340
         |||||||| |||| |||||||||||||| ||||||||||||||||||||| ||||||||
Db  1259 GGGAATGCCAGCGTCTGTGACTCGCGTCGTGATTGAATGCGCCCAACGGCCCCGGGTGGTTACCGGCCTTT 1318

Qy  1341 TGCCAGGCGGTTGGGTGGGGGCGACCCCATCACCCATTTGGAGCCACGGACAAAACCAGTGG 1400
         |||||||||  ||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  1319 TGCCAGCGATTGCCTGGGGTGGGTGATCCCACTACCCCATCACGCCACCGGACAAAATCAGTGG 1378

Qy  1401 CCCCTATCATGCCCCAATATGTCTATGGTCGTGTGTCCGTAACGTCGTGTGGGGTTCC 1460
         |||||| ||||||||||  ||||||||||||||||||||||||||| ||||||||||||
Db  1379 CCCCTTTCATGCCCCAGTTGTCTACGGGTCTGTCTCAGTCACTTGCGTGTGGGGCTCC 1438

Qy  1461 GTGTCTTGGTTGCCACGCTGTGTGTCGGCGTCGTGATTCTGGAAGATCGATGTGTGGAGTTTGGTG 1520
         | |||||||||||||||| || |||||||||||||||||| ||||||||||||||||||||||
Db  1439 GCTTCTTGGTTGCCCTGTGTGGGCTCGGCGTCGTGACTCGGAAGATCGATGTGTGGAGTTTGGTG 1498

Qy  1521 CCGGTTGGATCTGCCAGCTGCCACCATAGCCGCTCTAGGGTCATCGGCGCCACGGTG 1580
         || ||||||||||||||||||||||||||||||| ||| ||||||||||||||||||
Db  1499 CCAGTTGGATCTGCCACCTGCCACCATAGCCGCTCTCGGGTCTTCGGCGCCCACCAGTG 1558

Qy  1581 GTTGAGCTCTCCGAGTGGGGAGTCCCGTAAGGTGTATTCTGACCGGTGTATTCTCGGCCTGCT 1640
         | ||||||||||||||||||||||  ||||||||||||| ||||||||| |||||||||
Db  1559 GTCGAGCTCTCCGAGTGGGGAGTCCCCGTAAGGTGTCTATAGGACCGGTGTATCCCGGCCTGCC 1618

Qy  1641 TCATGTGGCACCTGTGTGCGGGACGGCCTGGCCCGAAACCGGTCGGTTAGATTCCCTTTC 1700
         ||||||||||||||||||||||| |||||||||||| ||||||||| ||||||||| ||
Db  1619 TCCTGCGCGGCACCTGTGTGAGGGACGGCCTGGCCCGAGACCGGTCGGTTAGATTCCCGTTC 1678

Qy  1701 CATCGGTGATCTGCCAGCTGCCACCTCGGGTGACAAAGGACTTGCCCTTCGTCAAC 1760
         |||||||||||||||||||||||||||||||||| |||||||||||||| |||||
Db  1679 CATCGGTGATCTGCCACCTGCCACCTCGGGTGACAAAGGACTTGGAAGCTGTCCCTTCGTCAAT 1738

Qy  1761 AGGACAACTCCCTCACCATAAGGGGCCCCATAGGGGCAACCAGGGGAGGCAACCCGGTG 1820
         ||||||||||||| |||||||| |||||||||  |||||||||||||||||||||||||
Db  1739 AGGACAACTCCCCTCACCATTAGGGGCCCCTGGGGCAACCAGGGGTCAGGCAACCCGGTG 1798

Qy  1821 CGGTCGGCCCCTGGGTTTTGGGTCCTACACCAAGATCCGGGATTCCCTGCATTTG 1880
         ||||||||||||||||||||||| || |||||| |||| ||||| |||||||||
Db  1799 CGGTCGGCCCCTGGGTTTGGGTCCTACCATGACCACCAGATCCGGGACTCCTTG 1858

Qy  1881 GTGAAATGTCCCACCACCAGCCATTGACCCTCCCACTGGGACGTTTGGTTCTCCCCGGA 1940
         ||||| ||||||||||||||||| ||||||  ||||||||||||||  ||  |||| ||
Db  1859 GTGAAATGTCCCACCACCAGCCATTGACCCTCCCACTGGGACGTTTGGTTCTCCCTGGG 1918

Qy  1941 GTCCCCGCCCATTAAACAACTGCATGCCCGTAGGCACGGAAGTGTCTGAGGCACGGCGGA 2000
         ||||| |||||  |||||||||  |||| || |  | |||| || | |||||||| |||||
Db  1919 (see right column)
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Db  1919 ACGGCGCCCCTAACAACTGTATGCTGTTGGGCACGGAAGTGTCCGAGGCACTCGGCGGG 1978

Qy  2001 GCTGGGCTTACGGGGGGGTTCTACGAGCCTTCGTTCCGCAGTGTTCGGAGCTGATGGGAA 2060
         ||||  |  |||||||||||||| |||| ||||| ||||||||||| ||||||||||||||
Db  1979 GCTGGCCTCACGGGGGGGTTCTATGAACCCCTGGTTCGGAGCTGATGGGAA 2038

Qy  2061 CGGCCAAATCCGGTTGCCCGGGGTACGGCCATGGCCGTCTCCTGTAGACCTGACGGGTTC 2120
         ||||||||| ||||  | ||||||  |||||||||||||||||||  |  |||||||||||
Db  2039 CGGCCAAATCCAGTTGCAGGGGGTTTGCATGGCCTCTCTTCGGGCAGACCTGATGGGTTC 2098

Qy  2121 ATACACGTCCAGGGGCCACCTGCAGGAGGTGGATGCGGGGCAACTTCATCCCTCCTTCCACGC 2180
         || ||||| ||||||||||||||  ||||||||||||||||||||| |||||||| ||||| |
Db  2099 ATACAGTTCAGGGGCCACCTGCAGGAGGTGGATGCGGGGCAACTTCATTCCGCCCCCGGCGC 2158

Qy  2181 TGGTTGCTCTTGGATTTGTTGTATTTGTCCTGCTGCTCTCATCTGATGAGCTGCTGAGGCACGG 2240
         |||||||||||| ||||  | | |||| |||||| ||||||| ||||| ||||||||||||||||
Db  2159 TGGTTGCTCTTGGACTTTGTGTATTTGTCCTTGTTTATACCTGTTATACCCTGGCTGAGGCACGG 2218

Qy  2241 TTGGCTCCCGTTGATCTTGCTTCTGCTGGCGGGTGTGTGTGGGTGAACCAGTTGGCGGTTCTAGGA 2300
         ||||||| |||||| ||||| ||||||| ||||||||||||||| |||| |||||| || |||||
Db  2219 TTGGTCCCCGCGATCTTGCTATTGCTGGTGTCTATGGTGGTGGGTGAACCAGCTAGCAGTTTTAGGA 2278

Qy  2301 CTGCCGGCTGTGGACGCTGCCGTGCGGGTGAAGTTTTGCGGGCCCCTGCCTTGTCATGG 2360
         || ||||||||||||||| |||||| ||||||||||| ||||| |||| |||| |||||
Db  2279 CTGCCTGTGTGGACGCCCGCTGAGCTGGTGAGGTTTTTGCGGGCTGCCCTGCCCTGTCCTG 2338

Qy  2361 TGTTTGGCCTTCCCACTGTCAGTATGATACTAGGTCTAGCAAACCTGTGTTGTACTTT 2420
         || |  |||  ||| | || |||| ||| ||||||||| |||||||||||||| ||||||
Db  2339 TGTCTGGGCTCCCCGGTCTCGAGTATGCGCTCGAGTATACTAGGGTTAGCAAACCTGTGTGTTGTACTTT 2398

Qy  2421 CGGTGGATGGGCCCTCAGCGCCTTGGGCTGGTGTGTGTTCCTCTGTGTGTGGGGAGCT 2480
         | ||||||||||||||  |||||| ||| | ||||||| |||| |||||||||||||||
Db  2399 AGATGGTTGGGCTTGGGCCGTGCCGCTTTGCGCCTCGAGCTCCTGTTGTGTGGGGAGCT 2458

Qy  2481 TTCCCGGTTGGCACTTTTGATGGGGATTTCGGCGACCCGGCGGCCACCTCTGTGCTCGGG 2540
         |||| ||||||||| || |||| ||||||||||||||||| ||||||||||| |||||||
Db  2459 TTCCCGGCTGGCACTTTTGATGGGGATTTCGTGGATGGGGATTTCGGCGGCCACCTCGTGTCGGG 2518

Qy  2541 GCCCAGTTCGTCGTTCGCTTGCGTCGTGATCGAGGTGACACTTCGGTGTTGGGCTGGGTGGTG 2600
         |||||||| |||||||| | | ||||||||||||| |||||||||||||| || |||||||||
Db  2519 GCCGAGTTCGTCGTTCGATGTGCGTCGTGATCGAGGTGACACTTCGGTGTTGGGCTGGTGGTG 2578

Qy  2601 GCCAGCGTGGTGGGCTTGGGCCGATGCGTCTGAGCTCAATGAGCGCAGGGGGGTGGAAG 2660
         |||||||||||||||| ||| |||| || |||||||||||| |||| |||||||||||||
Db  2579 GCCAGTGTGGTGGGCTTGGGTCGATGCGTCTGAGCTCAATGAGCGCGGGGGGGTGGAGG 2638

Qy  2661 CACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGTACCAGGGTGTGCGCCAGAGGGTG 2720
         ||||||||||| ||||||||||||||||||||||||||||||||||||||| ||||||||
Db  2639 CACAAAGCCGTGATCTATAGGACGTGGTCTATAGGACGTGGTGTAAGGGGTGTCCCAGAGGGTG 2698

Qy  2721 GTGCGGAGGCCCCCTCGGGAGGGGCGTCCTCCAAGCTTCTGACGTTCTGACGTTGCTTG 2780
         |||||| |||| || || |||||||||| ||||||| |||||||||||||||||||||||
Db  2699 GTGAGGAGTTCGGGTCCGGGAGGGGACGGCCCCAAACCCGACGTTCGGGCTTGGTGTGCTTG 2758

Qy  2781 GCCTCATACATCTGCCGCCGATGCGTGTGATGATGGGCCTACCTGTTGACCACTGGGCTCTTTC 2840
         ||||||| |||||||||||||||||| ||||| ||||| || || | || |||| |||||||||
Db  2759 GCCTCGTACACTCTGCCGCCGATGCGTGTGATGATGGGCCTATTGTTGTTGTCGGCTCTTTC 2818

Qy  2841 GGCTGTTCGACGCACTGGACTGGGCCCTGGAGGAGCTCCTGGTTCTCCCGGCCCTCGTTA 2900
         |||||||| ||| |||||||||||||||||||||||  ||||| ||| |||||||||||||
Db  2819 GGTCTGTTCGTCGCGTTGGACTGGGCTTTGGAGGAGATCTTGGTATCCCGGCCCTCGTTG 2878

Qy  2901 CGGCGACTGGCACGCGTGCTTGAGTCTGTTGAGATGGCGGCCGAGAAGGCCACCACCATC 2960
         |||||||| ||||| | |||||||||| ||||| |||||||||| |||||||||||| ||||
Db  2879 CGGCGTCTGCCTGCTCGGTGCTTGAGTCTGTGTGTGTCGTGTGTGGGCCTGAGAAGGCCAAACGGTC 2938

Qy  2961 CGACTGGTCTCCAAGATGTGCGCAAGAGGGGCCTACCGTTGACCACATGGGGCTCTTTC 3020
         ||  || ||| ||||||| ||| ||||||||| || ||||||||||| |||||||||||
Db  2939 CGGTCGGTCTCCAAGATGTGTCGCAGGGGAGCCTATTGTGTTCGATCATATGGGGTTCCTTC 2998

Qy  3021 TCGCGCGCTGTCAAGGAGCCGCTTGTTGGATGGGCACGCGCCCCTGGAGCCCTTGCAATTC 3080
         | |||||| ||| ||||||||||||||||| ||| |||| |||||||||||||||||||||
Db  2999 TCGCGCCGGCCGTTAAGGAGCGGCCTCTGTGAGTGGAGCGCGCCCCTTGAGCCCTTGCATTC 3058
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Qy   4161 CTGGCGCGGAGGATGTGGAGTGCAATTGGTGTCTACGCCACTGCCACCCTCCGGATCC 4220
          |||||| || ||| ||||||| |||||||||||||||||||||||||| ||||| |||
Db   4139 CTGGCACGTGGGTGCGGGGTGCCAACTTGTGCTCTACGCTACTGCCACTGCCCGGCTCC 4198

Qy   4221 CCGATGACCCAGCACCCATCAATCATTGAGACAAAACTGGACGTGGGAGAGATCCCCTTC 4280
          | ||||| |||||| ||||||||| || || |||||||||||||||||||||||||||
Db   4199 CCCATGACACAGCACCCACCCATCTATCATGTGGGATGTGGGAGAGAGTCCCCATTTT 4258

Qy   4281 TATGGCATGGCATACCTCTTGAGCGATGCGAAGGCATCTCGTATTCTGCCAC 4340
          |||||||||| |||||||||||||||||||||||||||||||||||| |||||
Db   4259 TATGGGCATGGCATACCCCTTGAGCGGATGCGGAGGCACCTCGTATTTTGCCAT 4318

Qy   4341 TCCAAGGCTGAGTGCGAGCGCCTGGCGGCCGGCCAGTTTTCGGCTGGGGGGTAAATGCCATC 4400
          |||||||||||||||||||| |||||||||||||||||||||||| ||| ||||||||||||
Db   4319 TCCAAGGCTGAGTGCGAGCGTCTGGCCGGCCAGTTTTCTCGTGCTAGAGGGGGTGAACGCCATT 4378

Qy   4401 GCCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATGGAGACTTGGTGGTGTGTGCT 4460
          ||||||||||||||||||||| |||| |||||||||||| ||||||||||||||||||||
Db   4379 GCCTATTATAGGGGCAAAGACAGTTCCATCATCAAAGACGGAGACTTAGTGTGTGTGCGT 4438

Qy   4461 ACAGACGCACTATCCACTGGGTACACTGGAACTTCGTGTCTGCCGATTCGTGTGTGGGTTA 4520
          ||||||||| ||||||||||||||||| ||||| || ||||| |||||||| ||||||||||
Db   4439 ACAGACGCGCTATCCACTGGGTACACTGGAATTTCGATTCTGTCACCGACTGCGGGGTTA 4498

Qy   4521 GTGGTGGAGGAGTCGTCGAGTGACCGTGACCTTGATCCCACCATTACCATCTCCCTGCCACG 4580
          ||||||||||||||||||||||||| ||||| ||||||||| |||||||||||||| ||||
Db   4499 GTGGTGGAGGAGTCGTCGAGTGACCGTGACCTTGATCCCACCATTACCATCTCCCTGCCGACA 4558

Qy   4581 GTGCCCGGTCGGCTGAACTGTCGATGCAGCGGCGAGGACGCACGGTCAGGGGCAGTCT 4640
          ||||| || |||||| |||| || ||||| ||||||||| ||||||||||||||||||||
Db   4559 GTGCCCGTTCGGCTGAATTGTCGATGCAGACGGACGAGGACGCACGGTAGGGGCAGTCT 4618

Qy   4641 GGGCGCTACTACTACGCGGGGTCGGCGCAAGGCCCTGCGGTGGTGTGGCGCTCAGGTCCT 4700
          |||| |||||||||||||||||||||||| |||| ||||||||||| |||||||||||||
Db   4619 GGGCGCTACTACTACGCGGGGTGGGCAAAGCTCCCCGACGTTCGTGTCGGTCGGGTCCT 4678

Qy   4701 GTCTGGTCGGCGGTGAAGCCGGTGAACTGGTACGGAATGGAACCTGACCTGACAGCA 4760
          |||||||||||||| ||||||||| ||||| ||||||| ||||| ||||||| |||||||
Db   4679 GTCTGGTCGGCGGTGGAAGCCGGTGACCTGGTATGGAATGGAACCTGACCTGACAGCT 4738

Qy   4761 AACCTACTGACACTTACGACAACTGCCCTTACACCCGCAGCCGTCGCAGCTGACATTGGG 4820
          ||||||||||||||||||||||| |||||||||||||| |||||||| ||||||||||||
Db   4739 AACCTACTGACACTTTACGACGACTGCCCTTACACCCGCAGCCGTCGCAGCTGACATCGGA 4798

Qy   4821 GAAGCGCGGTGTCTTCGCGGGCCTTGCCCCGGTTGAGGATGCATCCGATGTTAGCTGG 4880
          ||||||||||||| ||| ||| ||| || |||| |||||||| |||||||||| |||||
Db   4799 GAAGCGCGGTGTTCTTCTCTCGGGCTTGCGCCCCATTGAGGATGCGGATGCACCCGACGTTAGCTGG 4858

Qy   4881 GCAAAAGTTCGCGGCGTCAACTGGCCCTTCCTGGTTCAGCGGGACCATGTGCCGG 4940
          |||||||||||||||||||||||||||||||||| || || ||||||||||||||||
Db   4859 GCAAAAGTTCGCGGCGTCAACTGGCCCCTCTTGGTTCAGCGGGACCATGTGCCGG 4918

Qy   4941 GAAAACACTGTCTCCCGCCCATCGGATGACCCCCAGTGGGCAGGTCTGAAGGGCCCGAAT 5000
          |||||||||||||||||||||||| ||||||||||||||| ||||| ||||||||||||||
Db   4919 GAAAACACTGTCTCCCGCCCATCGGATGACCCCCAATGGGCAGGTCTGAAGGGCCCAAAT 4978

Qy   5001 CCTGTCCCACTCGTGCTGAGGTGGGCCAATGATTTACCATTACCATCTATGCGTCATCACC 5060
          ||||||||||| || |||||||||| |||||||||||| |||| ||||||||||||||||
Db   4979 CCTGTCCCACTGGTGCTGAGGTGGGCCAACGATTTACCATTACCATCTAAAGTGGCCGGCCATCAC 5038

Qy   5061 ATCGTGACGACCTGGTTCCGGTACGTTCGGGGTTGGCGAGGGTTACGTCCGCTGCGATGCG 5120
          ||| |||||||| ||| ||||| ||| ||||||| ||||||||| |||| ||||| |||||
Db   5039 ATAGTGACGACCTGGTTCCGGAGGCTCCGGTTATGTCCGCTGCGATGCT 5098

Qy   5121 GGACCCATCTTGATGGTGGGCCTCGCTATTGCGGGGCATGATCATGGTCATCACACC 5180
          ||| |||||||| || |||||| ||| ||| ||||||||||||| |||||||||||||
Db   5099 GGCCCCATCTTAATGGTGGGCTCGCTATCGCGGGGGGATGATGATCTTACGCCGTCTTACACC 5158

Qy   5181 GGGTCTCTGGTGGTGGTTAACGACTGGTAACTGGATGGATCGGAGGGGTTGGCGAGGGTTACGGGCCCTTTATCGG 5240
          |||| ||||||||||| |||| || ||||||||||||||||||||| |||||||||| ||||||||||||||||| |
Db   5159 GGGTCAATAGTTGGTGGTGACAGACTGGATGTGAAGGGGGTGGCGCCCCCCTTTATAGG 5218

Qy   5241 CATGGAGACCAGCCCACGCCCCAGCCCGTTGTGCAGGTCCCCGGTAGACCATCGGCCG 5300

Qy   3081 ACTAGGACGACTGCTGCATCATCAGAGATGCCGCGAGGACCCTGTCCTGCGGACAGTGC 3140
          ||||||||||| ||||||||||||| ||| ||||||||||||||| |||||||||||||
Db   3059 ACTAGGACGACGTGTCGCATCATACGAGAGCGCGGAGACGCCGGGACCCGTCCTGCGGGCAGTGC 3118

Qy   3141 GTCATGGGTTTACCCGTGGTAGCACGGCGCGGCGGCCGCGGTGATGATGAGTTCTTCATCGGCGTCTTTCAG 3200
          ||||||||||||||||| || ||||| || |||||||||| |||||||||||||||||||||||||||||||
Db   3119 GTCATGGGCTTACCCGTGTGCGCCGGTCCGGTGAGTGTCCATCGGCGTTTTCCAA 3178

Qy   3201 GATGTGAATCATTGCCTCCCGGGTTGTCCGACTGTCACCAGTTGTCATCCGTCGGTGC 3260
          |||||| || |||||||||||||||| ||||| ||| |||||||||||||||||| |||
Db   3179 GATGTGAACCATTGCCTCCCGGGTTCGTCCCGACTGTCATCCGGCGGTGC 3238

Qy   3261 GGAAAGGGCCTTCCTGGGGTCACGAAGGCAGCCTTGACAGTGGATCCTGACTTACAT 3320
          |||||||||| |||||||||||||||||| |||||||| || ||||||||||||||||
Db   3239 GGAAAGGGCTTCCTGGGGGTTACAAAGGCTGCCTTGACGGGGTCGGGGATCCTGACTTACAT 3298

Qy   3321 CCAGGGAACGTCATGTGTTGGGGACGGCGTACGTCACGAGCAGCATGGCACATGTCTGAAT 3380
          ||||| ||||||||||||||||||||||||||||||||||| ||| |||||| ||| |||
Db   3299 CCAGGGAACGTCATGTGTTGGGGACGGCGTACGTCGCGAAGCATGGCAACATGCTTGAAC 3358

Qy   3381 GGCCTGCTGTTCACAACTTTCATGGGCTTCATCCGAACCATCGCCACGCCCGTGGGG 3440
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3359 GGCTTGCTGTTCACGACTTTCATGGGCTTCATCCGAACCATCGCCACGCCCGTGGGG 3418

Qy   3441 GCCCTTAATCCCAGGTGGTGGTCAGCCAGTGATGACGTCACGGTTACCCGCTTCCAGAT 3500
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   3419 GCCCTTAATCCCAGGTGGTGGTCAGCCAGTGACGACGTCACGGTTACCCGCTTCCAGAT 3478

Qy   3501 GGGGCAACTTCGTTGACAGTGCTCCACTCTGGCGGCCAGGCGGGGGAGTCCGTGTTATTAGATCC 3560
          |||||||||||||||||||||| ||| |||| || ||||||||||||| ||||| |||||| |||
Db   3479 GGGGCAACTTCGTTGACAGTGCTCCAGGCCTGAGTCTTGTTTGGGTCATCAGATCC 3538

Qy   3561 GACGGGGCTTTGTGCCATGGCTTGAGCCAAGGTTGAGCTGGATGTGGCCATG 3620
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   3539 GACGGGGCTTTGTGCCATGGCTTGAGTAAGGGAGACAAGGTGGAGCTGGATGTGGCCATG 3598

Qy   3621 GAGGTCTCTGACTTCCGTGGTTCGTCTGGTCACCGGTCTCACCCGGTGCCACAAAGGGCACAGCA 3680
          |||||||||||| ||||||||| ||||||||||| ||||| ||| ||||||||||||||| |||
Db   3599 GAGGTCTCTGACTTCCGTGGTCGTCTGGTCACCCGTCTCACCCGCTGCGAAGGGCACGCG 3658

Qy   3681 GTAAGAATGCTCGTGTGTCAGTGCTCCACTCTGGCGGCGGTACTGCGGGCGGATTCACT 3740
          |||| ||||| ||||| || ||||||||||||| || ||||| || ||||||| |||||
Db   3659 GTAGGAATGCTCGTGTGTCCACTCTGGTGTAGGGTTACCCGCAGCTCGGTTCACT 3718

Qy   3741 AGGCCGTGGACTCAAGTGACGATGCCAAGACTACCACAGAACCCCTCCGGTGCCG 3800
          ||||||| || |||||||||||||||||||||||||||||||||||||||||||||
Db   3719 AGGCCGTGGACCAAGTGACGATGCCAAGACTACCACAGAACCCCTCCGGTGCCG 3778

Qy   3801 GCAAAAGGAGTTTCAAGGAGGCCCCGTTGTTTATGCCTACGGGGCGGGAAAGAGCACC 3860
          ||||||||||||||||||||||||||||||||| ||||||||||| |||||||||||||
Db   3779 GCAAAAGGAGTTTCAAAGAGGCCCGTGTTTATCCTCACGGAGCGGGAAAGAGCACC 3838

Qy   3861 CGCGTACCGTTGGAGTACGGCCAACATGGGCACCAAGAGTCTTGATCTTGAACCCGTCGGTA 3920
          ||||||||| ||||||||||||||||||| |||| |||||||||| |||||||||||||||
Db   3839 CGCGTTCCGGTTGGAGTACGGCCAACATGGGCCACCAAGGTCTTAATCCTGACCCCCTCGGTG 3898

Qy   3921 GCTACCGGAAGGTTTTGGGCCAACCCTAGCCCATCACATGGAGCCCAGTATT 3980
          ||| |||||||||||| |||||||| |||||||||||| || || |||||
Db   3899 GCCACTGTGAGAGCAGCCTTACATGGGGCCCTTGCGGGGAAAACATCCAAGCATA 3958

Qy   3981 TACTGTGGGCCATGACGACCACTGCTTTCACAAGGATCACTGCCCCTTACGTATTCC 4040
          ||||||||||||||| ||||||||||| |||||||||||||| ||||||||| ||||
Db   3959 TACTGTGGGCCATGAACGACCACTGCTTTCACGAGGATCACTGCGACGTACTCTA 4018

Qy   4041 ACTTACGGAAGGTTTTGGCCAACCTAGGCCAGTGCTGAGGGTGTGTGGTGCATT 4100
          ||| |||||||||| ||| |||||||||||||| ||||||||| ||||||| |||
Db   4019 ACCTACGGAAGGTTTTCTCGCCAACCCAACCCAGTGTTGGGGCGTCTCGGTGTCATT 4078

Qy   4101 TGTGACGAGTCCCAGACTCATGACTCAACTCTGTTTGGGGCGTGTCAGGGAG 4160
          |||| || ||||||||||||||| |||||||||| |||||||||||||||||
Db   4079 TGTGATGAAATGCCCAGTCATGACTCAACTGTGCTGTTTGGGGCCATTGGGAGGGTCCCGGGAG 4138

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Db  5219  ||||||||||||||||||  ||  ||||||  ||||||||||||||||||||||        5278
          CATGGAGCCAGCCACGCCACAACCGGTTGGTGCAGGTCCCCCGGTAGACGTGGCCG

Qy  5301  GGGGGAGGAGTCTGCGCCATCGATGCCAACACAGTGACAGATGCGGTGCGGCCATCCAG  5360
          ||||||||||||  |||||||||||  ||||  |||||||||||||  |||| |||
Db  5279  GGGGGAGGAGTCCGCGCCATCGGACGCCAAGAGCAGTGACAGATGCGGTGGCAGCCATTCAG  5338

Qy  5361  GTGGGATTGCGATTGGTCAGTCATGACCCTTCGATCGGGAGTGCTGTCCTTGGCCCAG  5420
          ||||||||||||||||||||||  |||| |||||||||| ||||||||||||| |||
Db  5339  GTGGGATTGCGATTGGTCAGTCATGACTCGTCGATCGGAGAGTGCTGTCCTTGGCTCAG  5398

Qy  5421  GCTAAGACGGGCCGAGGCCTACGCCAGCTACCACCAAGTGGCTTGCTGGCTACACGGGG  5480
          ||||||||||||||||||| ||  ||||||||||||||||||||| |||||||||||
Db  5399  GCTAAGACGGGCCGAGGCCTACACAGCGGCCAAGTGGCTTGCTGGCTGCTGCTACACGGGG  5458

Qy  5481  ACGCGGGCCCGTCCCCACTGTTTCAATTGTTGACAAGCTCTTCGCGGGGGCTGGGCGCG  5540
          ||||||||||||||||||||  |||||||||||||| ||| ||||||||||  ||||||
Db  5459  ACGCGGGCCCGTCCCCACTGTTTCAATTGTTGACAAGCTCTTCGCGGGGGGCTGGGCGGGGCT  5518

Qy  5541  GTGGTAGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGGCCGCCTATGGGGCTTCTAGG  5600
          ||||||||||||||||||||  |||| |||||||||||||||||| ||||||  |||
Db  5519  GTGGTAGGCCATTGCCACAGTCTGCAGCAGTGGCAGCCCTACGGGGCTTCAAGG  5578

Qy  5601  AGCCCTCCATTGGCTGCTGCCGCGCTCCTACCTCATGGGGTTGGGCGTCGGAGGCAACGCG  5660
          ||||||||||||||||||  |||||||||||  |||||||||||||||||||||
Db  5579  AGCCCTCCGTTGGCTGCGCCCTCCGCGTGATGGGGTTGGGCGTCGGGGGCAACGCT  5638

Qy  5661  CAAACCCGCTTAGCCTCCGCGTCTCCGCTTCCTACTAGGGGCCTCTGGGCACGCCT  5720
          |||| |||||||| ||||||||||  ||||| ||||||||||||||||||||| |||
Db  5639  CAAACGCGCTCTGGCATCCGCGCCCTCCTATTGGGGCCTGCTGGGACCGCGTGGGCCACTCCT  5698

Qy  5721  GTCGTGGGGTTAACCATAGGCGGCGCGTTCATGGGAAGTGCTAGCGTCTCCCCCTCTTG  5780
          ||||||||||||||||||||||  |||| ||||||| || |||||||||||||||
Db  5699  GTCGTGGGGTTTAACCATGGCGGGGGCGTTTATGGGAGTGCTAGCGTCTCCTCCTGTG  5758

Qy  5781  GTCACCATTTTACTGGGGGCCGTGGGAGGGCGTTGGTGAATGCGGCTAGCCTT  5840
          ||||||||| |||||||||||||| || |||||  ||  | |||| ||||||
Db  5759  GTCACCATCTTACTGGGGGCTGTAGGAGGTTGGGATGGGGCGTCGTCAACGCGGCGACCCTT  5818

Qy  5841  GTCTTCCACTTTATGGCGGGAAACTATCATCAGAGATCTGTGGTATGCCATCCCAGTG  5900
          ||||||  |||||||||||||| |||||||||||||  |||||||||||||||||||||
Db  5819  GTCTTTGACTTCATGGCGGGGAAACTTTCATCAGAAGATCTGTGGTATGCCATCCCAGTG  5878

Qy  5901  CTAACCAGTCGGGGGCAGGACTTGCCGGGATCGCCCTCGGGTTGGTGTTACTCAGCT  5960
          |  ||||||| ||| | |||||||||||| ||||||||||| ||||||||||||||||
Db  5879  CTGACTAGTCCGGGGGCGGGGGCGGGGCCGCTCTCGGGGTTGGTTTTGTACTCAGCT  5938

Qy  5961  AACAACTCGGCACTACCACTTGGTTGAACCGTCTCTGACTACATTACCTAGGTCTTCA  6020
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Db  5939  AACAACTTCGGGTACTACCACTTGGTTGAACCGTCTCTGACTACATTACCTAGGTTTTCA  5998

Qy  6021  TGCATCCCTGACAGTTACTTTCAGCAGGCCGATTACTGTGACAAGGTCTCAGCTGTCTC  6080
          ||||||||||||||||||||||  |||| |||||||||||||||  ||||||||||||
Db  5999  TGCATGCCAGACAGTTACTTTCCAGCAGGCCCTGTCACTACCTTTGTGTGTGCCCGTCTC  6058

Qy  6081  CGACGCTTGAGCGTCACTGGTTGCCCTGGTTCAACAGGGGAGCCTAAGGTGGAT  6140
          || ||  |||||||||||| ||||||||||||| | ||| | |||||||||||
Db  6059  CGCCGATTGAGCGTTACCCGCACTGTCGTGGTTGCCCTGGTTCAACAGGGAGCCTAAGGTGCGAC  6118

Qy  6141  GAGGTTCAGGTGGGGTACGTCTGGGGATCATGCGCCAAGGTGCGCATG  6200
          ||||| ||||||| |||||||||||| |||||  | |||| ||||||||
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Qy  6201  GTGATGGCCAGACTTACTTTCGGCCCTGTCATTACCCTTATGGCACTGCGGGG  6260
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Db  6179  GTCATGGCCAGACTTACTTTCGGCCCTGCCCGTCGTCACTACCTTTGTGTGCCACTGTGGG  6238

Qy  6261  GAGGGGTGGTTCCGGAGAATGTTCGTTGGACGGCCATGTTGAGTCGTTTGTGGT  6320
          |||||||  |||||||||||||||||| |||||| | ||||||||||||||
Db  6239  GAGGGGTGGTTCCGGAGAATGTTCGTTGGACGGCTCATGTTGAGTCCGTGTCTGTGG  6298

Qy  6321  TGCGTGATCACCGGTGATGTTTGAATGGCAACTCAAAGATTCCAGTTACTCTACCAAG  6380
          ||  ||||||||||||||  ||  |||||||||||| || |||||||||||||
Db  6319  GAGGGGTGGT...
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Db  6299  ||||||||||||||||||||||||||||||||||||||  6358
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Qy  6381  CTGTGCAGGCATTATTGGATGGGACAGCTCCCTGTGAACATGGCTATGGGCGAGACG  6440
          ||||| ||||||||||| ||||| |||| ||| ||| |  |||||||||||
Db  6359  CTGTGCCGCGCACTATTGGATGGGACAGTCCCTGTGAACATGGCTGGGTTACGGTGAAACA  6418

Qy  6441  TCGCCCTTTGCTCGCTCGTCAGACACCCCGAAGGTGGTACCATTCGGGACGTCTGGGCTGGGCT  6500
          ||||  ||  ||  ||  |||||||||  ||||||| |||  |||  | |||||||||||
Db  6419  TCGCCCTCCTGGCCCTTGCACACCCCGAAGGTTGTACCCTTCGGGACGTGTGGCTGGGCT  6478

Qy  6501  GAGGTGGTGGTGACCCCTACCCACGTTGTGATCAGGCGAACATCCGCCTACAAACTGCTG  6560
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Db  6479  GAGGTGGTGGTGACCCCCACCCACGTAGTCAGGTGATCAGGAGAACCTCCGCCTACAAGTTGCTG  6538

Qy  6561  CGGCAGCAAATCCTGTCGGCGTCGTGTCTTGCTGACGGGCCCTATTCGGACGGCATACCGGTC  6620
          ||||||||  ||||||  |  |  || | |||| ||||| || ||||||||||||||
Db  6539  CGCCAGCAAATCCTATCCGGCTGCTGTAGCTAGCGTGTGAGCCCTACACGTTGCGACGGTC  6598

Qy  6621  TCATGGGACGCGGACGCGCGAGCCCTGCATGGTCTATGGCCCTGGCAAAGTGTCACC  6680
          || |||||||  || ||||| ||||||||||||| || |||| ||||  |||||||
Db  6599  TCGTGGGACGCGGACGCGCGTCGGCCCGCATGGTCTATGGCCCTGGCAAAGTGTTACC  6658

Qy  6681  ATTGACGGGGAACGCTACACCCTTCCGCATCAACTGCGCGCCTTAGGGAATGTGGCGCCCTCT  6740
          ||||||||||||||||||||  ||||||||| | |||||||||||||||||||||| |||||
Db  6659  ATTGACGGGGAACGCTACACCCTCCCGCTCCTCACCAGCGCTGAGCTCAGGGAATGTGGCGCCCTCT  6718

Qy  6741  GAGGTGTCATCCGGAGGTGTCCATTGACACATTGGACGGAGGACTGAAGACTCAGAACTGACT  6800
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Db  6719  GAGGTTTCATCCGGAGGTGTCCATTGACACATTGGACGGAGGACTGAAGACTCAGAACTGACT  6778

Qy  6801  GAGGCCGACCTGCGCGCCGGCCTTCAGCGTCGGCTATCGGAGAATT  6860
          |||||  |||| ||||| ||||||  || |  |||| ||||||||||
Db  6779  GAGGCTGACTTGCCGCCGGCCTGCTGCTCTCCAAGCGATCGGCGGAGAATT  6838

Qy  6861  CTTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTGACACCCTCTCTTTGTGGGAGT  6920
          ||| ||||  | |||||||||||||| ||||| |||| ||||||||||| ||||||| ||
Db  6839  CTTGAACCTCCATATTGATGTCATCATGGGGGACTGCAGTCAGTACACCCTCTCTTTGTGGTGT  6898

Qy  6921  AGCCGAGAGATGCCTGTGTGGGGAGAAGCATACCCCACTCCATCGCCAGCACTTATC  6980
          ||||||| |||||||||||||||||||||||||||||  ||||||||||||||||||
Db  6899  AGCCGAGAGATGCCTGTGTGGGGAGAAGACACATCCCACTCCATCGCCCACTCTTATC  6958

Qy  6981  TCGGTTACTGAGAGCAGCAGATGGAGATGAGAAGACCCCGTCCTTCCGCAGGAGGAT  7040
          ||||  |||||||||| |||||||||||||| ||||||||||||||||||||||||
Db  6959  TCGGTTACTGAGAGCAGCAGATCAGATGAGAAGACCCCGTCGGTCCTTCCGCAGGAGGAT  7018

Qy  7041  ACCCCGTCTTCTGACTCATTCGAGGTCATCATTGACTCAGGTTGTGAGATGGAAGGGGAGGAAA  7100
          ||||||||||||||| || ||||||||||||||| ||||| || |||||||||||||||
Db  7019  ACCCCGTCTTCTGACTCATTCGAGGTCATCATTGACTCAGGTTGTGAGATGGAAGGGGAGGAA  7078

Qy  7101  AGGGTCTTCAACGTGGCTGCTCTTTCCGCTACTAAAAAGCCTGTTCGTTCCACAGAGCGCCACA  7160
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Db  7079  AGTGTCTTCAACGTGGCTGCTCTTTCCGCTACAAAAAGCCTATTATTTTCCACAGAGCGATGCGACC  7138

Qy  7161  AGAAAGCTTACCGTTAAGATGTCATGCTGTGTTGAGAAGAGCGTAACACGCTTCTTTTCA  7220
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Db  7139  CGGAAGCTTACCGTTCAAGATGTCATGCTGTGTTGAGAAGAGCGTCACACGCTTCTTTTCG  7198

Qy  7221  TTGGATTGACGGTCGCTGACGTCGCTGGAGATGGAAAATCAGAACCATACA  7280
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Db  7199  CTGGGGTTCAGGTTGACGGTTGCTGACGTCGCTGGAGATGGAAATCAGAACCATACA  7258

Qy  7281  GCCTATTGACAAGGTGCCGCACTCGGTTGGTGGTGGCAAT  7340
          ||| ||||||||||||  ||||||||| ||||| ||||||
Db  7259  GCCTATTGTGACAAGGTGCGCACTCGGTTGGTGTGCTGGGCAAT  7318

Qy  7341  GAACTTACCTTTGAAGTGACAAGTGACAGTCGTTTCTTGTGGT  7400
          ||||||||||||||  ||||||||| |||| ||||||||||||
Db  7319  GAACTTACCTTTGAAGTGACAAGTGAGGCCAAGAAACCTTGGCCTCTTTCTCC  7378

Qy  7401  TACATTTGGTCTGCGGTGCCACTCACGACGGGCCACTCCGTGTGTGAGG  7460
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Db  7379  TACATTTGGTCTGCGGTGCCACTCACGACTAGGGCTACTCCCGTGTGTGTAAGG  7438
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Qy  7461  CCGGTTGGCTCCTTGCTGCTGTGGCCGACACCACCAAGGTGTATGTCACCAACCCGGACAAT  7520
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Db  7439  CCGGTTGGCTCCTTGTTGTTGGGCAGACACCACCAAGGTGTATGTTACCAACCCAGGACAAT  7498

Qy  7521  GTTGGGAAAGAGTTGACAAGGTTACCTTCTGGCGTGCCCTAGGGGTTCATGACAAAATTC   7580
          ||  ||||||||  || ||||||||||||||||||||| || |||||||||||||||||||  7558
Db  7499  GTGGGAAGGAGGGTGGACAAGGTGACCTTCTCCGAGCTGTCCTAAGCCTGCCTAAGCATGGGTTAC

Qy  7581  CTCGTGGACTCCATAGAGCCGCGTAAGAGGGCAGCTCAAGCCTGCCTAAGCATGGGTTAC   7640
          |||||||| ||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  7559  CTCGTGGACTCGATCGAGCCGCGTAAGAGGGCCGCCTCAAGCCTGCCTAAGCATGGGTTAC   7618

Qy  7641  ACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCCATGGGCTGGGATCTAAG   7700
          |||||||||||||||||||| |||||||| ||||||| ||||||||||||||||||||||
Db  7619  ACTTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCCATGGGCTGGGATCTAAG   7678

Qy  7701  GTGTCGGTCAAGGACCTGCCACCCTGCGGGGAAGATGGCTGTCCATGACCGGCTCCAG   7760
          |||| |||||||| | |||||||||||||||||||||| || ||||||||||| |||||
Db  7679  GTGTCAGTCAAGGATCTTGCCACCCTGCGGGGAAGATGGCTGTCCACGACCGGCTCCAG   7738

Qy  7761  GAGATACTTGAAGGGACGCAGTCGTCCCTTTACTCTTGTGAAAAAGGAGTGTTCTTC   7820
          |||||||||||||||| || ||||||| |||||||||||||||||||||||||||||
Db  7739  GAGATACTTGAAGGGACTCCGGTCGTCCCTTTACTCTTTACTGTGAAAAAGGAGTGTTCTTC   7798

Qy  7821  AAAGACCGAAAGGAAGAAGGAGAGAGGCCCCCCGCCTCATTGTGTTCCCCCCTGGACTTCCGG   7880
          |||| || ||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  7799  AAAGATCGCAAGGAAGAAGGAGAGAGGCCCCCCGCCTCATTGTGTTCCCCCCTGGACTTCCGG   7858

Qy  7881  ATAGCTGAAAAGCTTATTCTGGAGACCTGGGACGGTAGCCAAGGCCGTGTTGGGGGGA   7940
          |||||||||||| |||||||| ||||||||||||||| ||||||||||||||||||||
Db  7859  ATAGCTGAAAAGCTCATCCTGGAGACCTGGGACGGTAGCCAAGGCCGTGTTGGGGGGG   7918

Qy  7941  GCCTACGCCTTCCAGTACACACCCCCAAATACCGGAATTAGGGAGATGCTCTAAACTGTGGAA   8000
          |||||||||||||||||||| |||||||||| || |||||||||||| ||||||||||| ||||
Db  7919  GCCTATGCCTTCCAGTACACACCCCCAAAACCGGGTAGGGAGATGCTCAAGCTATGGGAG   7978

Qy  8001  TCAAAGAAGACACACCATGCGCCATCTGTTGTGGACGCCACATGCTTCGACAGTAGCATAACT   8060
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Db  7979  TCAAAGAAAATACACCTTGCGTCGATGCGTGTGCGACGCTGCTTCGACAGTAGTATAACT   8038

Qy  8061  GAAGAGGACGTGGCCTGAGACAGAGCTTTATCGCCCTGCTTCAGCACCATCCAGAATGG   8120
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Db  8039  GAAGAGGACGTCGCGTTTGGAGACAGAGCTGTATGCTCTGCCTCTGCCCTGTACCACCCAGAAATGG   8098

Qy  8121  GTGCGTGGCCCTGGGGAAATACTATGCCCTCTGGCACAATGGTAACCCCCGAGGGGGTGCCA   8180
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Db  8099  GTGCAGTGGCCCTGGGGAAATACTATGCCCTCTGGCACCATGGTCACCCCCGGAAGGGGTTCCC   8158

Qy  8181  GTGGGTGAGAGGTATTGTGATCCTTCAGGGGTCTTGACCACCAGTGCGAGCAACTGCTTG   8240
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Db  8159  GTTGGTGAGAGGTATTGTGATCCTTCAGGGGTCGTGACGGCGGCTAGCCGGCAACTGCCCTG   8218

Qy  8241  ACTTGCTATATCAAGGTGAAAGCCCGCCTGGTGGGGCTGAGAAAAATGTCTGCTCTC   8300
          |||| || |||| |||||||||||||||||||||||||||||||||||||||||||| |
Db  8219  ACCTGCTACATTAAGGTGAAAGCCCGCCTTGTGAGAGGGCTGAGAAAAATGTCTCACTC   8278

Qy  8301  CTCATCGCTGGCGATGACTGTTGATCATATGCGAACGCGTGTGTCGGATCCTAGCGAC   8360
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Db  8279  CTCTAGCTGGCGATGACTGTCGATCATATGTGAACGCGTCACCGGCCCAGTGTGCGACCCAGCGAC   8338

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Db  8339  GCTCTGGGGCAAAGCGCTATCAAGCTATGGGTACCGCGCCTTCATATCATCATCA   8398

Qy  8421  CTGGACAACGGCGCCCCCCCCTCTGGCCTAGCTGGCTGCGCAATGCGAGATGCAGATGGGAAACGC   8480
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Qy  8481  CATTTCTTCCTGACCACGACTTTCGGAGGCCCCTCGCTTCGCCTTCGCTCGAGCGAGTACAGT   8540
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Db  8459  CATTTCTTCCTGACTACGACTTTCGGAGGCCCCTCGCTCCGCCTTCGCTCGAGCGAGTACAGT   8518
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Qy  8541  GACCCAATGGCTTCGGCCATCGGTTACATCTCTCCTATACCCTTGGCATCTATCACACGG   8600
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Db  8579  TGGGTCATCATCCCTCATGTGCTAACATGCGCATTCAGGGGGTGTGGCACACCGTCTGAT   8638

Qy  8661  CCTGTGTGTGCCAGGTACATGGTAATTACTACACAGTTTCCACTGGACAAAACTGCCTAAC   8720
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Db  8819  AAGAGGGCCGGGACTCGCATCGTCCTGGGCGCTGCAGGTCGGCCGTGAGTTGGCC   8878

Qy  8901  AGGGGCTTGTTGTGGCGTCCAGGCCTGCGGCCTTCCCCCTCCGGAGATTGCTGGTATCCCC   8960
          |||||||| |||||||| |||||||| |||| ||||||||||||| ||| || |||||||||
Db  8879  AGGGGCCTGTTGTGCGGCATCCAGGCCTTCCCCCCCCCCCAGAGATTGCTGGTATCCCC   8938

Qy  8961  GGGGTTTCCCCCTTTCCCCCTATATGGGGTGGTTCATCAATTGGATTCACAAGC   9020
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Db  8939  GGGGTTCCCCCCTTTCCCCCCTACATTGGGGTGGTTCATCAATTGGATTCATCAACAGC   8998

Qy  9021  CAGAGGAGTGCTGCTGGGTGGTGTTCTTAGCCCTCTCATCGTAGCCCTCTTCGGG   9080
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Db  9059  TGAACTAAATTCATCTGTTGCGGCAAGGTCTGGTGACTGATCATCACCACCGGAGGAGGTTCC   9118

Qy  9141  CGCCCTCCCCGCCCCAGGGGTCTCCCCGCCGGGGCCTTGGTAAAAAGGGCCGGCCTTGGGAGGCAT   9200
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          || ||||||| || |||||||| ||||| || |||||| || |||||||||||||
Db  9239  GTGGCGGGGTCGCTACCTTATAGCGGACCGGCTGACGCGCTCGCAGAGCCCTCCC   9298

Qy  9321  CGGATGGGGCACAGTGCACTGTGATCTGAAGGGTGCACCCGGTCGGCGCCCAA   9380
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Db  9299  CGGATGGGGCACAGTGCACTGTGATCTGAAGGGTGCACCCGGTAAGAGCCCGGCGCCAA   9358

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Db  9359  AGGCCGGGTTTTATT   9373
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RESULT 7

REFERENCE   1 (bases 1 to 9292)
AUTHORS   Kempfer,M., Nuebling,M.C. and Loewer,J.
TITLE   Direct Submission
JOURNAL   Submitted (01-OCT-2000) FG 2/4, Paul-Ehrlich-Institut,
             Paul-Ehrlich-Str. 51-59, Langen 63225, Germany
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             IPRTPSPALISVTESSSDEKTPSVSPSQEDTPSSDSFEVIQESETAEGEESVFNVALS
             VLXALFPQSDATRKRLTVKMSCCVEXSVTRFFSLGLTVADVASLCEMEIQNHTAYCDKV
             RTPLELQVGCLVGNELTFECDKCEARQETLASFSYIWSGVPLTRATPAKPVVRPVGS
             LLVADTTKVYVTNPDNVGRRVDKVTFWRAPRVHDKYLVDSIERAKRAAQACLSMGYTY
             EEAIRTVRPHAAMGWGSKVSVKDLPTPXGKMAVHDRLQEILEGXPVPFTLTVKKEVFF
             KDRKEEKAPRLIVFPPLDFRIAEKLILGDPGRVAKAVLGGAYAFQYTPNQRVREMLKL
             WESKKTPCAICVDATCFDSSITEEDVALETELYALASDHPEWVRALGKYYASGTMVTP
             EGVPVGERYCRSSGVLTTXASNCLTCYIKVKAACERVGLKNVSLLIAGDDCLIICERP
             MCDPSDALGRALASGYACEPSYHASLDTAPFCSTWLAECNADGKRHFFLTTDFRRPL
             ARMSSEYSDPMASAIGYILLYPWHPITRWVIIPHVLTCAFRGGGTPSDPVWCQVHGNY
             YKFPLDKLPNIIVALHGPAALRVTADTTKTKMEAGKVLSDLKLPGLAVHRKKAGAXRT
             RMLRSXGWAELARGLLWHPXLRLPPPEIAGIPGGFPLSPPYMGVVHQLDFTSQRSRWR
             WLGFLALLIVALEG"

BASE COUNT   1653 a   2480 c   2937 g   2046 t   176 others
ORIGIN

Query Match   85.3%; Score 8018; DB 14; Length 9292;
Best Local Similarity   90.2%; Pred. No. 0;
Matches 8383; Conservative 158; Mismatches 750; Indels 1; Gaps 1;

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Qy  1082 GGTTTGGGTGGCCGCATTGCTTTGCTGGAGCAACGGATTGTCATGGTTTCCTGCTCGT 1141
         ||| || |||| ||| |||||||||||||||||||| ||||||| |||||  ||
Db  1082 GGTCTGCGTAGCCGCCTTGCTCCTGCGGAGCAACGGGTTGTCATGGCTTCCTGTTGGT 1141

Qy  1142 GACGATGGCGGGGATGGTTGCAAGGCGCCCCGCCTCCGTTTGGGGTCCCGCCCTTTGA 1201
         |||||||  ||||||: ||||||||||||||||||||||| |: |||||| |:||
Db  1142 GACCATGGCGGGGATGYCCCAAGGCGCCCCTGCCGCCCTGCGTTTGGGGTCTCGCCCTTTYGA 1201

Qy  1202 CTACGGGTTGAAGTGGCAGTCATGCTCCTGCAGGGTCAACGGGTCGCCTATTCCCACTGG 1261
         ||||||||| || |||||||  ||| ||||||| ||| || |||||||||||||| |||||
Db  1202 CTACGGGTTGACATGGCAGTCCTGCTCCTGCAGGTCAACGGCTCACGTTYGATCACTGG 1261

Qy  1262 GGAGAGGGTGTGGGATCGAGGGAATGTCACGCTCTTGTGTGACTGCCCCAACGGCCCCTG 1321
         :||| |||| ||  |||||||||| ||   |||||| || : |||||| ||||:|| ||
Db  1262 KGAGAAGGTCTGGGAYCGAGGGAATGTGACACTTYTGTGTGATTGCCCCAACGGYCCGTG 1321

Qy  1322 GGTTTGGGTCCCGGCCTTTTGCCAGGCGGTTGGGTGGGGCGACCCCATCACCCCATTGGAG 1381
         |||||||| |||||||||| |||||||| ||| ||||| ||||||||||||  | ||||
Db  1322 GGTGTGGGTCCCGCTGCYCARGCAGTGGGCGTGGGGTGATTCCATTCACTCACTGGAG 1381

Qy  1382 CCACGGACAAAACCAGTGGCCCTATCATGCCCCAATATGTCTATGGTCTGTGTCCGT 1441
         ||||||||||||| ||||| || :|||| ||||||||| || ||||||||| |
Db  1382 CCACGGACAAAATCAGTGCGCCCCTGTCTCTGCCTCCAAYGTCTATGGTCTGTGTCAGW 1441

Qy  1442 AACGTGCGTGTGGGGTTCCGTGTTGGTTTGCCTGCAGTGGCACCTGTGATTCGAAGAT 1501
         || | |||||||||||| ||| :|||||| ||| |||| |||||| |||| |||||
Db  1442 CACTTGCGTGTGTGGGGCCTGCYCCTTGGTTTGGTCGGTCGGATTCAAAGAT 1501

Qy  1502 CGATGTGTGGAGTTTGGTGCCGGTTGGTTCCATCGGTGATCTGCCAGTGCACCATAGCCGCTTCTAGGGTC 1561
         |||||||| ||||| |||| ||| ||| ||| :|| || |||||||||||| |||||||
Db  1502 CGATGTGTGGAGTTTGGTTYCTGCCASCTGTACCATGGTCGCACTCGCCACTCGGGTC 1561

Qy  1562 ATCGGATCGCGACACGTGGTTGAGCTCTCCAGTGGGGAGTCCCGTTGCGTAACGTGTAT 1621
         :||| ||:+ ||||| | ||||||||||  || |||| || :||||||||||||| |
Db  1562 RTCCGGATYGTGACACCGTGGTGGGGCYCTCCAGYGGGGGTCCCGAGYGGGGTGACGTGTAT 1621

Qy  1622 TCTCGACCCTCGGCCTGCTTCATGTGGCACCTGTGTGCGGGACTGCTGCCGCGAAACCGG 1681
         |||||| |||||||||| |||| |||||| |||||||||||||||||
Db  1622 TCTCGGATCGCGTCGCGRTCGTGTGGCACCTGTGTGCGGGACTGTTGCCCGAAACCGG 1681

Qy  1682 GTCGGTTAGATTCCCTTTCCATCGGTCGCCATGCTGCACCATAGCCGCTGCAAAGGACTTGGA 1741
         ||| | ||||| ||| ||||||||||| || ||| ||||| ||||||| ||||||||||
Db  1682 GTCGTCAGATTCCCATTCCCATMGGTGTGGCACGGGCCTCGCCGGCTGACARAGGACTTGGA 1741

Qy  1742 AGCTGTGCCCTTCGTCAACAGGACAACTCCCCTTCACCATAAAGGGGCCCCCTGGGCACCA 1801
         :|||||||: :|||||| ||||| |||||| :|||| ||||||| |:||||||||||||
Db  1742 RGCTGTGCCYTTCGTCAATAGGACAACYCCCCTTCGCCTATARGGGYCCCCTGGGCAACCA 1801

Qy  1802 GGGGAGAGGCAACCCGGTCGCGAGCTGGTTTCGGGTCCTACACCATGACCAAGAT 1861
         |||||||||||||||||||||||||| || ||||||||||||||||||||||||||
Db  1802 GGGGAGAGGCAACCCGGTCGCGAGCTGGTTTCGGGTCCTACACCATGACCAAGAT 1861

Qy  1862 CCCGGGAATTCCCTGCATTTGGTGAAATGTCCCACCACCAGCCTCCCGACTGGAAC 1921
         ||||| || ||||| ||||||||| ||||||||||||||||||||||||||: ||
Db  1862 CCCGGAYACCCTRCATTYGGTGAAATGTCCCACCACCAGCCTCCCACTGGRGAC 1921

Qy  1922 GTTCGGGTTCTTCCCCGAGTCCCGGGTTCTTACGGACCACGGAAGT 1981
         |||||||||||||::|||||| |||| | ||||||||||||||||||
Db  1922 GTTCGGGTTCYTCCCCGAGTGCCGAGCTGGTTCCTGGGCACGGAAGT 1981

Qy  1982 GTCTCGAGGCAGTTGGGCGGAGCTGGGCGTTCTACGGGTTCGGAG 2041
         |||||||||||: |:|||||||||||||||: :||||||||||||
Db  1982 GTCTCGAGGRCTGRGGTGGCGTGGGGCTGCYCYCACGGGGTTGGCGCAG 2041

Qy  2042 GTGTTCGGAGCTGATGGGACGCCGAAATCCGGTTTGCCCGGGTACCCATGGCCTGTCCTC 2101
         ||||||||:||||||||| |||||| | |||||| |:||||| |||||| ||||||||
Db  2042 GTGTTCGGARCTGAYRGGACGCCGGAATCCAGTYTGCCCGGGGTATGCGATGGCTTTCCTC 2101

Qy  2102 TGGTAGACCTGACGGGTTCATCACGTCCAGGGACGTGGATGCGGGCAA 2161
         |||| |||| ||||| ||| |||||||:||||| |||||| ||||||||
Db  2102 GGGTCGACCTGACGGGTTCATCACATGTCCAGGGACATCGCAGGAGGTCGAGTGCGGGCAA 2161

Qy  2162 CTTCATCCCTCCTCCACCGCTGGTTGCTCTGCCCTARTTTGTCCTGCTGATATCTGAT 2221
         ||| ||||||| ||| ||||||| ||: || |||| ||||| ||||||| |||||
Db  2162 CTTCATCCCTCCTCCACCGCTGGTTGCTCCTGGAYTTTGTRTTTGCCTGTGTGGTGGTGA 2221

Qy  2222 GAAGCTGGCTGAGGCACGGTTGGTCCGTTGATCTTGCTTCTGCTGCTGCGGTGGGGTGGAA 2281
         |||||||||||||||||||||||| ||||||| ||||  :||
Db  2222 GAAGCTGGCTGAGGCACGGTTGGTCCGTRATCTTGCTYGCTGCTGCTGGTGGTGGTGGYGAA 2281

Qy  2282 CCAGTTGGCGGTTCTAGGACTGGGCTGGACGCTGCCGTCGCCGGTGAAGTTTTGC 2341
         :|||| |:::||:+ ||  |||||||||| || ||||| |||||||||||||||
Db  2282 YCAGCTGGCAGTCCKMGGGCGTGGCCYGGGACGCCGGCGGTGGGGCGAGGTTTTGC 2341

Qy  2342 GGGCCCTGCCTTGTCATGGTGTTTGGGCCTCCCACTGCGTCAGTCAGTGATACTAGGTCTAGC 2401
         ||||||| ||| | |||| ||||||||||||| |||||||| |:||||:||||||| |||||
Db  2342 GGGCCCTGCCCTGTGTCGTGTTTGGGCCTCCCACCGGTTAGTAGTATGATACTAGGCTTAGC 2401

Qy  2402 AAACCTGGTTGTGTACTTTCGGTGGATGGGCCCTCAGCGCCTCATGTTCCTGTGTTGTG 2461
         |||||||| |||| |||:|| ||| |||||||||| ||| |||||||||||||||||||
Db  2402 AAACCTGGTTGTGTGTTTCCGGTGGATGGGCCCTCAACGCCTCATGTTCCTTGTGTTGTG 2461

Qy  2462 GAAGCTCGCTCGGGGAGTTTCCCGCTGGCACTTTGATGGGATTTCGGCGACCCGCCG 2521
         ||||||||||||||||| || |||| |||||| |||||||| ||||| | || |
Db  2462 GAAGCTCGCTCGGGGRGCTTCCCGCTGGCACTTCGATGGGATTGGGGCGACTCGCGG 2521

Qy  2522 GCGGCACCCTGTGCTCGGGGCCCAGTTCTGCTCGATGCGATGCAGATCGGGGACACTTC 2581
         |||||||||||||||||||||||||||||||||| ||||||||| || || |||||||||
Db  2522 GCGGCACCTGTGCTCGGGGRCCCAGTTCTGCTCGACGTTGCTTCGACGTGGCGACACTTC 2581

Qy  2582 GGTGTTGGGGCTGGGCTGGCTGGGCTTGGGCCAGCGCTCCTCTGAGCTCAAT 2641
         |||||||||||||||| |||||||| ||||||||||| ||| ||||||||
Db  2582 GGTGTTGGGGCTGGGCTGGCTGGGCTTGGGCCAGCGCTCCTCATGAGCTCCAT 2641

Qy  2642 GAGCGCAGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCA 2701
         |||||||  |||:||||||||||||||||||| |:||||  :||:|||||||| ||||||
Db  2642 GAGCGCGGGAGGGTGGAAGCACAAAGCCRTRATCTATAGGACGTGGTGTAAGGGGTACCA 2701

Qy  2702 GGCTGTGCGCCAGAGGGTGTGCGCACTGCCTCGGGAGGGCGTCCTACCAAGCTTCT 2761
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Db  2702 GGCCATACGTCAGCGGGTGTGCGCGCTGCCTCGGGAGGGCGTCCTACCAAACCCTT 2761

Qy  2762 GACGTTCGCCTGGTGCTTGGCCTCATACATCTGGCGGATGGTGGTGGT 2821
         |||| |||||||||| |::|| |||||||||| ||||| |||||:|||
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Qy  2822 GGCCTTGGTCCTCTCGTGTTCGACGGACTGACTGGGCCCTGGAGGAGCTCCT 2881
         |||||||||||:|||  |||||||||||| || || ||| ||||||||||:
Db  2822 AGCCTTGGTGCTCTTTCGCGTGTTCGCGTGTTGGACGTGGGCGTTTGGAGGAGCTCTT 2881

Qy  2882 GGTCTCCCGGCCCTCGTTACGGCGACTGCCACGGGTGGTTGAGTGCTGTGATGGCGG 2941
         ||| ||  |||| ||||| | ||| ||||| ||| ||||||| |||||| |||||||
Db  2882 GGTGTCCCGGCCCTCGTTTGCGGCGTTGCCGACGGGTGGTTGAGTGCTGTGATGGCRGG 2941

Qy  2942 CGAGAAGGCCACCAATCGACTGGTCTCCAAGAGCCTCCGACTGTTT 3001
         ||||||:  :|||||||||| ||:|| ||| |||| ||||| :||||
Db  2942 TGAGAAGCCACACAATCCGGCTGGTCTCCAAGAGCTGCCAGAGGGGCCTATTTGTT 3001

Qy  3002 TGACCACATGGGCTCTTTTCTCGCGCTGTGTCAAGGACGCGCGGCGC 3061
         |||| ||||||||| |||:|| |||||||||| |||||||||||||||
Db  3002 CGACCATATGGGCTCTTCTYTGCTCTCTTCGCGCTGTGTCAAAGAGCGCTTGCTTGGACGGCGCGGCGC 3061

Qy  3062 TTTGGAGCCCTTGCATTCACTAGGACGCGTCGCATCACTAGGAGGACGCCCCGAGGAC 3121
         ||||| || |||| ||||| |||||| | |:||||||||  |||||||||||||||||
Db  3062 TTTGGAACCTCTCATTYCATTCACCAGGACCGGTTCGCATCATCAGACGCCCGAGGAC 3121

Qy  3122 CCTGTCCTGCGGACAGTGCGTCATCAGGGTTTACCCGTGGTTAGCACGCGCGGTGATGAGGT 3181
         |||||| :||||||| ||| || || |||||||||||| ||||| |||||||||:||||
Db  3122 CCTGTCCTGYCGGCCAGTGCGTCATGTGTAGTTACCTGGTAGCACCGGGTTAGCACGCGCGGYGATGAGGT 3181

Qy  3182 TCTCATCCGGCGTCTTTCAGGATGTGAATCATTTGCCTCCCGGTTGTTCCGACTGCACC 3241
         ||:||  |||||||| || ||||||||| | |||||||||| || ||| |||||||||
Db  3182 TCTYATCGGCGTCTTTTCCAGGATGTGAAYCAYTTGCCACCGGGGTTTGTCCCAACCGCGCC 3241

Qy  3242 AGTTGTCATCCGCTCGGTCGCGGTGCGGAAAAGGCGTTCTGTGGGGTCACGGAGGCAGCAGG 3301
         ||| ||||||||||||  ||:|| | |||||||:||
Db
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Db  3242  AGTAGTCATCCGGCGTGCCGAAAGGGCTTCCTGGGAGTYACAAAGGCAGCCTTGACAGG  3301

Qy  3302  TAGGGATCCTGACTTACATCCAGGAACGTCATGTGTTGGGGACGGCTACGTCACGCAGAAG  3361
          ||||| ||||||||||||||||||||||||||||||||| ||||||||||||| |||||
Db  3302  TCGGGAYCCTGAYCCTGACTTACATCCAGGAACGTCATGTGTTGGGRACGGCTACGTCGCGGAAG  3361

Qy  3362  CATGGGCACATGTCGAATGCCTCGTGTTCACAACTTTCCATGGGCTTCATCCCGAAC  3421
          ||||| |||| |||||||||||||||||||||| ||||||||||||||||||||||||
Db  3362  CATGGGGCACATGCCTGCTGTTCACTTTCCATGGGCTTCATCCCGAAC  3421

Qy  3422  CATGCCCACGCCCGTGGGGCGCCCCTTAATCCCAGGTGGTCGTCAGCCAGTGATGACGTCAC  3481
          ||||||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||
Db  3422  CATCCCCACGCCCGTGGGGCGCCCCTCAATCCCAGGTGGTGCTCGCCAGTGACGACGTCAC  3481

Qy  3482  GGTGTACCCCGCCTTCCAGATGGGGCAACTTCGTTGACGCCCTGCACTTGCCAGGCGGAGTC  3541
          |||||||||||||||||||||| |||||||||| |||||||||| |||||||||||||||||
Db  3482  GGTGTACCCCACTTCCGGATGGGCACCTCGTTGACRCCCTGCACGTGCCCGAGTCGCAGGCGGAGTC  3541

Qy  3542  CTGTTGGGTTATTAGAATCCCACGGGCCTTTGTGCCGACTTCAAGTACCAACAGAGGGGACAAGGT  3601
          |||||||| ||||||||||||||||||||||| ||||||||||||||||||||||| ||||||||
Db  3542  TTGCTGGGTCATTAGAATCCGACGGGCGTTGTGCCGACCACCAAGTTGTGTAAGGGGGACAAGGT  3601

Qy  3602  TGAGCTGGATGTGGCCATGGACGTCTCTGAGGTTCGTCTGGTTCACCGGTCCT  3661
          ||||||| |||||||||||||||||||||||||||||||| |||| ||| |||
Db  3602  GGAATTGGATGTGGCTATGGACGTCTCAGARTCCTGTCGGTTCCTCCGCGTCTTT  3661

Qy  3662  TTGGCGACAAAGGGCACGCAGTAAGAAAGTGCTCGTTGGACTCGTCGTGGCGCAGGGT  3721
          ||||||||||||||||| ||||||| ||||||||| ||||||||| |||||||| ||||
Db  3662  GTGCCACGAGGGGGCACGCRGTAGGGAATGGGCGTACCCGTGGTCMGTTCCYCACGTGGTAGGGT  3721

Qy  3722  TACTTCGGGCCCGATTCACTAGGCCCGTGGGACTCAAGTACCAACAGATGCCAAGACTACCAC  3781
          ||||||||||||||||||||||||||||| ||||||||||||||||||||| ||||||||||||
Db  3722  CACCGGGCCCGTTTCACTCGGTGCRGTGGARGGCCCGTACATGGAGCGGCTGGC  3781

Qy  3782  AGAACCCCCTCCGGTGCCGGCAAAGAGAGTTTCAAGGAGGCCCGTTGTTATGCCTAC  3841
          ||||||||||||||||||||||||||||||| |||||||||| ||| ||||||||||
Db  3782  TGAACCCCCTCCGGTGCCGGCAAAGAGAGTTTCAAGGAGGCCCATTGTTTATGCCTAC  3841

Qy  3842  GGGGCGGAAAAGCACCCCGGTACGGTTGGAGTAGGCCAACATGGGCCACAAGGTCTT  3901
          ||||||||||||||||||||| |||||| ||||||| ||||||||||||||| ||||
Db  3842  GGGGCGGGAAAGAGCATTTACTGCGGTGCCCGRTACCCGTAYGGCCACAARGTCTT  3901

Qy  3902  GATCTTGAACCCGTCGGTAGCTACCACCGGTGAGGGCCATCATGAGCGGCTGGC  3961
          ||| ||||||||||| |||| ||||||||||| |||||||||||| ||||||||
Db  3902  GATTYTGAACCCGTCRGTGCCTAYGGAGGTGARGGCCATCATTGGGAGCGGCTGGC  3961

Qy  3962  GGGGAAACACCCCAGTATTTACTGTGGCCATGAGCACCACTGCTTTCACAAGGATCACTGA  4021
          |||||||||||| |||| ||||| |||||||||||| |||||||||||||||||||||||
Db  3962  AGGAAAACATCCAAGCATYTACTGTGGCRACGACAACAGCTTTCACRAGAATCACTGA  4021

Qy  4022  CTCGCCCCTTACGTATTCCACTTACGGAAGGTTTTTTGGCCAACCCTAGGCAGATGCTGAG  4081
          |||||||||||| |||||||||||||||||||| ||||||||| |||||||||||||||||
Db  4022  CTCGCCTCTTAAGTATYTCTACCTAYGGGAGGTTTYTTGGCCAACCCTARGCAGATGCTGAG  4081

Qy  4082  GGGTGTGTCGGTGTGTCATTTGTGACGAGTGCCCAGGATGTGCCCACAGTCTGTTGTTGGG  4141
          |||||||| ||||| |||||| ||||| |||||||| |||||||| |||||||||||||||
Db  4082  GGCCGTGTCGTCGGTGTATTTTATGGGCATGGATGAGTGTGATACCCCTCGGAGGATGTTGTTGGG  4141

Qy  4142  CATTGGGCGTGTCAGGAGACTGGCCGAGGATGTTGGAGTGCAATTGGTCTGTCTACGCCAC  4201
          ||| |||||||||||||||||||||||||| ||| |||||||||||||| |||| ||||||
Db  4142  GATTGGGCGTGTCAGGAGACTGGCCGACGCCGGTGGGTGTGTGCAGCTTGTGCTNTACACTAC  4201

Qy  4202  TGCCACCCCTACGTATTCCACTGGGCCATGGATGACCACCAGCAACCATCAATCATTGACACAAAACTGGA  4261
          |||||||||||||||||||||||| ||||| ||||||| ||||||||||||||||||| ||||||||||||
Db  4202  GGCCACGCACCGGGGTCCCCCATGACTTCAACATCCCTATCATTGAGACAAAACTGGA  4261

Qy  4262  CGTGGGAGAGATCCCCTTCTATGGGCATGCGATACCCTTGAGCCGGATGGGACCGGAAG  4321
          ||||||||||| |||||||||||||||||| ||||||| ||||||||| ||||||||||
Db  4262  TGTCGGGAGAAATCCCCTTTTATGGGCATGGATGAGTGATCCACCTGTGATGACCCGTGTCGTCGGGAG  4321

Qy  4322  GCAATCTCGTATTCTGCCACTCCAAGGCTGCGAGTGCCGAGCCCTGCGGCCCAGTTTCGGC  4381
          |||| |||| |||| |||||||||||||| ||||||||||| |||||| ||||||||| ||
Db  4322  ACACCTCGTTTTTCGCCACTCACGGAGGCGGAGTTGCCCACAGGCGGTTCAGTTTTTTCTGC  4381
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Db  4382  TAGGGGGTAAATGCCATCGGCCTATTACAGGGGGCGAAAGACACAGTTCATCATCAAAGATGG  4441
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Qy  4382  CAGAGGGGTCAATGCCATCGCCTATTACAGGGGCAAAGACAGTTCCATCATCAAGGACGACG  4441

Qy  4442  AGACCTGGTGGTGTGTGCTACAGACGCACTATCCACTGGGTACACCGGCACTATTCCGATTC  4501
          |||||||||||||||| |||||||| ||||||||||||||| ||||||||| ||||||||||
Db  4442  AGACCTTGTGGTGTGTGCTGGTGTGCTACAGACGCGCTATCCACTGGGTACACTGGGAAYTTCGGAATTC  4501

Qy  4502  TGTCACCGATTGTGGGTTAGTGTGGAGGAGTCGTCAGGTGACCCTGATCCACCAT  4561
          |||||| |||||||||||||||| |||||| |||||||||||||||||||||||||
Db  4502  TGTCACCGATTGTGGGTTAGTGTGGAGGAGTCGTGACCTGACCCTTGATCCCCACCAT  4561

Qy  4562  TACCATCTCCCTGCGCACGGTGCCCGCGTGCCGCTGAACTGTCGATGCAGGCGGAGGACG  4621
          |||||||||||||| ||||||||||||||||||||||||| ||||||||| ||||||||||
Db  4562  AACCATCCCCGCGCACAGTGCGCAGTGCCGCAGAGACTGTCGCATGCAAAGGCGGAGGACG  4621

Qy  4622  CACGGGTAGGGGCCAGGTCGGCGGCTACTACGCGGGGTCGGCAAGGCCCCCTGCTGG  4681
          |||||| ||||| ||||||||||||| ||||||||||||| ||||||||| |||||||
Db  4622  CACGGGGTAGAGGCAGATCGGGCGCTACTACGCTATGCGGGGGTGGGCAAAGCCCCYGCTGG  4681

Qy  4682  TGTGGTCGCTCAGGTCCGTGGGTCGCGGGTCGGCCGGTGGAAGCCGGTGTGACCTGTACGGAAT  4741
          ||||||||||||||||| ||||| ||||||||||||||| |||||||||||||| ||||||| 
Db  4682  TGTGGTCGCTTCARGTCCGTTGGTCGGCCAAAGTGCGCCGGCGGTCAACTGCCCAACTGGTATGGTAT  4741

Qy  4742  GGAACTTGACTGACAGCAACTACTTACGACTTCGATTTACGACACCGCCAGC  4801
          |||||||||||||||||||: ||||| |||||||||||| ||||||||||||
Db  4742  GGAACTTGACTGACAGCAACCYTCTGAGACCYTTCGAGACTTACGACCACCAGCAGC  4801

Qy  4802  CGTCGCAGTGACACATTGGGAAGGCCCGAATCCTGCTCCACTCGTGCTGAGGAT  4861
          |||||||||||||||| ||||||||| |:|||||||||||||||||| |||||||
Db  4802  CGTCGCAGCTGACATTGGTGAAGGCCCGAATCCTGCTCCACTCGTGCTYGCGGCTGAGGAT  4861

Qy  4862  GCATCCGATGTTAGCTGGGCAAAAGTTCGCGGCGCGTTCCTGCGCCTTCCTCGGTGGGTGT  4921
          |||||||||||||||||| ||||||||| ||||||||||||:|||||||||||||||||||
Db  4862  GCATCCGATGTTAGCTGGGCAAAAGTGCGCGGCGCGGTTCAACTGCCCYSCTGGTGTGGGTGT  4921

Qy  4922  TCAGCGGACCATGTGCCGGGAAACACTGTCTCCCGGCCATCGGATGACCCCAGTGGGC  4981
          ||:|:|||||||||||||| |||| ||||| ||||||||| ||||||| ||||||||||
Db  4922  TCRGCGGACCATGYGCGGGGAAACAYTGTCTCCCGGCCATCGGATGACCCCAGTGGGC  4981

Qy  4982  AGGTCTGAAGGCCCGAATCCTGCTCCACTCCGTGCTGGGCAATGATTTACCATC  5041
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  4982  AGGTCTGAAGGCCCGAATCCTGCTCCACTCCTGTGCTGAGGTGGGCAATGATTTACCATC  5041

Qy  5042  TAAAGTGCGCGGCCATCCAGTCGGTCTCGGGGTCCGGCGGAGGG  5101
          |||||||||||||||||||||||||| ||||||||||:||||||
Db  5042  TAAAGTGCGCGGCCATCCAGTCGGTCTCCTAGGCTGGRGTGGCCGAGGG  5101

Qy  5102  TTACGTCCGGCTGCGATGCGGGACCCATCTTGATGGTGGCGCCATTGCCGGGGGCAT  5161
          |||| |||||||||| ||||||||||| |||||| |||||| ||:|||||||||||||
Db  5102  TTATGTCCGGCTGTGACGCTGGGCCGATCTTAATGGTCGGTCTTGCTCATCGCGGCGGGGGGAT  5161

Qy  5162  GATCTATGGCGTCATACACCCGGTTCTCCGTGGTGGTGACTGGTGTGGGG  5221
          |||||||||||||| ||||||||||||| ||||| |||||||| ||||||
Db  5162  GATCTACGCGTCATCAACACCGGTGGTGGTGGTGGTCAGTGGTCGGTGATGTAAAGGGGGG  5221

Qy  5222  TGGCAGCGCCCCTTTATCGGCCATGCGATGACGGCACCGCCCCAGCCGGTTGTGCAGGTCCC  5281
          |||||||||||| |||| |||| |||||||| |||||||||||| ||||||||||||||||
Db  5222  TGGCAGCAGCCCGTTTATGGCCATGCGATGGTGACCAGCCGGTTGTGCAGGTCCC  5281

Qy  5282  CCCGGTAGACCATCGGCCGCCGGGGGGAGAGTCTGCCAACAGTCGACAGA  5341
          ||||| ||||||| ||||||||||| |||||| ||||| ||||||||| ||||||||||
Db  5282  CCCGGTAGACCATCGGCCGCCGGGGGGGAATCGCCCGGGGGGATGCCAAGCACAGTGACAGA  5341

Qy  5342  TGCGGTGGCGGCCATCCAGTCGGTTCGATTGCTCAGTTCATGGACACCTGTCGATCCGGGGA  5401
          |||||||| ||||||||||||||||| |||||||| ||||||||||||||| |||||||||
Db  5342  TGCGGTGGYGCCGGTTGGYCAGTGGACTGTGATTGTGATTGGTCATGGACCCTGTCGATCCGGGGA  5401

Qy  5402  AGTGCTGTCTTCCTTGGCCACCAGGCTAAGACGCGGCGCTACCCGACCAAGTGCT  5461
          |||||||||||| ||||||||||||||||||| ||| |||||||||||| ||||||
Db  5402  AGTGCTGTCTTCCTTGGCCACCAGGCTAAGACTGCCACAGCGACCGCGTAAGTGCTT  5461
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Db  6542 CTCCKCGTACAAGCTGCTCGCGCCAGCAAATCCTATCGGCTGCTGTGTARCTGGACCCTACTA 6601

Qy  6602 CGTCGACGGCATACCGGTCTCATGGGACGGCGAGCGGCCGCTGCCATGGTCTATGG 6661
Db  6602 CGTCGATGGCATTCCGGTCTCATGGGACGGGACGGCTCGGCGCGCCCATGGTCTACGG 6661

Qy  6662 CCCTGGCAAAGTGTCACCATTGACGGGAACGTACACCCTTCGCATCAACTGCGGCT 6721
Db  6662 CCCCGGRCAAGTGTTACCATTGACGGGACGCGCTACACATRCCCACATCCCCCGCAC 6721

Qy  6722 TAGGAATGTGGCGCGCCCTCTGAGGTGTCATCCGAGGTGTCATTGACATTGGGACGGAGAC 6781
Db  6722 CAGGAAYGTRGCGCCCTCTGAGGTTCATCCGAGGTGTCATAGACATTGGGACGGAGAC 6781

Qy  6782 TGAAGACTCAGAACTGACTGAGGCCGACCTGCCGCGGCCGCTGCAGCCGGCTAT 6841
Db  6782 TGAAGACTCAGAACTGACTGAGGCCGAYCTGCCCACCGGCGGCTCTCCAGGCTGC 6841

Qy  6842 CGAGAATGCTGCAGAAT TCTTGAACCTCACATAGATGTCATCATGGGAGATTGCAGTAC 6901
Db  6842 CGAGAATGCTGCGAGAATTCTGGAGCCACACATAGATGTCATCATGGGAGATTGCAGTAC 6901

Qy  6902 ACCCTCTCTTGTGGGAGTAGCCGGAGAGATGCGTCTGTGGGGAGAAGACATACCCCGCAC 6961
Db  6902 ACCCTCTCTGTGGTAGTAGCCGGAGAGATGCCYGTGTGGGGAGAAGACATCCCCCGCAC 6961

Qy  6962 TCCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCCCAGATGAGAAGACCCCGTCGGT 7021
Db  6962 TCCATCGCCAGCACTTATCTCGGTTACGGAGAGCAGCTCAGATGAGAAGACCCCGTCGGT 7021

Qy  7022 GTCTTCCTGCAGGAGGATACCCCGTCTTCTGACTCATTCGAGTGTCATCCAAGAGTCCGA 7081
Db  7022 GTCCCCTCCGCAGGAGGATACCCCGTCCTCTGACTCATTCGAGTGTCATCCAAGAGTCTGA 7081

Qy  7082 GACAGCCGAAGGGAGGAGGGAAAGCGTCTTCAACGTGCTCTTCCGTACTAAAAGCCTTGTT 7141
Db  7082 GACAGCCGARGGGAGGGAGGAAAGTGTTCTTCAACGTGCTCTTTCYGTATTAARAGCCTTGTT 7141

Qy  7142 TCCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGATGTCATCGTCGTTGAGAAGAG 7201
Db  7142 TCCCAGAGCGAYGCTACAAGGAAGCTTACCGTTACCGTTCAAGATGTCTTGCTGTGTCGAGARGAG 7201

Qy  7202 CGTAACACGCTTCTTTTCATTGGGATTGACGTGCGCTGGCAAGCCTGTGTGTGAGAT 7261
Db  7202 CGTCACRCGCTTCTTCTTCTCGTTAGGGTTGACGTGCGCTGGCCAGCCTGTGTGTGAAAT 7261

Qy  7262 GGAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCGCACTCCGCCTTGAATTGCAGGT 7321
Db  7262 GGAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCGCACTCCGCCTTGAATTGCAAGT 7321

Qy  7322 TGGGTGCTTGGTGCTGGCAATGACAACTTTACCTTTGGTCTGGGGTGCAAGTGTCAGGCTAGGCAAGA 7381
Db  7322 TGGGTGCTTGGTGGTGGCAATGACAACTTTACCTTTGTGACAAGGTGACAAGGTAGGCAAGA 7381

Qy  7382 GACCTTGGCTTCCTTCTCTTTACATTGGTCTGGGGTCCACTGACGACGAGGGCCACTCCGGC 7441
Db  7382 GACCTTGGCYTCCTTCTCTCCTCCTACATTTGGTCTGGGCTCGGAGGGCCACTCCGGC 7441

Qy  7442 CAAGCCCCCGTGTGGGGTGAGGCCGGGTGGGTTGGCTGCTCCGTGGTCCCGTTGGTCGGTGGCTGTCGACCACCAAGGTGTA 7501
Db  7442 CAAGCCNCCTGTGGGGTGAGGCCGGGTGAGGTCCCGTTGGTGGCTGTCGACCACCAAGGTGTA 7501

Qy  7502 TGTCACCAACCCGGACAATGTTGGGGAAGAGTTGACAAGGTTACCTTCGGCCGTGCCCC 7561
Db  7502 TGTGACCAACCCGGACAATGTTGGGGAGGTGACAAGGTRACCTTCTTCGGCCGAGCTCC 7561

Qy  7562 TAGGGTTCATGACAAATTCCTCGTTGGGACTCCATAGAGGGGCAGTCAAGC 7621
Db  7562 YAGRGTTCACGACAAATATCTCGTGGGATTCTATTGAGCAGGTCAATAACGACTGTAAGGCACATGCTGC 7621

Qy  7622 CTGCCTAAGCATGGTTACCTTATGAGGAGCAATAAGGACTGTAAGGACATGCTGC 7681
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Qy  5462 TGCTGGCTGCTACACGGGGACGGCGGGCCGTCCCCACTGTTTCAATTGTTGACAAGCTCTT 5521
Db  5462 AGCTGGCTGCTACACGGGGACGGCGGCGGCGGGCCGTCCCCACTGYWTCCATTGTTGACAAGCTCTT 5521

Qy  5522 CGCCGGGGCGGTGGGCGGCCGGTGTGGTGGGCTGGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGC 5581
Db  5522 TGCCGGCGGTYGGAGGCCAACGCRCAGACCCGCCGTGTCACACGTGTAATAGCTGCGGCRGTGC 5581

Qy  5582 GGCCTATGGGGCTTCTAGGAGCCCTCCATTGGCTGCTGCGCCGCTTCCTACCTCATGGGGTT 5641
Db  5582 GGCCTACGGGGCTTCAAGGAGTCCCGCGTTGGCAGCTGCTCGGCGTTCYTACCTRATGGGATT 5641

Qy  5642 GGGGCTCGGAGGCAACGGCAAACCCGCTTAGCCTCCGCTCTCCTACTAGGGGCCGCTGG 5701
Db  5642 GGGGCTYGGAGGCAACGCRCAGACCGCRCAGACCCGCGTTGGCGTCGCTTCATGCGGGCGSGCTGG 5701

Qy  5702 GACCGCTCTGGCCACGCGCTGCTCGTGGGGTTAACCATGCGCGGCGCGGCCGTCATGGGAAGTGC 5761
Db  5702 YACTGCCCCGTGGGCACACCCGTCGTGGGGATTAACCATGCGCGGCGGGCTTCATGCGGGGGTGC 5761

Qy  5762 TAGCGTCTCCCCCTCCTTGGTCACCATTTTACTGGGGCCGTGTGGGGGGCTGGGAGGGCGT 5821
Db  5762 CAGCGTTTCCCCCTCCTTGGTCACCATCCTTCTGGGGCCGTGTGGGGGGYTGGGAGGGCGT 5821

Qy  5822 GGTGAATGCGGCTAGCCTTGTCTTGCGACTTTATGGCGGGAAACTATCATCAGAAGATCT 5881
Db  5822 CGTCAACGGCGTAGCCGCTAGCCTTGTCTTGCGACTTCAGTGGCGGGAAACTTTCTTCAGAAGATCT 5881

Qy  5882 GTGTATGCCATCCCAGTGCTAACCAGTCCGGGGCAGGACTTGCCGGGGATCGCCCTCGG 5941
Db  5882 GTGTATGCGATCGCCAGTGCTGCTAACCAGTCCGGGGCAGGACTTGCCGGGGATCGCCCTTRG 5941

Qy  5942 GTTGGTGTTGTACTCAGCTAACAACTCTGGCACTACCTGGTTGACACCGTCTGCTGCGAC 6001
Db  5942 GTTGGTTCTTGTACTCAGCTAACAACTCTGGCACTACCACCATGTTGAACCGTCTGCTGCTAAC 6001

Qy  6002 TACATTGCCAAGGTCCTCATGCATCATCCCTGACAGTGACTTTCAGCAGGCCGATTACTGTGA 6061
Db  6002 AACATTGCCRAGATCGTGTGCATTCGCATTCCAGCAGCYTACCAGCAGGCCGACTACTGYGA 6061

Qy  6062 CAAGGTCTCAGCTGTGCTGTCCGACGCTTGAGCCTCACTCGCACCGTTGGTTGCCCCTGGTCAA 6121
Db  6062 CAAGGTCTCCRAGATCGTGGCATTCCGGCCCTGAGCCTGACGCTGTGTGGGSCCTAGTCAA 6121

Qy  6122 CAGGAGCCTAAGGTGGATGAGGTTCAGGTGGGTACGTCTCGGGAGTTGTTGGGAGTGGAT 6181
Db  6122 CAGGGAACCTAARGTGGATGAGGTTACCAGGTGGGTACCTGTGTGGGAGTGGGAGTGRGAT 6181

Qy  6182 CATGCGTCAAGTGCGCATGGTGATGGGCCAGACTTCGGGGCCCTGTGCCCGTGGTGTCATT 6241
Db  6182 CATGCGCCAGGTGGCGTATGGTGATGGGCCAGGCGTCCCGTTGGTGTCGCT 6241

Qy  6242 ACCCTTATGGCACTGCGGGGAGGGGTGTCGGATCACCGGTGATGCTTTTGAATGGCAACTCAAAGA 6301
Db  6242 ACCATTGTGGCACTGGGGGGAGGGGTGTCGATAAGGTGAATGGGCAACTGTTCTGAAYGGACAATGTTGA 6301

Qy  6302 GAGTCGTTGTCTTTGTGCTGCCTGATCACCGGTGATGGTTTTGAATGGGACAACTGTCAAAGA 6361
Db  6302 GAGTCGCTGCCTGTGGRTGCGGTCTGCCTGATAACAGGTGTTCTGAATGGGACAATGTTGA 6361

Qy  6362 TCCAGTTTACTCTACCAAGCTGTGCAGGCATTATTGGATGGGGACAGTTCCCTGTGAACAT 6421
Db  6362 ACCAGTTTACTTCTACACAAAGCTGTGCAGGCATTACTGGAGGCCGGGTCCCCTGTCAACAT 6421

Qy  6422 GCTGTCCGTATGGCGAGAGCGTCGCGCTTGCCTCCCTTTGCTCGCCCTCCAGACACCCCGAAGGTGGTACCATT 6481
Db  6422 GTTGGGGTACGGTGAAACATCGCCCCTGCCTCCCTGCCTCCCAAGGTAGTACCCTT 6481

Qy  6482 CGGGACGTCTGGGCTGCTGAGTGTGGTGTGCTACCCCACGTTGTGATCAGGCCGAAC 6541
Db  6482 CGGGACGTCCCGGCTGGGCAGAGTGGTGGTGACCCCACCACGTGGTGATCAGGAGAGAAC 6541

Qy  6542 ATCCGCTACAAAACTGCTCGCGCCAGCAAATCCTGTCGGCTGCTGTTGCTGAGCCGTATTA 6601
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Db   7622  CTGCCTAAGCATGGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCCATGCTGC  7681

Qy   7682  CATGGGGATCTGGGTGTCGGTCAAGAGACCTCGCCACCCTGCGGGGAAGATGGC  7741
           ||||||||||||||||||||||||||| ||||| :|:|||||||||||||
Db   7682  CATGGGGCTGGGGATCTYAAGGTGTCGGTCAAAGACCTGCCCACCCCCGYGGGGAAGATGGC  7741

Qy   7742  TGTCCATGACCGGCTCCAGGAGATACTTGAAGGACGCCAGTCCCCTTACTCTTACTGT  7801
           |||||| ||| |||||||||||||:|| ||||||||:: |||||||||||||||
Db   7742  GGTCCACGACGACTTCGARGGGATYCCGGTYCCGGTCGACTCCACTCTTACTGT  7801

Qy   7802  GAAAAAGGAAGTGTTCTTCAAAGACCGAAAGAAGGAGAAGGCCCCGCCCCTCATTGTGTT  7861
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   7802  GAAAAAGGAGGTGTTCTTYAAAGACCGRAAGGAGGAGGAAGGCCCCGCCCCTCATTGTGTT  7861

Qy   7862  CCCCCCTGGACTTCCGGATAGCTGAAAAGCTTATTCTGGGAGACCCTGACGGGGTAGCC  7921
           |||||||||||||||| || |||||||| ||:|||||||||||| ||
Db   7862  CCCCCCTGGACTTCCGGATAGCTGAAAAGCTCATCTTGGGAGACCCCGGGSCGGGGTGGC  7921

Qy   7922  CAAGGGCGGTGTTGGGGGGGCCTTACGCCTTCAGTACACCCCAAATCAGCGAATTAGGGA  7981
           |||||||||||||||||||||||| |:|||||||| |||| |||||
Db   7922  CAAGGGCGGTTGGGGGGGGCCTTACGCCTTCAGTACACCCCAAACCAGCGCGTTAGGGA  7981

Qy   7982  GATGCTCAAAACTGTGGAATCAAAGAGAGACACCATGCGCCATCTGTGTGGACGCCACATG  8041
           |||| | |||| |||||| || |||||||||||| || ||||||||||||||||||||||
Db   7982  GATGCTCAAAAGCTATGGGAGTCAAAGAGAAAAACACCATGCGCCATCTGTGTGGACGCTACGTG  8041

Qy   8042  CTTCGACAGTAGCATRACTGAAGAGACGCTGGCGTCGGAGACAGAGCTTTATGCCCTGGC  8101
           ||||| || || |:|||||||||||||||||||||||||||| | ||||||||
Db   8042  CTTCGACAGTAGCATWACTGAAGAGACGCTGGCACTRAGAGACGGAGCTTTATGCYCTWGGC  8101

Qy   8102  TTCAGACCATCCAGAATGGTGCGTGCCCTCTGGGGAAATACTATGCCTCTGGCCACAATGGT  8161
           |||| || |||||||||||||||||| || |||||||||||||||||||||||||||
Db   8102  CTCTGACCATCCAGAGTGGGTGCGAGCCTGGGGAAATACTATGCCTCTGGCCACCACAATGGT  8161

Qy   8162  AACCCCGAGGGGTGCCAGTGGGTGAGAGTTATTGTAGATCCTCAGGGGTCTTGACCAC  8221
           ||::|| | |||||||||||||||||||||||||:|| ||||||:|:||
Db   8162  GACYCCGAAGGGGTGCCAGTGGGTGAGAGTTATTGTAGTCCTACCTTATACGTTGACTAC  8221

Qy   8222  CAGTGCGGAGCAACTGCTTGACGTGCTATATCAAGGTGAAAAGCCGCCTGTGAGAGGGTGGG  8281
           |:::|| |||||||||:|||| ::|||| | |||||| |||||||||||||||||||||
Db   8222  WRGCCGCAAGCAACTGCYGYTGACCTGCTACCTGCTACATCAAGGTGAAGGGCCGCCTGTGAGAGGGTGGG  8281

Qy   8282  GCTGAAAAAATGTCTCGCTCCTCATCGCTGGCGATGACTGTTTGATCATATGCGAACGGCC  8341
           |||||||||||:||||||||||||||||||||||||: |||||||||||||||||||||
Db   8282  GCTGAAAAAATGTCTCYCTCCTCCATAGCCGGCGATGACTGYTTGATCATATGCCGAACGGCC  8341

Qy   8342  TGTGTGCGATCCTAGCGACGCTTTGGGCAGAGCCCTGGCGAGCTACGGGTACGCATGCGA  8401
           |||||||||||||||||||||||||||||||| |||||||||||||||||||||:||||
Db   8342  TATGTGCGATCCTAGCGACGCTTTGGGCAGAGCCCTGGCGAGCTAYGGGTACGCGTGTGA  8401

Qy   8402  GCCTTCGGTCGTCATCAGCGACACGGGCCCCCCCTTCTGCCACTTGGCTAGCTGAGTG  8461
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8402  GCCTTCGTCGTCATCAGCGACACGGGCCCCCCCTTCTGCCACTTGGCTGCTGAGTG  8461

Qy   8462  CAATGCAGATGGGAAACGCCATTTCTTCGGAGGCCCCGACTTTCGGAGGCCCCACTCCGCTCG  8521
           ||||||||||||||||| ||||||||||||:|:||
Db   8462  TAATGCAGATGGGAAGCGCCATTTCGGAGGCCCCGACTTTCGGAGGCCCCACTCCGCYCG  8521

Qy   8522  CATGTCGAGCGAGTACAGTGACCCAGTGACCATCCTTCGGCCATGACTTACATCCTCCTATACCC  8581
           ||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   8522  CATGTCGAGCGAGTACAGTGACGCCAGTGACCATCCTTCGGCCATGTTACATCCTCCTATACCC  8581

Qy   8582  TTGGCATCCTATCACACGGTGGGTCATCATCCTCACGTGCCTGCGGCCGTTTAGGGG  8641
           |||||||:::||||||||||||||||| ||:||||||||||||||||| ||||||||||
Db   8582  CTGGCAYCCATCACACGGTGGGTCATCATCCTCACYTGTGCCTGCGGCCGTTTAGGGG  8641

Qy   8642  TGGTGGCCACACCGTCTGATCCTGTCGTGTGCCAGGTACATGGTAATTACTACACAAGTTCC  8701
           ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   8642  TGGTGGCACCGTCTGATCCTGTCGTGTGCCAGGTACATGGTAACTACTACACAAGTTCC  8701

Qy   8702  ACTGGACAAAACTGCCTAACATGCCTGCCTGCCTGCCCTCCACGGACCAGCGCGTTGAGGGTTAC  8761
           || || ||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   8702  TCTRGACAAACTGCCTAACATGCCTGCCTGCCCTCCACGGACCAGCGCGTTCACCTTTGTGGGT  8761
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Qy   8762  CGCAGACACAACTAAGACAAAAATGGAGCTGCTGGCCAAGGTGCTGCTGACGCGACTTCAAGCTCCC  8821
           ||:|||||||||||||||:||::||||||||||||||:|||||||||||:|||||||||:||||
Db   8762  CGCAGACACAACCAARACAACAAAATCGAAGCGCGGCAAGGTGCTGAGCGGATCTCAAGCTACC  8821

Qy   8822  TGGCCTAGCAGTCCACCGGAAGAAGGCCGGCCATTGCGAACGCCGTATGGCTCCGGTCGCGG  8881
           ||||||||||:||||||||:|||||:|||||||:|:|||||:||||||||||::|||||||
Db   8822  TGGCCTAGCGGTCCACCGGTCCACGCGGCRMTGCGGCAGCGMTGGCCATGGCWTCTCCGGTCGCR  8881

Qy   8882  CGGTTGGGCTGAGTTGGCTAGGGGCCTTCAGGCGTCTCCAGGCGCTTCCCCCTC  8941
           ||||||||||||||||||||||||||||| ||:| |:||||:|||:|||||
Db   8882  CGGTTGGGCTGAGTTGGCTAGGGGCCTTCCARCCYTACGGGCCTCCCYCCTCC  8941

Qy   8942  GGAGATTGCTGGTATCCCGCGGGGGTTCCCCCCTTTTCCCCCCATATAGGGGGTTGGTTCA  9001
           ||||||||||||||:||||:|||||||||||||||| |||||:|:||||||||||:||||:
Db   8942  CGAGATTGCTGGTATCCCGGGGGTTCCCCCCTTTCCCCCCTAYATGGGGGTGTGCA  9001

Qy   9002  TCAATTGGATTTCACAAGCCAGAGAGTCGCTGGCGTGTTCTGGGGTTCTTAGCCCTGCT  9061
           ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   9002  TCAATTGGATTTCACAAGCCAGAGAGTCGCTGGCGTGTTGGGGTTCTTAGCCCTGCT  9061

Qy   9062  CATCGTAGCCCTCTTCGGGTGAACTAAAATTCATCTTGTGGACGGGGTCTCCCCGCTGGGACTGAT  9121
           ||||| |||||||||||||||||||||||||||||||||||||||||| ||||
Db   9062  CATCGTGGCCCTTTCGGGTGAACTAAATTCATCTTGTGGACGGGTCTCCCCGCTGGGACTGAT  9121

Qy   9122  CATCACTGAGGAGGTTCCCCGCGTCTCCCCGCTGGGTAAAAAGG  9181
           |:||| |||||||||||||||:|||||||||||||||||||||||
Db   9122  CACCACTGAGGAGGTTCCGSCCTCTCCCCGCTGGGTAAAAAGG  9181

Qy   9182  GCCCGGCCTTGGGAGGCATGGTACTAACCCCTGGTACTAACCCCTGCAGGGTCAAAGCCTGATGGTG  9241
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9182  GCCCGGCCTTGGGAGGCATGGTACTAACCCCTGGTACTAACCCCTGCAGGGTCAAAGCCTGATGGTG  9241

Qy   9242  CTAATGCACTGCCACTTCGGTGGCCGGTCCTACCTTATAGGCGTAATCCGTG  9293
           ||||||||| :| ||| || ||||||||||||||||||||||||||||||||
Db   9242  CTAATGCACT-SCGCTACGGCGCGGGTCCTACCTTATAGCGGTAATCCGTG  9292
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RESULT 8
AR026694

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LOCUS       AR026694               Sequence 14 from patent US 5856134.          9392 bp    DNA        linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5856134.
ACCESSION   AR026694
VERSION     AR026694.1  GI:5937534
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 9392)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie., Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5856134-A 14 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1..9392
                     /organism="unknown"
BASE COUNT     1694 a   2551 c   2998 g   2148 t   1 others
ORIGIN

Query Match        84.9%;  Score 7979;  DB 6;  Length 9392;
Best Local Similarity   90.7%;                 Pred. No. 0;
Matches 8515;  Conservative 1;  Mismatches 876;  Indels 1;  Gaps 1;
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Qy      3  ACGTGGGGGTGTGATCCATCCCCCCCCGCACTGGTGCAAGCCCCATAAACCGACGCCT  62
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ACGTGGGGAGTTGATCCCCCCCCCGCACTGGTGCAAGCCCCAGAAACCGACGCCT  60

Qy     63  ATCTAAGTAGACGCAATGACCCTGGCAGGTAATGGTAATTACTACAGAAGTTTCC  122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ATCTAAGTAGACGCAATGACCCTGGCAGGTAATGGTAACTACTACAGAAGTTTCC  120

Qy    123  GTGGTGACAGGGGTTGGTAGGTCGTAAATCCGGTGCACTATAGGTGGGT  182
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GTGATGACAAACTGCCTAACATGCCTAACATCCGGTGAATCCGGTGCACTATAGGTGGGT  180
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Qy    183  CTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTGCGGGCGAGACCGCCGCACGGTCCACAGGT  242
           ||||||||||||||||  |||  |||||||||||||||||||||||||||||||||||||||
Db    181  CTTAAGAGAAGGTTAAGATTCCTCTTGTGCCTGCGGGCGAGACCGCCGCACGGTCCACAGGT  240

Qy    243  GCTGGCCCTACCGGTGAATAAGGGCCCACGTCAGCGTCGTCGTTAAACCGAGCCCGT      302
           ||||||||||||||  || ||||||||||||||||||||||||| ||||||||||||
Db    241  GTTGGCCCTACCGGTGGAATAAGGCCCCACGTCAGCGTCGTCGTTAAACCGAGCCCGT      300

Qy    303  CACCCACCTGGCAAACGACGCCCACGTACGGTCCACGTCGCCCTTCAATGTCTCTTG  362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  TACCCACCTGGCAAACGACGCCCACGTACGGTCCACGTCGCCCTTCAATGTCTCTTG  360

Qy    363  ACCAATAGGTTTATCCGGCCAGTTGACAAGGACCAGTGGGGGCCGGGGTTATGGGGAAG  422
           |||||||||||||||  |||||||||||  |||||||||||||||||||| |||||||
Db    361  ACCAATAGGCGTAGCGGCCAGTTGACAAGGACCAGTGGGGGCCGGGGCT-TGGAGAGAG  419

Qy    423  GACCCCAAAACCTGCCCTTCCCGGTGGGCCCGGGAAATGCATGGGGGCCACCCAGCTCCGCG  482
           ||||| ||  || |||  |||||||||||||||||||||||||||||||||||||||||||
Db    420  GACTCCAAGTGCCCGCCCTTCCCGGTGGGCCCGGGAAATGCATGGGGGCCACCCAGCTCCGCG  479

Qy    483  GCGGCCTGCAGCCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCCGGTGGCATTTCTCTT  542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480  GCGGCCTGCAGCCGGGGTAGCCCAAGAATCCTTCGGGTGAGGGCCGGTGGCATTTCCTTT  539

Qy    543  TTCTATACCATCATGGCAGTCCTTCTGCTTCGTGTTGAGGCCGCAATATTCCTCACAAATTGCTGTGCC  602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540  TTCTATACCATCATGCAGTCCTTCTGCTCTCTGCTGTGTTGAGGCCGCAATATTCCTCACAAATTGCTGTGCC  599

Qy    603  GCCCCGGCCACCCACCGCTTGTCGCGAGCGAATGGCAATATTCCTCACAAATTGCTGTGCC  662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600  GCCCCGGCCACCCACCGCTTGTCGCGAGCGAATGGCAATATTTCCTCACAAATTGTTGTGCC  659

Qy    663  CCGGAAGACATCGGGTTCTCGCCGGAAGGCGATGCCTGGTGCGGTTTGGTCCTGGTGCACGGTT  722
           ||||||||||||||||  ||||||||||  |||| ||||||||||||||||||||||||||||
Db    660  CCGGAGGACATCGGGTTCTCGCCGGAAGGCGATGCCTGGTGCGGTTTGGTCCTGGTGCACGATT  719

Qy    723  TGCACCGAGCGTTGCTGGCCACTGTATCAGGCGGTTTGGCTGTGCGGCCTGGCAAGTCC  782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720  TGCACTGACCAATGCTGGCCACTGTATCAGGCGGTTTGGCTGTGCGGCCTGGCAAGTCC  779

Qy    783  GCGGCCCAGTCGTTGGGAACTGGGGAGCCTGTACGGGCCCTGTCGTGTCGTCGGCTTAC  842
           ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db    780  GCGGCCAACTGGTGGGGAGCTGGGGAGCCTATACGGGCCCTGTCGTGTCGTCGGCCTAT  839

Qy    843  GTAGCCGGGATCCTGGGCTGGGGCCGAGGTTTACTCCGGGTCCTGACAGTTGGTGTTGCG  902
           ||||||||||||||||||||  |||||||||||||||||||||||||||||||||||||
Db    840  GTGGCTGGGATCCTGGGCTGGGGAGGGTTCTCTGGGTCCTAACGGGTGGGAGCTGGGTGCG  899

Qy    903  TTGAGGCGGCCGCAATGCTTTGCTGGACGCAACCGGAGTAGAAGTGACGTTAAG  962
           ||||||||||||||||  |||||||||||||||||||||||||||||||||||
Db    900  TTGACGCGGCCGCAATTGCTTGCTGAGCAACGGAGTGCAGTGCAGTCGTAAAAG  959

Qy    963  TGGGAAGTGAGTTTTGGAGATGGGACTGAGCAGTTGAGCCTTCCAATTACTGGATTTTGGAA  1022
           ||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||||||
Db    960  TGGGAAAGTGAGTTTTGGAGATGGGACTGAACAGCTGGCCTTCCAACTACTGGATTCTGGAA  1019

Qy   1023  TACCTTGGAAGTCCCATTTGAATTTGGAGGAGTGATGAGCCTGACCCCCTGTTG  1082
           ||||||  |||||||||  |||||||||||||| ||||||||||||||||||||
Db   1020  TACCTCTGGAAGTCCCGATTCGATTTCTGGAGAGGGTGATAAGCCTGACCCCCTGTTG  1079

Qy   1083  GTTTGGGTGGCCGCATTGCTTTTGCTGGAGCCAACCGGATTGTCATGGTTTTCTGGTG  1142
           ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1080  GTTTGCGTGGCCGCATTGCTTTTGCTGCTGAGCAACCGGATTGTCATGGTTTTCTGGTG  1139

Qy   1143  ACGATGGCGGGGATGTTGCAAGGCGCCCTCCGGCCTCCTGCAGGGTCGCCGTATTCCCACTGAC  1202
           ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db   1140  ACGATGGCGGGGATGTTGCGCGCAGTGTTGCAAGGCGCCCTCCGGCCTCCTGCAGGGTCACGGCCCTTTGAC  1199

Qy   1203  TACGGGTTGAAGTGGCAGTCCTTGGCAGGGGTCGCCGTATTCCCACTGGG  1262
           |||||||||||||||||||||||||||||||||||||||||| |||||||
Db   1200  TACGGGTTGACTTGGCAGACCGGTCGCTCTTGCAGGGGCCAACCGGTTCCGCAGGTTTTTGGACTGGG  1259
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Qy   1263  GAGAGGGTGTGGGATCGAGGGAATGTCACGCTCTTGTGTGACTGCCCCAACGGCCCCTGG  1322
           ||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db   1260  GAGAAGGTGTGGGACCCTGGGAACGTTACGCTTCAGTGTGACTGCCTGCCCCTGGAGC  1319

Qy   1323  GTTTGGGTCCCGGCTTTTGCCAGGCGGTTGGGTGGGCGACCCCATCACCCATTGGAGC  1382
           ||||||||||| || ||||||||||| || ||||||||||||||||||||||||||||
Db   1320  GTGTGGTTGCCAGCCTTTTGCCAAGCAATCGGGTGGGGTGACCCCATCACTTATTGGAGC  1379

Qy   1383  CACGGACAAAACCAGTGACGTCGCCCTATCATGCGCCCCAATATGTCTATGGTGTCTGTGTCCGTA  1442
           |||| |||  ||||||||||||||||||||||||  |||||||||||| |||||||||| |  ||
Db   1380  CACGGGCAAAATCAGTGGCCCCTTTCATGCGCCCCAGTATGTCTATGGTCTGTCGTCTGCTACAGTC  1439

Qy   1443  ACGTGCGTGTCGGGTTCCGTGTCTTGTTCGGTTGCCTCGCAGCGGCGGTCTGATTCGAAGATC  1502
           ||||||||||||||  ||  ||| ||||||| ||| |||||||||||||||||||  ||||||
Db   1440  ACTTGCGTGTGGGGTTCCGTGTCTTGTTGCCTCGCACCAGTGGTCGCGACTGGACTGAAGATA  1499

Qy   1503  GATGTGTGGAGTTTGTGCCGGTTGACGTCGATCTGCCAGCTGCACCAGTCGCACCATAGCCGCTCTAGGGTCA  1562
           ||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   1500  GATGTGTGGAGTTTAGTGCCAGTTGGCTCTGCCACCTTGCTGCACCATAGCCGCCACTTGGATCA  1559

Qy   1563  TCGGATCGGACACGGTGGTTGAGCTCTCCGAGTGGGGAGTCCCGTTGCGTAACGTGTATT  1622
           |||| ||||||| ||  |||| |||||||||||||||||  |||||||||||||||||||
Db   1560  TCGGATCCGGACACGGTGCCTGCCTCCGAGTGGGGAATCCCGTCGCGTGACGTGTGTT  1619

Qy   1623  CTGGACCGTCGGCCTGCTTCATGTGGCCACTGTGTGCGGGACTGCTGGCCCGAAACCGGG  1682
           |||||||||||||||||| || ||||| ||||||||||||||||||||||  |||||||||
Db   1620  CTGGACCGTCGGCCTGCCTGCCTCCTGCGGCCACTGTGTGGGGGACTGCTGGCCCGAGACCGGG  1679

Qy   1683  TCGGTTAGATTCCCTTTCCATCGGTGCGGCACGAGCAACTCCCTCGGCTCAACCAG  1742
           |||||| ||||||||||||||||||||| ||| ||||||||||||||||| ||||||
Db   1680  TCGGTTAGGTTCCATTCCATCGGTGCGGCGTGCGTGGGGGCCTCGGCTCAACCAG  1739

Qy   1743  GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATAAGGGCCCCTGGCAACCAG  1802
           |||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db   1740  GCTGTGCCCTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGCACCTGGCAACCAG  1799

Qy   1803  GGGAGAGGCAACCGGTGCGGTCGCCCTCCGGGTTTGGGTCCTACACCATGACCAAGAATC  1862
           ||  ||||||||||||||||| |||||||| ||||||||||||||| ||||||||||||
Db   1800  GGCCGAGGCAACCGGTGCGGTCGGCCCTTCTTGGGTCCTTACGCGTGACCATGACCAGAGATC  1859

Qy   1863  CGGGATTCCCTGCATTGGTGAAATGTCCCAGCCATAGAGCCTCCGACTCCGACGAACG  1922
           || |||||||| || |||| || ||||||||| ||||||||||||||||| |||||||
Db   1860  CGAGATACCCTACATCTGGTGGAGTGTCCCACCAGCCATTGAGCCTCCACCACCGGGACG  1919

Qy   1923  TTCGGGTTCTTCCCCGAGTCCCGGGTCCTGACAGTTGGTGTTGCG  1982
           |||||||||||| |||||||||| ||||||||||||||||||||||
Db   1920  TTTGGGTTCTTCCCCGGGGGGGGTCTCATGAACCCCTGGTGCGCGCAGG  1979

Qy   1983  TCTGAGGCATTGGGCGGAGCGTGGGCTTCTACGGGCTCTGGTTCGCAGG  2042
           ||  |||||||||| |||||| |||||||| |||||| ||||| ||||||
Db   1980  TCCGAGGCACTTGGGGGGGGTGGCTGGCCTACGCGGGTGCGCGCAGG  2039

Qy   2043  TGTTCGGAGCTGATGGGACGGCCGGAAATCCGGTTGTTGCCGGGTACGGCACGCATGGCTGTCTTCT  2102
           |||| ||||||  ||||| || |||||||||||||||| |||||||| |||||| |||||||||||| |
Db   2040  TGTTCGAAGCTGATGGGAGGAAGCCGAAATCCGGTTGTTGCCATGGCTCTTCTTCG  2099

Qy   2103  GGTAGACCTGACGGGTTCATCACGCGGTTGATGAGGGTGGATGCGGGCCAAC  2162
           || ||| ||| ||||||||| |||||| || ||||||||||||||||||||||
Db   2100  GGCAGCCTGATGGGTTTATACATGTCCAGGGTCACTGCAGGGTGGATGCAGGCAGGCAAC  2159

Qy   2163  TTCATCCCTCCTCCACGCGTTGCTCTGTTGATTTCTGTTGATTTTGTCCTTGTCGTCGATCTGATG  2222
           |||||| ||||| ||||||||||||||  ||  ||||| |||| ||| ||||  |||  |||||||
Db   2160  TTCATCCCGCCCCCCGCGCGCGCTGGCCTGGTTCATACCCTGATGGACTTTGTATTTGTCCTGTCTTTATACCTGATG  2219

Qy   2223  AAGCTGCTGAGGCAGTTGCTCAGGACTGAGCACGTTGGTGGCGACGACGCATGGTGGTGAAC  2282
           ||||||||||||||  |||  |||||||| ||||||||||||||||||||||||||||||||
Db   2220  AAGCTGCTGAGGCAGTTGGTCCTAGGGCTGCGGCACGGTGGTGAAGCCGCTGCGGTGGGGTGAAC  2279

Qy   2283  CAGTTGGCGGTTCTAGGACTGCTGGGG  2342
           |||||||| |||||| |||||  ||
Db   2280  CAGCTGGCAGTCCTAGGGCGTGTGGAAGCCGGCTGCGGTGGGGTGGGGTGAAC  2339

Qy   2343  GGGCCCTGCCTTGTCATGGTGTTTTGGGCCTTCCCACTGTCAGTATGATACTAGGTCTAGCA  2402
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          ||||||||| |||| |||||| |||| || ||    |||||||||||| | ||| | |||
Db   2340 GGCCCTGCCCTGTCCTGGTGTCTGGGACTCCCGGTCGTCAGTATGATATTGGGTTTGGCA 2399

Qy   2403 AACCTGGTGTTGTACTTTCGGTGGATGGGCCCTCAGCGCCTCATGTTCCTCGTGTTGTGG 2462
          ||||||||| |||||||| | ||| |||| || || ||||| ||||||||||||||||||
Db   2400 AACCTGGTGCTGTACTTTAGATGGTTGGGACCCCAACGCCTGATGTTCCTCGTGTTGTGG 2459

Qy   2463 AAGCTCGCTCGGGGAGCTTTCCCGCTGGCACTTTTGATGGGGATTTCGGCGACCCGCGGG 2522
          ||||| ||||||||||||||||||||||| || ||||||||||||||||||||||||||
Db   2460 AAGCTTGCTCGGGGAGCTTTCCCGCTGGCCCTCTTGATGGGGATTTCGGCGACCCGCGGG 2519

Qy   2523 CGCACCTCTGTGCTCGGGGCCGAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCG 2582
          |||||||| ||||||||||||||||||||||||||||  |||||||||||||||||||||
Db   2520 CGCACCTCAGTGCTCGGGGCCGAGTTCTGCTTCGATGCTACATTCGAGGTGGACACTTCG 2579

Qy   2583 GTGTTGGGCTGGGTGGTGGCCAGCGTGGTGGCTTGGGCCATAGCGCTCCTGAGCTCAATG 2642
          ||||||||||||||||||||||| ||||| ||||||||||| |||||||||||||| |||
Db   2580 GTGTTGGGCTGGGTGGTGGCCAGTGTGGTAGCTTGGGCCATTGCGCTCCTGAGCTCGATG 2639

Qy   2643 AGCGCAGGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCAG 2702
          |||||||||||||||| |||||| |||||||||||||||||||||||||| |||||||||
Db   2640 AGCGCAGGGGGGTGGAGGCACAAAGCCGTGATCTATAGGACGTGGTGTAAGGGGTACCAG 2699

Qy   2703 GCTGTGCGCCAGAGGGTGGTGCGGAGCCCCCTCGGGGAGGGGCGTCCTACCAAGCTTCTG 2762
          ||  | || || ||||||||| |||||||||||||||||||||| ||| ||||| |  |||
Db   2700 GCAATCCGTCAAAGGGTGGTGAGGAGCCCCCTCGGGGAGGGGCGGCCTGCCAAACCCCTG 2759

Qy   2763 ACGTTCGCCTGGTGCTTGGCCTCATACATCTGGCCGGATGCTGTGATGATGGTGGTGGTG 2822
          || || ||||||||||||||||| |||||||||||| ||||||||||||||||||||||
Db   2760 ACCTTTGCCTGGTGCTTGGCCTCGTACATCTGGCCAGATGCTGTGATGATGGTGGTGGTT 2819

Qy   2823 GCCTTGGTCCTCCTCTTCGGCCTGTTCGACGCACTGGACTGGGCCCTGGAGGAGCTCCTG 2882
          ||||||||||| ||||| ||||||||||||||  |||| |||||| |||||||| || ||
Db   2820 GCCTTGGTCCTTCTCTTTGGCCTGTTCGACGCGTTGGATTGGGCCTTGGAGGAGATCTTG 2879

Qy   2883 GTCTCCCGGCCCTCGTTACGGCGACTGGCACGGGTGGTTGAGTGCTGTGTGATGGCGGGC 2942
          || |||||||||||||| |||||  |||| |||||||||||||||||||||||||||||
Db   2880 GTGTCCCGGCCCTCGTTGCGGCGTTTGGCTCGGGTGGTTGAGTGCTGTGTGATGGCGGGT 2939

Qy   2943 GAGAAGGCCACCACCATCCGACTGGTCTCCAAGATGTGCGCAAGAGGGGCCTACCTGTTT 3002
          ||||||||||| ||| |||| ||||||||||||||||| || ||||| ||  ||  ||||
Db   2940 GAGAAGGCCACAACCGTCCGGCTGGTCTCCAAGATGTGTGCGAGAGGAGCTTATTTGTTC 2999

Qy   3003 GACCACATGGGCTCTTTCTCGCGCGCTGTCAAGGAGCGCTTGTTGGAATGGGACGCGGCT 3062
          || || ||||||||||| ||||| ||||||||||||||| |||||||||||||||| |||
Db   3000 GATCATATGGGCTCTTTTTCGCGTGCTGTCAAGGAGCGCCTGTTGGAATGGGACGCAGCT 3059

Qy   3063 TTGGAGCCCTTGTCATTCACTAGGACGGACTGTCGCATCATCAGAGATGCCGCGAGGACC 3122
           | || ||  ||||||||||||||||||||||||||||||||||  | ||||||||||||||
Db   3060 CTTGAACCTCTGTCATTCACTAGGACGGACTGTCGCATCATACGGGATGCCGCGAGGACT 3119

Qy   3123 CTGTCCTGCGGACAGTGCGTCATGGGTTTACCCGTGGTAGCACGGCGCGGTGATGAGGTT 3182
           |||||||||| ||||||||||||||||||||||||||| || || || ||||||||||||
Db   3120 TTGTCCTGCGGGCAGTGCGTCATGGGTTTACCCGTGGTTGCGCGCCGTGGTGATGAGGTT 3179

Qy   3183 CTCATCGGCGTCTTTCAGGATGTGAATCATTTGCCTCCCGGGTTTGTCCCGACTGCACCA 3242
          |||||||||||||| ||||||||||||||||||||||||||||||||| ||||| || ||
Db   3180 CTCATCGGCGTCTTCCAGGATGTGAATCATTTGCCTCCCGGGTTTGTTCCGACCGCGCCT 3239

Qy   3243 GTTGTCATCCGTCGGTGCGGAAAGGGCTTCCTGGGGGTCACGAAGGCAGCCTTGACAGGT 3302
          ||||||||||| |||||||||||||||||| ||||||||||| ||||| ||||||||||||
Db   3240 GTTGTCATCCGACGGTGCGGAAAGGGCTTCTTGGGGGTCACAAAGGCTGCCTTGACAGGT 3299

Qy   3303 AGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTTGGGGACGGCTACGTCACGAAGC 3362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   3300 CGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTTGGGGACGGCTACGTCGCGAAGC 3359

Qy   3363 ATGGGCACATGTCTGAATGGCCTGCTGTTCACAACTTTCCATGGGGCTTCATCCCGAACC 3422
          ||||| |||||  |||| |||||||||||||| || ||||||||||||||||||||||||
Db   3360 ATGGGAACATGCTTGAACGGCCTGCTGTTCACGACCTTCCATGGGGCTTCATCCCGAACC 3419

Qy   3423 ATCGCCACGCCCGTGGGGGCCCTTAATCCCAGGTGGTGGTCAGCCAGTGATGACGTCACG 3482
          |||||||| |||||||||||||||||||||||| ||||||||||||||||||| ||||||
Db   3420 ATCGCCACACCCGTGGGGGCCCTTAATCCCAGATGGTGGTCAGCCAGTGATGATGTCACG 3479

Qy   3483 GTGTACCCGCTTCCAGATGGGGCAACTTCGTTGACGCCCTGCACTTGCCAGGCGGAGTCC 3542
          ||||| || || || |||||||| |||||||| || || || | |||||||||| ||||||
Db   3480 GTGTATCCACTCCCGGATGGGGCTACTTCGTTAACACCTTGTACTTGCCAGGCTGAGTCC 3539

Qy   3543 TGTTGGGTTATTAGATCCGACGGGGCTTTGTGCCATGGCTTGAGCAAGGGGGACAAGGTT 3602
          |||||||| || ||||||||||||||  | |||||||||||||||||||||||||||||
Db   3540 TGTTGGGTCATCAGATCCGACGGGGCCCTATGCCATGGCTTGAGCAAGGGGGACAAGGTG 3599

Qy   3603 GAGCTGGATGTGGCCATGGAGGTCTCTGACTTCCGTGGTTCGTCTGGTTCACCGGTCCTT 3662
          |||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||
Db   3600 GAGCTGGATGTGGCCATGGAGGTCTCTGACTTCCGTGGCTCGTCTGGCTCACCGGTCCTA 3659

Qy   3663 TGCGACAAAGGGCACGCAGTAAGAATGCTCGTGTCAGTGCTCCACTCTGGCGGCAGGGTT 3722
          || ||| ||||||||||||| |||||||||||||| ||||| ||||| ||  || |||||
Db   3660 TGTGACGAAGGGCACGCAGTAGGAATGCTCGTGTCTGTGCTTCACTCCGGTGGTAGGGTC 3719

Qy   3723 ACTGCGGCGCGATTCACTAGGCCGTGGACTCAAGTACCAACAGATGCCAAGACTACCACA 3782
          || ||||| || |||||||||||||||| ||||| |||||||||||||| || || ||
Db   3720 ACCGCGGCACGGTTCACTAGGCCGTGGACCCAAGTGCCAACAGATGCCAAAACCACTACT 3779

Qy   3783 GAACCCCCTCCGGTGCCGGCAAAAGGAGTTTTCAAGGAGGCCCCGTTGTTTATGCCTACG 3842
          |||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||||
Db   3780 GAACCCCCTCCGGTGCCGGCCAAAGGAGTTTTCAAAGAGGCCCCGTTGTTTATGCCTACG 3839

Qy   3843 GGGGCGGGAAAGAGCACCCGCGTACCGTTGGAGTACGGCAACATGGGCCACAAGGTCTTG 3902
          || |||||||||||||| ||||| ||||||||||||  |||||||| |||||||||||
Db   3840 GGAGCGGGAAAGAGCACTCGCGTCCCGTTGGAGTACGATAACATGGGGCACAAGGTCTTA 3899

Qy   3903 ATCTTGAACCCGTCGGTAGCTACCGTGAGGGCCATGGGCCCATACATGGAGCGGCTGGCG 3962
          ||||||||||| || || ||  || ||| ||||||||||||| ||||||||||||||||||
Db   3900 ATCTTGAACCCCTCAGTGGCCACTGTGCGGGCCATGGGCCCGTACATGGAGCGGCTGGCG 3959

Qy   3963 GGGAAACACCCCAGTATTTACTGTGGCCATGACACCACTGCTTTCACAAGGATCACTGAC 4022
          || ||||| || ||||| |||||||| ||||| || ||||||||||||||||||||||||
Db   3960 GGTAAACATCCAAGTATATACTGTGGGCATGATACAACTGCTTTCACAAGGATCACTGAC 4019

Qy   4023 TCGCCCCTTACGTATTCCACTTACGGAAGGTTTTTGGCCAACCCTAGGCAGATGCTGAGG 4082
          || ||||| |||||||| || || || |||||||||||||||||||||||||||||  ||
Db   4020 TCCCCCCTGACGTATTCAACCTATGGGAGGTTTTTGGCCAACCCTAGGCAGATGCTACGG 4079

Qy   4083 GGTGTGTCGGTGGTCATTTGTGACGAGTGCCACAGTCATGACTCAACTGTGTTGTTGGGC 4142
          || || |||||||||||||||||| ||||||||||||||||||||||| ||| |||| |||
Db   4080 GGCGTTTCGGTGGTCATTTGTGATGAGTGCCACAGTCATGACTCAACCGTGCTGTTAGGC 4139

Qy   4143 ATTGGGCGTGTCAGGGAGCTGGCGCGAGGATGTGGAGTGCAATTGGTGCTCTACGCCACT 4202
          |||||| | ||| ||||||||||||| || || |||||| | ||||||||||||||
Db   4140 ATTGGGAGAGTCCGGGAGCTGGCGCGTGGGTGCGGGGTGCAACTAGTGCTCTACGCCACC 4199

Qy   4203 GCCACCCCTCCCGGATCCCCGATGACCCAGCACCCATCAATCATTGAGACAAAACTGGAC 4262
          || || |||||||||||||| ||||| |||||||| || || |||||||||||| |||||
Db   4200 GCTACACCTCCCGGATCCCCTATGACGCAGCACCCTTCCATAATTGAGACAAAATTGGAC 4259

Qy   4263 GTGGGAGAGATCCCCTTCTATGGGCATGGCATACCTCTTGAGCGGATGCGGACCGGAAGG 4322
          ||||| ||||| ||||| ||||||||||| ||||| || ||||||||||| |||||||||
Db   4260 GTGGGCGAGATTCCCTTTTATGGGCATGGAATACCCCTCGAGCGGATGCGAACCGGAAGG 4319

Qy   4323 CATCTCGTATTCTGCCACTCCAAGGCTGAGTGCGAGCGCCTGGCGGGCCAGTTTTCGGCT 4382
          || ||||| |||||||| || |||||||||||||||||||| || |||||||| || |||
Db   4320 CACCTCGTGTTCTGCCATTCTAAGGCTGAGTGCGAGCGCCTTGCTGGCCAGTTCTCCGCT 4379

Qy   4383 AGGGGGGTAAATGCCATCGCCTATTACAGGGGGAAAGACAGTTCTATCATCAAAGATGGA 4442
          |||||||| ||||||| |||||| |||||| ||||||||||||||||||||||| |||||
Db   4380 AGGGGGGTCAATGCCATTGCCTATTATAGGGGTAAAGACAGTTCTATCATCAAGGATGGG 4439

Qy   4443 GACCTGGTGGTGTGTGCTACAGACGCACTATCCACTGGGTACACTGGGAACTTCGATTCT 4502
          ||||||||||| |||||||||||||| || ||||||||||||||||| || ||||| ||
Db   4440 GACCTGGTGGTCTGTGCTACAGACGCGCTTTCCACTGGGTACACTGGAAATTTCGACTCC 4499

Qy   4503 GTCACCGATTGTGGGTTAGTGGTGGAGGAGGTCGTCGAGGTGACCCTTGATCCCACCATT 4562
          |||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db   4500 GTCACCGACTGTGGATTAGTGGTGGAGGAGGTCGTTGAGGTGACCCTTGATCCCACCATT 4559
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Qy   4563 ACCATCTCCCTGCGCACGGTGCCCCGCGTCGGCTGTGATGCAGCGGCGAGGACGC 4622
          ||||||||||||| ||  ||||||| | |  |||||||||  |         ||
Db   4560 ACCATCTCCCTGCGGACAGTGCCGCGGTCCGCTGTGATGTCGAAGACGAGGACGC 4619

Qy   4623 ACGGGTAGGGCAGTCTTGGCGCGCTACTACGCGGGGTCCCCTGCTGT 4682
          |||||| ||||||||||| |||||||||||||||||||  | |||||
Db   4620 ACGGGTAGGGCAGTCTGCGGACGCTACTACGCGGGGTGGGCAAAGCCCCTGCGGGT 4679

Qy   4683 GTGGTGCCTCAGGTCCTCTGTCTGGTCGGCGGTGGAAGCCGGTGTGAACTGGTACGGGAATG 4742
          ||||||||||||| | ||||||||||||||||||||    |||||||||||||||
Db   4680 GTGGTGCGCCTCAGGTCCTGTCGGCGGTGGAAGCTGGAGTGAACCTGGTACGGGAATG 4739

Qy   4743 GAACCTGACCTGACAGCAGCAAACTACTGAGACAACTGCCCTTACACCGCAGCC 4802
          ||||||||||||||||||||| ||||||||||||  |||||||||||||||||||
Db   4740 GAACCTGACCTGACAGCTAACCTTACGACGACTGCCCTTCACACCGCAGCC 4799

Qy   4803 GTCGCAGCTGACATTGGGGAGGCCGCGGTGTCTTTTCGGGCCTTGCCCCGTTGAGGATG 4862
          ||||||||||| ||| ||||||||||||||||  ||||||  |||||||||||||||||
Db   4800 GTCGCGGCTGATATCGGCGAGAAGCGCGGCGTGTCTCTGGGCTCGGCTCGGCCATTGAGGATG 4859

Qy   4863 CATCCCGATGTTAGCTGGGGCAAAAGTTCGCGGGGCCTTCCTGGTGGGTGTT 4922
          |   ||||||||||||||||||||||||||||||||||||  || ||||||||
Db   4860 CACCCTGATGTCAGCTGGGGCAAAAGTTCGCGGCGTCCAACTGGTTGGGTGTT 4919

Qy   4923 CAGCGGACCATGTGCCGGAAACACTGTCTCCCGGCCATCGGATGACCCCCAGTGGGCCA 4982
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   4920 CAGCGGACCATGTGCCGGAAACACTGTCTCCCGGCCATCGGATGACCCCCCAATGGGCCA 4979

Qy   4983 GGTCTGAAGGGCCCGAATCCTGTCCCACTCCTGCTGAGGTGGGCAATGATTTACCATCT 5042
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   4980 GGTCTCAAGGGCCCAAATCCTGTCCCACTCCTGCTGAGGTGGGCAATGATTTACCATCT 5039

Qy   5043 AAAGTGGCCGGCCATCACATCGTGGACGACCTGGTCCGGCGCCCAGCCGGTGCGCGAGGGT 5102
          ||||||||||||||||||||  ||| ||||| || || ||||||||||| ||||| |||||
Db   5040 AAAGTGGCCCGGCCACCACATAGTGGACGACTCGGTCCGGACTCGGTGTGGCCGGAGGGT 5099

Qy   5103 TACGTCCGCTGCGATGCGGGGACCCATCTTGATGGTGGGGCTCGTTATTGGGGGGCATG 5162
          |||||||||||||||||| |  |||||| ||||| ||||||||   ||||||| |||||
Db   5100 TACGTCCGCTGCGACGTGGGGGCCCATCTTGATGATGCGGGGCTCTAGCTATCGCGGGGGAATG 5159

Qy   5163 ATCTATGCGTCATACACCGGTCTCTCGTGGTTACAGACTGGATGTGAAAGGGGGT 5222
          |||  |  |||| |||||||||||||| ||| |||||||||||||||||||||||
Db   5160 ATCTACGCGTCATACACCGGTCTCGTGGTGGTCACTGGATGTGGTCGACTGGATGGGGGT 5219

Qy   5223 GGCAGCCCCCTTATCGGACATGGAGACAGGAGACCACAGGCCCAGCCGGTTGTGCAGTCCCC 5282
          |||   |||||||||| ||||| |||||||||||||||||||||||||||||||| |||||
Db   5220 GGCGCCCCCCTTATCCGACATGGAGACGGCGCAGGCCACGCCGGTTCGCAGTCCCT 5279

Qy   5283 CCGGTAGACCATCGGCCGCGGGGAGAGTCTGCGGCCATGACAACAGTGACAGAT 5342
          |||||||||||||| ||||||||||||||  ||  || | ||||||||||||||
Db   5280 CCGGTAGACCATCGGCCGCGGGGAGAGTCGGAATCAGCACCATCAGAACAGTGACAGAT 5339

Qy   5343 GCGGGTGGCGGCCATCCAGGTGGATTGCGATTGGTCAGTCGATGCGGGGAA 5402
          ||||||| |||||||||||||| ||||||||||||||| |||||| ||||
Db   5340 GCGGTTGTCCTGGCGCCATCCAGGTGGACTATCATGACTCTGTCGATCGGAGA 5399

Qy   5403 GTGCTGTCCTTGGCTACACACGGGCCGAGGCCTACACCACCAAGTGGCTT 5462
          ||||| |||| ||||||||||||||||||||||||| ||||||||||||
Db   5400 GTGTGTCCTTGGCTATACGGGCCGAGGCCTACACCACCACACCAAGTGGCTC 5459

Qy   5463 GCTGGCTGCTACACACGGGGCCGTGCCCCACTGTTTCAATTGTTGACAAGCTCTTC 5522
          |||||||||| ||||||||||||||||||||||| ||| || |||| ||||||||
Db   5460 GCTGGCTGCTATACGGGGCCGTGCCCCACTCCCCACTGTATGAGTCTGCGCAGTCCTTC 5519

Qy   5523 GCCGGGGGTGGCGGGACGGGCGTGGTAGGCCATTGCCACAGTGTAATAGCTGCGCAGTGGGG 5582
          ||||||| ||||||||||||| |||||||||||||||||  ||||||||||||||||||
Db   5520 GCCGGAGGGTTGGGCCGGGTCGTGTGGTGGTGGCCATTGCCACAGCGCGGGGCCGTGGGCG 5579

Qy   5583 GCCTATGGGGGCTTCTAGGAGCCCTCCATTGCTGCTACCTCATGGGGTTG 5642
          ||||  ||||| ||||||||||||||| ||||||||| ||| |||||||
Db   5580 GCCTACGGCGGCTTCAAGGAGCCCGGCGCTTGCAGCCGCGCCGGCTTCGATGGGGGTTG 5639
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Qy   5643 GGCTCGGAGGCAACGCGCAAACCCGCTTAGCCTCCTCCTACTAGGGGCCGCTGGG 5702
          ||||  | |||||||||  ||||  ||||| |  ||||  || |||||||| ||||
Db   5640 GGCGGTTGGAGGCAACGCTCAGCACGCGCTCAGACGCGCTCGCGTCCCTCCGTTCATTGGGGGGCTGCTGGA 5699

Qy   5703 ACCGGTCTGGCCACGCGCCTGTCGTGGGTTAACCATGGCGGGCGCGTCATGGGAAGTGCT 5762
          |||| |||||||| ||| ||| ||||||||||| |||||||||| |||||||| ||||||
Db   5700 ACCGCCTTGGGGCACTCCGTGTCGTTGGGCTTGACCAGTGGCGTTGCGTTCATGGGGGGGCC 5759

Qy   5763 AGGGTCTCCCCTTCTTGGTCACCATTTACTGGGGCGGCTGGGGGGCTGGGAGGGCGTG 5822
          |  ||||||||||||||||||||||||||| |||||  || | | |||| |||| |||
Db   5760 AGTGTCTCCCCTTCCTGGTCACCATTTATTGGGGCGCTCGGGACGTTGGGAGAGGTGTGTT 5819

Qy   5823 GTGAATGCGCTAGCCTTGTCTTCGACTTTATGGCGGGAAACCATCATCAGAAGATCTG 5882
          || ||||||||   ||| |||  |||||| |||| ||||||| ||||||||||||||||
Db   5820 GTCAACGCGGCGGAGCCTAGTTCGTTTGACTTCATGGCGGGAAACTTTCATCAGAAGATCTG 5879

Qy   5883 TGGTATGCCATCCCAGTGCTAACCAGTCCGGGGCCGTTGCGGGGATCGCCCTCGGG 5942
          ||||||||||||||  ||||||||||||| |||||||||||||  ||||||| ||||
Db   5880 TGGTATGCCATCCGGTACTGACCAGCCCGGGGCCGCTTGCGGGGATCGCTCTCTCGGG 5939

Qy   5943 TTGGTGTTGTTACTCAGCTAACAACTCTGGCACTAACACTTGGTTGCACCGTCTGCTGACT 6002
          ||||| |||| ||||||||   |||  ||||||  |||||||||||||||  || ||||||
Db   5940 TTGGTTTGTTATTCAGCTAACAACTCTGGCACTCAACACTTGGTTGAACCGTCTGCTGACT 5999

Qy   6003 ACATTGCCAAGGTCTCATCCACCTCGACAGTTACTTTCAGGATTACTGTGAC 6062
          ||  |||||||||| || |||||| ||||||||||||||||   |||||||||
Db   6000 ACGTTACCAAGGTCTTCATGTATCCCGGCAGTTACTTTGACTACTGCGAC 6059

Qy   6063 AAGGTCTCAGCTGTGCTGCTCCCGACGCGTTGAGCCTCACTGCTGGTCAAC 6122
          ||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   6060 AAGGTCTCAGCCGTGCTGCTCCGGCCTGAGCCGTCCACCGTGGTTGCCCTGGTCAAC 6119

Qy   6123 AGGGAGCCTAAGGTTGGATGAGGTTCAGGTGGGGTACGCTCGGGACTGTGTGGGAGTCGATC 6182
          |||||||||||||| ||||||||||||||||  |||||  |||||||||||| ||||||||
Db   6120 AGGGAGCCTAAGGTGGGATGAGTGAGTACAGGTGGGGTATGTCTGGGACCTGTGGGAGTCGATC 6179

Qy   6183 ATGCGTCAAGTGCGCATGGTGATGGTCGCAGGCATTATTGATGGGGACAGTCCCTGTGTCATTA 6242
          ||||  ||||| |||||||| ||||| || ||  ||||||||||||||| ||| |||||||
Db   6180 ATGCGGCCAAGTCGCGCGTGGTCATGGCTGTGATGGTGCATGGGACACTCAGGGTGTGTCACTA 6239

Qy   6243 CCCTTATGGCACTGCGGGGAGGGGTCCCGGAGAATGGTTGTTGGACGGGCCATGTTGAG 6302
          ||||| |||||||||| ||||||||| |||||||||||| || |||||||||||||||||
Db   6240 CCCTTGTGGCATTGCGGGGAGGGGTGGTCCCGGGAATGGTTGCTTGACGGGTCATGTTGAG 6299

Qy   6303 AGTCGTTGTCTTTGTGTTGGTCGATCACCGTGATCGTGTTTGAATGGCAACTCAAAGAT 6362
          ||||  |||| ||| |||||||  |  |||||||||||| |||||||||||||||||||
Db   6300 AGTGTCTGCCTCTGTGTCGGTGATCACGTGTGACGTTCTGAATGGCAACTCAAAGAA 6359

Qy   6363 CCAGTTTACTCTACCAAGCTGTCGCAGGCATTATTGATGGGGACAGTTCCCTTGTGAACATG 6422
          |||||||||| |||||||||| | ||  |||||||||||||||||||| ||| |||||||
Db   6360 CCAGTTTACTCTACCAAGCTGTCGCCGCACTATTGGATGGGGACTGCCTGTGAACATG 6419

Qy   6423 CTGGGCTATGGCGCAAATCCTGTCCGGCGTTGCTCGGCCTTCAGACCCGGAGGTGTACCATTC 6482
          |||||| ||||| |||||| |||||  | ||||| |||||| ||||||| ||||||||| ||
Db   6420 CTGGGTTACGGTGAAACGTCGCCGCTCCGGCCTCCTGGCCTCCGCAGACCCGGAGGTTGTGCCCCTTC 6479

Qy   6483 GGGACGTCTGGTGGCTGAGTCTGGGCTGAGTCGTCCCCGAGGTGTTGTGATCAGGCGGAACA 6542
          |||| |||||||||||| |||||| |||||  |||||  ||||| || ||||||||| ||| |
Db   6480 GGGACGTCTGGTGGCTGGGTGAGTGAGTGTGTCGTGTGATCAGGAGGAGACC 6539

Qy   6543 TCCGCCTACAAAATCGTGCGGGCAGCAAATCCTGTCGGCTGTGTTGTGAGCCCTATTAC 6602
          ||||| |||||||| ||||| |||||  ||||| | |  || ||||| ||||| |  |||
Db   6540 TCCGGTTACGGTGAAACGTCGCCGCGCAAATCCTATCGGTTGCGTGTAGCCCTACTAC 6599

Qy   6603 GTCGACGGCATACCGTCTCATGGGACGCGGCCTGCCAGCCCTATGATGTGCTCATGGGC 6662
          ||||||||| || ||| |||||||||||||||||||||| | || ||||| |||||||
Db   6600 GTCGACGGCATTCCGGTTCCATGGGGACGCGGCCTGCCAGCCGCTCATGATGTGCTCATGGGC 6659

Qy   6663 CCTGGGCAAAGTGTCACCATTGACGGGGAACGCTCACACCCTTCCGCATCAACTGCGCGCTT 6722
          ||||||| |||||||||||||||| ||||| || || ||||||| |||||||| ||| |||
Db   6660 CCTGGGCAAAGTGTTACCATTGACGGGGAGGGAGGCTACACTTCCTCCTCATCAACTGCGAGCTC 6719

Qy   6723 AGGAATGTGGCGCCCTCTGAGGTGTCATTGACATTGGGACGGGAGACT 6782
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Db   7800 AAAAAGGAGGTGTCTTCAAAGACCTGGAAGGAGGAGGAGAGGCCCCGCCTCATTGTGTTC 7859
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy   7862 AAAAAGGAGGTGTCTTCAAAGACCTGGAAGGAGGAGGAGAGGCCCCGCCTCATTGTGTTC 7803
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Db   7863 CCCCCCTGGACTTCCGGACTTCATCCGAGGTGTCCATTGACCATTGACCGGACGGAGACT 7922
          ||||||||||||||||||||||||||||||||| || |||||||||||||||||||||||
Qy   7860 CCCCCCTGGACTTCCGGACTTCATCCGAGGTGTCCAGCCGTTCAGGCTATC 7919
```

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Db   7923 AAGGCGGTGTTGGGGGGGCCTACGCCTACGCGGGGGGGGCCTACGCGGGGGGGCCTACGCG 7982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   7920 AAGGCGGTGTTGGGGGGGCCTACGCGGGGGGGCCTACGCGGGGGGGCCTACGCG 7979
```

```
Db   7983 ATGCTCAAACTGTGGAATCAAAGAACACACATGCGCCATCTGTGTGGACGCCACATGC 8042
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   7980 ATGCTCAAGCTATGGGAGTCTAAGAAGACCCCTGCGCCATCTGTGTGGACGCCACCTGC 8039
```

```
Db   8043 TTCGACAGTAGCATAACTGAAGGACCTGGCGTCCGCGGAGACAGCAGAGCTTTATGCCCTGGCT 8102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   8040 TTCGACAGTAGCATAACTGAAGGACCTGGCGTCCGCGGAGACAGCAGAGCTATACCGCTCTGCGCC 8099
```

```
Db   8103 TCAGACCATCCAGAATGGGTGCGTCGTCCTCCATCGCCTGGCACAATGTA 8162
          | |||||||||||||||||||| || |||||||||||||||||||||
Qy   8100 TCTGACCATCCAGAATGGGTGCGTCGTCCTCCATCGCCTGGCACCATGTC 8159
```

```
Db   8163 ACCCCCCAGAGGGGTGCCAGTGGTGAGAGGTATTGTAGATCCTCAGGGGTCTTGACCACC 8222
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   8160 ACCCCCGGAGGGGTGCCGTCCGTGAGAGGTATTGCAGATCCTCGGGTGTCCTAACAACT 8219
```

```
Db   8223 AGTGCGAGCAACTGCTTGCGTCCTTGACTTGCTATATCAAGGTGAAAGCCCGCTGTGGGG 8282
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   8220 AGCGCGAGCAACTGCTTGCGTCCTTGACTTGCTACACTCAAGGTGAAAGCTGCCTGTGTGAGAGTGGGG 8279
```

```
Db   8283 CTGAAAAATGTCTCGCTCCATCGCTCGGCGATGACGTGTTGATCATATGCGGAACGGCCT 8342
          ||||||||||||| |||| |||||||||||||||||||||||||||||||||||||
Qy   8280 CTGAAAAATGTCTTGATCATAGCCGGCGATGACGTGTTGATCATATGTGAGCGGCCA 8339
```

```
Db   8343 GTGTGCGATCCTAGCGACGCGTTTGGGCAGAGCCCTGGCTCGCGAGCTACGGTACGCGGTT 8402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   8340 GTGTGCGACCCCAGCGACGCGTTTGGGCAGAGCCCTGGCTCGCGAGCTATGGGCGTACGCGTGCGAG 8399
```

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Db   8403 CCTTCATATCATGCATCACTGACACCGCCATTTCTTCCTGACCACGACTTTCGGAGGCCCCTCGCTGC 8462
          || ||||| | ||||||||||||||||||||||||||||||||||||||||||||||
Qy   8400 CCCTCATATCATCATTGGACACCGCCCATTTCTTCCTGACCACGACGCTTGCTGAGTGC 8459
```

```
Db   8463 AATGCAGATGGGAAACGCCATTTCTTCCTGACCACGCCATTTCTTCGGAGGCCCGCC 8522
          ||||||||||||||||||||||||||| || || ||||||||||| ||||||||
Qy   8460 AATGCAGATGGGAAGCCGTCGTGACAAGTGCCATGGTAACTACACAAGTTTCCA 8519
```

```
Db   8523 ATGTCGAGCGAGTACAGTGACCCAATGCTTCGGCCATCGGTTACATCCTCCTATACCCT 8582
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   8520 ATGTCGAGTGAGTAGTGACCCGATGCGGTTACATCCTCCTTTATCCT 8579
```

```
Db   8583 TGGCATCCTCATCACACGGTGGGTCATCATCCTCACGTGCTCACCTGCGCGTTTAGGGGT 8642
          | ||||| |||||||||||||||||||||||||||||||||||||||||
Qy   8580 TGGCACCCCATCACACGGTGGGTCATCATCCTCATGTGCTCAACGTGCCATTCAGGGGT 8639
```

```
Db   8643 GGTGGCACACCGTCTGATCCTGTGTGGTGCCAGTAGCTGCCTGGGGCATTGCAACAGTTCCA 8702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   8640 GGCTTGGCACACCGTCGTGATCCTGTGGTGCCAGTGACTTGCCTGTGGTAACTACACAAGTTCCA 8699
```

```
Db   8703 CTGGACAAACTGCCTAACATCGTGCCCTAACATCGTGACCGTTGAGGGTTACC 8762
          ||||||||||||||||||||| ||||||||||||||||||||||||||
Qy   8700 CTGGACAAACTGCCTAACATCGTGACCGTTGAGGGTTACC 8759
```

```
Db   8763 GCAGACACAACTAAGACAAAATGGAGGCGGACCTGAGCGACCTGAAGCTCCCT 8822
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||
Qy   8760 GCAGACACAACTAAAACAAAGATGGAGGCGTGGTTAAGGTTCTGAGCGACCTCAAGCTCCCT 8819
```

```
Db   8823 GGCTTAGCGTCCACCGGAAGAAGGCCGGGAACACGCCATGCTCCCGCGCGCG 8882
          |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   8820 GGCTTAGCGTCCACCGGAAGAAGGCCGGGCGTTGCGAACACGCCATGCTCCCGCGCGCG 8879
```

```
Db   8883 GGTTGGGCTGAGTTGGCTAGGGGCGTTGGCATCCAGGCGCTTACGCGGCTTCCCCCGCCG 8942
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   8880 GGTTGGGCTGAGTTGGCTAGGGGCGTTGTGTGCGCATCCAGGCGGCTTCCCCCCT 8939
```

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Qy  8943  GAGATTGCTGGTATCCCGGGGGTTTCCCCCTTTCCCCCCCTATATGGGGTGTGGTTCAT  9002
          ||||||||||||||||||||||||||||||| |||||||||||||||||||| ||||||
Db  8940  GAGATTGCTGGTATCCCGGGGGTTTCCTCTCTCCCCCCCTATATGGGGTGTGGTTACAT  8999

Qy  9003  CAATTGGATTCACAAGCCAGAGAGAGTTGCTGGCGTGCTGGGGTTCTTAGCCCTGCTC  9062
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9000  CAATTGGATTCACAAGCCAGAGAGAGTTGCTGGCGTGCTGGGGTTCTTAGCCCTGCTC  9059

Qy  9063  ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCGTGTTGCGGCAAGGTCCGGTGACTGATC  9122
          ||||||| |||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  9060  ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCGTGTTGCGGCAAGGTCCGGTGACTGATC  9119

Qy  9123  ATCACTGGAGGAGGTTCCGCGCCTTCCCGCCCCAGGGGGTCTCCCCGCGTGGGTAAAAAGGG  9182
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9120  ATCACCGGAGGAGGTTCCGCGCCCTTCCCGCCCCCCAGGGGGTCTCCCCGCGTGGGTAAAAAGGG  9179

Qy  9183  CCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCTGCAGGGTCAAAGCCTGATGGTGC  9242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9180  CCCGGCCTTGGGAGGCATGGTGGTTACTAACCCCTGCAGGGTCAAAGCCTGATGGTGC  9239

Qy  9243  TAATGCACTCGCACTTCGGTGGCGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC  9302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9240  TAATGCACTCGCACTTCGGTGGCGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC  9299

Qy  9303  TGCTCGCAGAGCCCTCCCCCGATGGGCACAGTGCACTGCACTGTGATCTGAAGGGGTGCACCCC  9362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9300  TGCTCGCAGAGCCCTCCCCCGATGGGCACAGTGCACTGCACTGTGATCTGAAGGGGTGCACCCC  9359

Qy  9363  GGTAAGAGCTCGGCCCAAAGGCCGGGTTCTACT  9395
          || |||||||||||| ||||||||||||||||||
Db  9360  GGGAAGAGCTCGGCCCGAGGCCCGGSTTCTACT  9392
```

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Query Match        84.9%;  Score 7979;  DB 6;  Length 9392;
Best Local Similarity  90.7%;  Pred. No. 0;
Matches 8515;  Conservative 1;  Mismatches 876;  Indels 1;  Gaps 1;

Qy     3  ACGTGGGGGGTTGATCCCCCCCCCCCCCGGCACTGGGTGCAAGCCCATAAACCGACGCCT   62
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db     1  ACGTGGGGGAGTTGATCCCCCCCCCCCCGGCACTGGGTGCAAGAAACCGACGCCT   60

Qy    63  ATCTAAGTAGACGCAATGACCTCGGCGACCGGCCAAAAGGTGTGGATGG  122
          ||||||||||||||||||||||| |||||||||||||||||||||||||
Db    61  ATCTAAGTAGACGCAATGACCTCGGCGACCGGCCAAAAGGTGTGGATGG  120

Qy   123  GTGGTTGACAGGGTTCGTAGGTCGTAAATCCCGGTCGTCATCCTGTAGCCACTATAGGTGGGT  182
          ||| |||||||||||||||||||||||||||| || |||||||||||||||||||||||
Db   121  GTGATGACAGGGTTGGTAGGTCGTAAATCCCGGTCGTCATCCTGTAGCCACTATAGGTGGGT  180

Qy   183  CTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTCGGCCGAGACCGCGACGGTCCACAGT  242
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CTTAAGAGAAGGTTGGGACCGTGGGAACGTTAGACGTTACGCTTCAGTGTGACCGTGCCCTAACGCACGAGT  240
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(continued alignment blocks, second column)

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Qy   243  GCTGCCCTACCGGTGTGAATAAGGCCCACGTCAGGCTCGTCGTCGTTAAACCGAGCCCGT   302
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   241  GTTGCCCTACCGGTGTATCGGGAATAAGGCCCACGTCAGGCTCGTCGTCGTTAAACCGAGCCCGT   300

Qy   303  CACCCACCTGGGCAAACGACGACGCCCACGTACGGTCACGTCGCCCTTCAATGTCTCTCTTG   362
          ||||||||||||| |||||||||||||||||||||||||| ||||||||||||||||||
Db   301  TACCCACCTGGGCAAACGACGACGCCCACGTACGGTCGTTCAATGTCTCTCTTG   360

Qy   363  ACCAATAGGTTATCCGGCCAGTTGACAAGGACCAGTGGGGCGGCGGGGTTATGGGGAAG   422
          ||||||| |  |||||||||||||||||||||||||||||||||| |||||||||||
Db   361  ACCAATAGGCTAGCCGGGTGAACTAAATTGACAAGGACCAGTGGGGCGGCGGGGCT-TGGAGAGG   419

Qy   423  GACCCCAAACCCTGCCCTTCCCGTGGGCCGGGAAATGCATGGGGCGCACCCAGTTCCGCG   482
          ||||||| |||||||||||| || ||||||||||||||||||||||||||||||||||
Db   420  GACTCCAAGTTCCCGCCTTCCCGCCGGGCCGGGGAAATGCATGGGGCCGGGGTGCCACCCAGTCCGCG   479

Qy   483  GCGGCCTGCAGCCGTGGTAGCCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCCGCGGGTGGCCATTCTCTT   542
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480  GCGGCCTGCAGCCGTGGTAGCCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCCGCGGGTGGCCATTCCTTT   539

Qy   543  TTCTATACCATCATGGCAGTCCTTCTCTCTGTTTATAGCGTAATCCGTGACTACGGGC   602
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540  TTCTATACCATCATGGCAGTCCTTCTCTCTGTTTATAGCGTAATCCGTGACTACGGGC   599

Qy   603  GCCCGGCCACCCACGCGTTGTCGAGCGAATGGCAATATTTCCTCACAAATTGCTGTGCC   662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   600  GCCCGGCCACCCACGCGTTGTCGAGCGAATGGCAATATTTCCTCACAAATTGCTGTGCC   659

Qy   663  CCGAAGACATCGGGTTCTGCTGGCCACTGTATCAGGCGGGTTTGCGTGTCGCCTGGCAAGTCC   722
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   660  CCGAGGGACATCGGGTTCTGCTGGCCACTGTATCAGGCGGGTTTGCGTGTGCGGCTGGCAACGATT   719

Qy   723  TGCACCGACCGTTGCTGGCCACTGTATCAGGCGGGTTTGCGTGTCGCCTGGCAAGTCC   782
          ||||| ||| |||||||||||||||||||||||||||||||||| ||||||||||||
Db   720  TGCACTGACCAATGCTGGCCACTGTATCAGGCGGGTTTGCGGTCGCCTGGCAAGTCC   779

Qy   783  GCGGCCCAGCTCGTTGGGAACTGGGAGCCTGTACGGGCGTCTCGGTCTCCGGCTTAC   842
          |||||| || |||||||||||||||||||||||||| ||||||||||||||||||||
Db   780  GCGGCCAACTGGTGGGGAGCTGGGGAGCCCCGTGTCGGGTCGGGTCCGGCCTAT   839

Qy   843  GTAGCCGGATCCTGGGCTCGGGGTGGGGCGAGGTTTACTCCGGGAGGTTGGTTGTTGGCG   902
          || || |||||||||||| ||| ||||||||||||||||||||||||||||||||||||
Db   840  GTGGCTGGATCCTGGGCTCGGGGTGGGGTGAGGTGTACTCGGGGTGTCCTAACGGTGGGAGTCGCGG   899

Qy   903  TTGAGGCGCCGGGTCTACCTGATGCCCAACCTGAGAGTGTGCAGTAGAATGTGACGTTAAG   962
          |||| |||||||||||| ||||||||| |||||||||| |||| |||||| |  ||||||
Db   900  TTGACGCGCCGGGTCTACCTGAGTGCCTAACCTGACGTGTGCAGTCGCGTGTGAGCTAAAG   959

Qy   963  TGGGAAGTGAGTTTGGAGATGAGGACTGAGCAGTTGGCCTCCAATTACTGGATTTTGGAA  1022
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   960  TGGGAAGTGAGTTTGGAGATGAGGACTGAGCAGCTGGCCCTCCAACTACTGGATTCTGGAA  1019

Qy  1023  TACCTTGGAAAGTCCCATTTGAATTTGAATTTGAATTTCTGGAGCGCGTGATGAGCCTGACCCCTTGTTG  1082
          |||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Db  1020  TACCTTCTGGAAAGTCCCATTTGATTTCTGATTTCTGGAGAGGCGTGATAAGCCTGACCCCCTTGTTG  1079

Qy  1083  GTTTCGGTGCCGCCATTGCTTTTGCTGGCAACGGATTGTTCATGGTTTCCTGCTGGTG  1142
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  1080  GTTTCGGTGCCGCCATTGCTTGCTGCTGCTGTGCAACGGATTGTTCATGGTTCCTGTTGGTG  1139

Qy  1143  ACGATGGCGGGGATGTTGCAAGGCGCCCCGCCTTCGTTTTGGGGTCCCGCCCCTTTGAC  1202
          ||| ||||||| ||||||||||||||||||||||| |||||||| ||||||||||||||
Db  1140  ACGATGGCGGGGATCTCGCAAGGCGCCCCGCCTTCGTTTTGGGGTCACGCCCCTTTGAC  1199

Qy  1203  TACGGGTTGAAGTGGCAGTCATGCTCGTATTCCCACTGGGT  1262
          |||||||||||| ||||||||| |||||||||||||||||
Db  1200  TACGGGTTGACTTGCAGACCTGCTCGTTGCGGCTTGCGGTTTTCGACTGGG   1259

Qy  1263  GAGAGGGTTGGGGATCGAGGGAATCGCGCGCGAGACCGCGACGGTCCACAGT  1322
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1260  GAGAGAGGTGTGGGGAACCGTGGGAACGTTAGCTGTTCAGTGTGACTGTCCCCTAACGTGTGCCCCCTGG  1319
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Qy  1323 GTTTGGGTCCGGCCTTTGCCAGGCGGTTGGGTGGGCGACCCCATCACCCATTGGGAGC 1382
         ||  |||  || ||||||||  |  || ||||||  ||| ||  |||||| ||||||||
Db  1320 GTGTCGGTTGCCAGCCTTTTGCCAAGCAATCGGCTCGGGGGTGACCCCATCACTTATTGGGAGC 1379

Qy  1383 CACCGGACAAAACCAGTGGCCCTATCATGCGCCCCAATATGTCTATGGGTCTGTGTCCGTA 1442
         ||||||  |||| |||||||||  ||  |||||||| ||| || |||| |||| ||
Db  1380 CACGGGCAAAATCAGTGGCCCTTTCATGCGCCCCAGTATGTCTATGGGTCTGCTACAGTC 1439

Qy  1443 ACGTCGGTGTGGGGTTCCGTGTCTTGGTTGCCTCGACCGGCGGTCGTGATTCGAAGATC 1502
         || ||||||| |||| |||||  || |||||||  |  |||| ||  | ||||||||
Db  1440 ACTTCGTGTGTGGGGTTCCGCTTCTTGGTTGCCTTCCACCAGTGGTCGCGACTCGAAGATA 1499

Qy  1503 GATGTGTGGAGTTTGTGTCCGGTTGATCTGCCAGTGCACCATAGCCGCTCTAGGGTCA 1562
         ||||||||| ||| |  |||| ||||  ||||||||||||||||  |||  || ||
Db  1500 GATGTCTGGGAGTTTAGTGCCAGTGCCTGCCACCGCCAGTGCCTCCTGGGGTCAGTCA 1559

Qy  1563 TCGGATCGGCACACGGTGGTTGAGCTCTCCGAGTGGGGAGTCCCGTGCCTGTAACGTGTATT 1622
         |||||||||||||||||| |||  ||||  ||||||  |||||  ||||||||||| |||
Db  1560 TCGGATCGGCACACGGTGCCCGGGGCTCTCCGAGTGGGGAATCCCGTGCCGTGACGTGTGTT 1619

Qy  1623 CTGGACCGTCGGCCTGCTTCATGTGCCACCTGTGTGGCCACGGGGGCCTCGGTTGACAAACCGGG 1682
         |||||||| ||||||||||  |  ||||||||||| |||  |||||  |||| |||||||||||
Db  1620 CTGGACCGTCGGCCTGCCTCTGAGGACTGCTGTGGGGCCTCGGTTGACAAAGGACTTGGAA 1679

Qy  1683 TCGGTTAGATTCCCTTTCCATGGTTCAACAGGACAACTCCCTTCACCATAAGGGGCCCCCTGGGCAACCAG 1742
         |||||||| ||||| || ||||||||||  |  ||||||||||  ||||||||||||||  ||||||||
Db  1680 TCGGTTAGGTTCCCATTCCATCGTTGCCTCGGGGCGTGTCGACAGTGTGACAAAGGACTTGGAA 1739

Qy  1743 GCTGTTGCCCTTCGTCAACAGGACAACTCCCTTCACCATAGGGGGCCCCCTGGGCAACCAG 1802
         || |||||||  || ||||||||| |||||||||  ||||||||||  ||||||||||||
Db  1740 GCTGTGCCCTTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGCCCCCTGGGCAACCAG 1799

Qy  1803 GGGAGGAGCAACCCGTGCCGCCGGTTTGGGTTCTACCACCATGACCAAGAATC 1862
         || ||||||||||||||||  ||  |||||||  ||||||| |  ||||||||
Db  1800 GGCCGAGGCAACCCGCGCGGCGTTGGGTTCCACCACCATGACCAAGGATC 1859

Qy  1863 CGGGATTCCCTGCATTGGTGAAATGTCCCACACCAGCCATGACCCGTCCTCT 1922
         |||| || || ||  ||||||||||| ||||||| |||||| ||||
Db  1860 CGAGATACCCTGGTGGAGTGTGCGTCCCGCTGTCTCCACCGCTCTCCTCG 1919

Qy  1923 TTCGGGTTCTTCCCCGGAGTTCCGGCCCATTAACAACTGCGATGCCCCGTAGGCACGGAAGTG 1982
         |||||||||   |||||    ||||||||||  |||||||| |||||  ||||||||||
Db  1920 TTTGGGTTCTTTCCCCGGGGACGCCGCCTCTCAACAACTGCGATGCCCCGTAGGCACGGAAGTG 1979

Qy  1983 TCTGAGGCATTGGGCGGAGCTGGGTTACGGGGTTCACGAGCCTCGGTTCGCAGG 2042
         || |||||||||| |  |||||| || ||||| |||||||  |||||||||||
Db  1980 TCCGAGGCACTTGGGGGGGCTGGGCTGGCCTCACGGGGGGTTCATGAACCCCTGGTCGCGCAGG 2039

Qy  2043 TGTTCCGAGCTGATGGGACGCCGGAAATCCGGTTTGCCCATGGGTACCGTGTCCTCT 2102
         ||||||||||||||||||||||||||||||||||||||  |||||||||  ||
Db  2040 TGTTCCGAAGCTGATGGGAAGCCCGAAATCCGGTTGTTGCCATGGGTTTGCATGGGTGAGGTT 2099

Qy  2103 GGTAGACCTGACGGGTTCATCACACGTCCAGGGGAGTTCAGGAGTGGATGCGGGCAAC 2162
         |||||||| ||||||||||  |  ||  |||||||||||||||||| ||| ||||||
Db  2100 GGCAGGCCTGATGGGTTTATACATGTCCCGGGGGCACCTGGTCGCAGGTGGATGCAGGCAAC 2159

Qy  2163 TTCATCCCTCCACGCGTGGTTCCTCGATTTTGTATTTCCTCTATCTGATG 2222
         ||||||||  ||  |||||||||   |||||| ||| |||  |  |||||
Db  2160 TTCATCCGCTCCACGACGGTGGGGGCCGGTTCATCCTGCTTGGATTTTTGTATTCCTCTATCTGATG 2219

Qy  2223 AAGCTGGCTGAGGCACGGTTCATCCAGGGGACTGCGTGGTCCGGTGGGTGAAC 2282
         |||||||||||||||||||||||  ||||  | |||||   || |||||||||
Db  2220 AAGCTGGCTGAGGCACGGTTCATCCAGGGAACGCTGCGTGGTCCGGTGGGTGAAC 2279

Qy  2283 CAGTTGGCCGGTTCATGTCTCATGGTGGGGCCCTTCCCACTGTTCGGGGTGAAGTTTTTGCG 2342
         || ||||| |  ||  |  ||||||||| |||  |||||  ||| | ||||||||||  ||
Db  2280 CAGCTGGCAGTGGCTCCTTCCGGGGCCCGTGGAAGCGGCCAGGTGAGGTCTTCGCG 2339

Qy  2343 GGGAGGCCTTGTCATGGTGTTGGGCCCTTCCCACTGTCATGATACTAGGTCTAGCA 2402
         |||||||||| |||| |||||| ||||||||||||| | ||||  ||||||||||
Db  2340 ATCGCCACCCCTGGGGGCCCCTTAAATCCACGAGATGGTGTGCCAGTGTCAGCACG 2399

Qy  2403 AACCTGGTGTTGTACTTTCCGTGGATGGGCCCTCAGCCGCCTCATGTTCCTCGTGTTGTGTGG 2462
         |||||||| || |  ||||||||||| |||||||||||  || |||||||||||||||||
Db  2460 AAGCTGCTCGGGGAGCTTGCCGGTGATTGCGGATTTCCCGGATTTCGGTGATGTGTCGGTGGG
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Db  2400 AACCTGGTGCTGTACTTTAGATGGTTGGGACCCCAACGCCTGGTGTCCTCGTGTTGTGG 2459

Qy  2463 AAGCTCGCTCGGGGAGCTTTCCGCTGCCACTTTGATGGGGATTTCCGGCGACCCCGCGGG 2522
Db  2460 AAGCTGCTCGGGGAGCTTTCCGCTGCCCTCTTGATGGGGATTCGGCGACCCCGCGGG 2519

Qy  2523 CGCACCTCTGTGTCTGCTGGGGCCGAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCG 2582
Db  2520 CGCACCTCAGTGTCTGCTGGGGCCCGAGTTCTCGATGTCGATGTCGATGTCGAGGTGGACACTTCG 2579

Qy  2583 GTGTTGGGCTGGTGGTGGTGCCAGCGTGTGGCCATAGCCGCTCGGCTTGAGCTCAATG 2642
Db  2580 GTGTTGGGCTGGGTGGTGGTGGCCAGTGTGGTAGCTGGTGCCATTGCGCGTCCTGAGCTCGATG 2639

Qy  2643 AGCGCAGGGGGGTGGAAGCACAAGGCCGTGATCTATAGGACGCTGGTGTGTAAAGGGTACCAG 2702
Db  2640 AGCGCAGGGGGGTGGAGGCACAAAGCCGTGATCTATAGGACGTGGTAAGGGGTACCAG 2699

Qy  2703 GCTGTGCGCAGAGGGTGGTGCGGAGCCCCCTCGGGGAGGAGGGGCCGTCCTACCAAGCTTCTG 2762
Db  2700 GCAATCCTCAAAGGGTGGTGAGGAGCCCCTCGGGGAGGGGGCGTCCCAAACCCCTG 2759

Qy  2763 ACGTTCCCGTGCTGCTTGGCCTCATACATCGGCCGGATGTCTGTGATGATGGTGGTGTG 2822
Db  2760 ACCTTTGCCTGGTGCTTGGCCTCTGTACATCTGGCCGCAGATGTCTGTGATGATGGTGGTGTT 2819

Qy  2823 GCCTTGGTCCTCCTCGTTCGACGACTGGACTCGACGCACTGGGGCCCTGGGAGCTCCTG 2882
Db  2820 GCCTTGGTCCTTTGTTTTCGACGCCTTGACGGCGTTGGGATTGGGGCCCTTGGGAGAGGATCTTG 2879

Qy  2883 GTCTCCCGGCCCTCGTTACGGCGACTGGCACCGGGGTGGTTGAGTGCTGTGTGATGGCGGGC 2942
Db  2880 GTGTCCCGGGCCCCGTTCGGTTGGCGTTTGCTCGGGGGTTGAGTGCTGTGTGTGATGGCGGGGT 2939

Qy  2943 GAGAAGGCCACCACCATCCGACTGGTCTCCAAGATGTCGCGAAGAGGGGGCCTACCTGTTT 3002
Db  2940 GAGAAGGCCACAAACCGTCCGGCTGGTCTCCAAGATGTCGCGAGAGGAGCTTATTTGTTC 2999

Qy  3003 GACCACATGGGCTCTTTCTGCGCCATTAACAACTGCGATGCCCCGTAGGCACGGAAGTG 3062
Db  3000 GATCATATGGGCTCTTTTGCGCCATTAACAACTGCGATGCCCCGTAGGCACGGAAGTG 3059

Qy  3063 TTGGAGCCCTTGTCATTCACTAGGACCGGTTCATTCACTAGGACGCCTGGGTCCGGTCCGGACC 3122
Db  3060 CTTGAACCTCTGTCATTCACTAGGACCGGTTCATTCACTAGGACGTCGCGGATGCGCGGAGGACT 3119

Qy  3123 CTGTCCTGCGGGACAGTGCGTCATTGGTTGCCATGGCTGTAGCACGGCGGCGGTGATGAGGTT 3182
Db  3120 TTGTCCTGCGGGACAGTGCGTCATGGGTTGCCATGGGTTGCCGCCGGTTGGTGATGAGGTT 3179

Qy  3183 CTCATCGGCGTCTTGCACCTTCAGGATGTGAATCATTGGAATCATTTGCCTCCGGGTTGTCCCGACTGCACCA 3242
Db  3180 CTCATCGGCGTCTTGCACCTTCAGGATGTGAATCATTTGAATCATTTGCCTCCGGGTTGTTCCGACCGCCGCCT 3239

Qy  3243 GTTGTCATCCGTCGGTCGGTGCCGGAAAGGGCTTCCTGGGGTCACGAAGGCAGGT 3302
Db  3240 GTTGTCATCCGACGGTGCGGAAAGGGCTTCTTGGGGTCACAAAGGCTGCCTTGACAGGT 3299

Qy  3303 AGGGATCCTGACTTACATCCAGGGAACGTCATGGTCATGGGGACGGCTTCACGGAAGC 3362
Db  3300 CGGGATCCTGACTTACATCCAGGGAACGTCATGGTCATGGGGACGGCTTCACGCGGAAGC 3359

Qy  3363 ATGGGCACATGTCTGAATGGCCTGTTCACAACTTCCATGGGCTTCATCCCGGAACC 3422
Db  3360 ATGGGAACATGTCTGAACGGCCTGTTCACCACTTCCATGGGCTTCATCCCGGAACC 3419

Qy  3423 ATCGCCACGCCCTGGGGGCCCTTAATCCCAGTGGTGTCAGTGACGTCACG 3482
Db  3420 AATCGCCACCACCCGTGGGGGCCCCTTAATCCCAGTGGTGTCAGCCAGTGTCAGCACG 3479

Qy  3483 GTGTACCCCGCTTCGTTGACGGCCCTGCAGCACTTGCGCACTGGCCAGGCGGAGTCC 3542
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Db   3480 GTGTATCCACTCCCGATGGGCTACTTCGTTAACACCTTGTACTTGTGTAACACCTTGTACTTGCCAGGCTGAGTCC 3539

Qy   3543 TGTTGGGTTATTAGAATCCACGACGGGCTTGTGCCATGCATGCTTGAGCAAGGGGGACAAGGTT 3602
          |||||||| || ||||||||||  |||||||||| -| ||||||||||||||||||| |||||||||
Db   3540 TGTTGGGTCATCAGATCCAGATCCGACGCGGCCCTATGCCATGCATGCTTGAGCAAGCAAGGGGGACAAGGTG 3599

Qy   3603 GAGCTGGATGGCCATGGAGTCTCTGACTTCGTCGTGGTTCGTGGTTCACCGGTCCTT 3662
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   3600 GAGCTGGATGGCCATGGAGTCTCTGACTTCCGTGGTTCGGCTCGTGGCTCACCGGTCCTA 3659

Qy   3663 TGCCACAAAGGGCACGCAGTAAGAATGCTCGTGTCAGTTGCTCCACTCTTGGCGCCAGGGTT 3722
          |||| ||||||||||||||| |||||||||  |||| |||||||||||||||||||||||||
Db   3660 TGTGACGAAGGGCACGCAGTAGGGAATGCTCGTGTCTGTCTGTCCACTCCCGTTGGTAGGGTC 3719

Qy   3723 ACTCGGCGCCGATTCACTAGGCCGTGGGACTCAAGTACCAACACAGATGCCAAGAGACTACCACA 3782
          || |||||| || ||||||||||||||  |||||||||||||||||||||| |||||
Db   3720 ACCGGCGCACGGTTCACTAGGCCGTGGGACCAAGTACCAACAGATGCCAAAACCACTACT 3779

Qy   3783 GAACCCCTTCCGGTGCCGCAAAAGGAGTTTCAAGGAGCCCCGTTGTTTATGCCTACG 3842
          ||||||||||||||||||||||| |||| |||||||||||||||||||||||||||
Db   3780 GAACCCCTTCCGGTGCCGCCGCCAAAAGGAGTTTCAAAGAGCCCCGTTGTTTATGCCTACG 3839

Qy   3843 GGGGCGGGAAAAGAGCACACCCGTACCGTTGGAGTACGGCAAATGGGCCACAAGGTCTTG 3902
          ||||||| |||| || |||||||||||||| ||||| |||||||||||||||||||||
Db   3840 GGACGCGGGAAAGAGCACTCGCGTCCCGTGGGAGTACGATAACAATGGGCCACAAGGTCTTA 3899

Qy   3903 ATCTTGAACCCGTCGGTAGCTACCTGAGGGGCCATGGGCCCATACATGGAGGGCGCTGGCG 3962
          || |||||||| |||||||||||  |||| ||  ||||||||||||| |||||||||||
Db   3900 ATCTTGAACCCCTCAGTGCCACTGCGGGCCATGGGGCCCATACATGGAGGCGGCTGGCG 3959

Qy   3963 GGGAAACACCCCAGTATTTACTGTGGGCCATGACACCACTGCTTTCACAAGGATCACTGAC 4022
          || ||| ||||||| |||| ||||||||||||||| |  ||||||||||||||||||||||
Db   3960 GGTAAAACATCCAAGTACTGTGGGCATGATACACAACTGCTTTCACAAGGATCACTGAC 4019

Qy   4023 TCGCCCCTTACGTATTCCACTTACGGAAGGTTTTGGGCCAACCCTAGGCAGATGCTAGG 4082
          |||||| |||| ||||||||||||| | ||||||||||||||||||| |||||||| ||
Db   4020 TCCCCCCTGACGTATTCCACGTATTGGGGCAGTTTTGGGCCAACCCTAGGCAGATGCTACGG 4079

Qy   4083 GGTGTGTGGTGTCATTTGTGACGAGTTGCCACAGTCACTGTTGTTTGGGC 4142
          || ||| |||||| ||||||||| || || ||||||||  || |||| |||
Db   4080 GGGCGTTTCGGTGGTCATTTGTGATGAGTTGCCACAGTCACTGCTGCTGTTAGGC 4139

Qy   4143 ATTGGGCGTGTCAGGGAGCTGGCCGCGGGATGTGGAGTGCAATTGGTGCTCTACGCCACT 4202
          |||||||||||||||||||||||||||||||| ||| ||| |||||||| ||||||||||
Db   4140 ATTGGGAGGGCTGTCAGGGAGCTGGCCGGTGGCTGGTGCAACTAGTGCTCTACGCCACC 4199

Qy   4203 GCCACCCCTCCCCGATGACCCCAGCAACCCCATCATTGAGACAAAACTGGAC 4262
          || ||||||| |||||  |||||||| ||||| ||| | |||| |||||||
Db   4200 GCTACAACCTCCCCGGATGACCCCAGCAACCCCTTCATCATCAAGGGAACAAAATTGGAC 4259

Qy   4263 GTGGGAGAGATCCCCTTCTTATGGCCATGCCATACCTCCTTGAGCCGGATGCGGACCGGAGG 4322
          |||||| ||||||| |||| |||||||  |||||||||  ||||||||||||||||||||
Db   4260 GTGGGAGAGATTCCCTTTTTATGGGCCATGCATGGGCGGATGCCGAGCCGGATGCGAACCGGAGG 4319

Qy   4323 CATCTTGTATTCTGCCACTCCAAGGCCGCTATTACAGGGGGGAAAGACAGTTTTCGGCT 4382
          || || ||||| ||||||||||||||||  |||||||||||| ||| |||||||| |||
Db   4320 CACCTGGTGTTCTGCCATTGTCCATTCTAGGCCTATTATAGGGGGTAAAGACAGTTCTCCGCT 4379

Qy   4383 AGGGGGTAAATGCCATCCGCCTATTACAGGGGGGAAAGACAGTTCTATCATCAAAGATGGA 4442
          || |||||||  |||||||| |||||||||||||| ||||||||| |||||||||| ||
Db   4380 AGGGGGTCAATGCCATTGCCCGTCTATTATAGGGGTAAAGACAGTTCTATCATCAAGGATGGG 4439

Qy   4443 GACTGGTGGTGTGTCTACAGACGCACTATCCACCTGGGGAACTTCGATTCT 4502
          |||||||| |||||| |||||||| |||  | |||||||||||||||| | |
Db   4440 GACTGGTGGTCTGCTCTACAGACGCTACACTGGGGTACACTGGGAACTTCGACTCC 4499

Qy   4503 GTCACCGATTGTGGTTAGTGGGTTAGTGTTGGAGGAGTCGTTGGAGAGTCTTCATCCCAATT 4562
          ||||||||||| |||||| ||||| || ||||||||| |||||||||| ||||||||||||
Db   4500 GTCACCGACTGTGGATTAGTGGGTCGTTGGAGTGGGTGACCCCTTGACCCCTGATCCCCACCATT 4559

Qy   4563 ACCATCTCCCTGCCAGTGCACGGTGCGCTCGGCTGAACTTGTCAGTGCGCGGAGGACGC 4622
          ||||||||||| |||||||||||||||||||||||||| ||||||||| |||||||||||
Db   4560 ACCATCTCCCTGCCAGCAGCGCTCAGACGCCCTGAACTTGTGATGCCGATCAAAGACGAGGACGC 4619
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Qy   4623 ACGGGTAGGGCAGGTCAGTTCCTGGGCGCTACTACTACGCGGGGTCGGCAAGGCCCCTGCTGGT 4682
          ||||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||||||
Db   4620 ACGGGTAGGGCAGGTCAGTTCTGACGCGTCTGGACGCGCTACTACTACGCGGGGTGGGCAAGCCCCTGCGGGT 4679

Qy   4683 GTGGTGCGTCAGGTCCTTCGGTCGGCGGTGGTCTCGTGGCGGTGGAAGCCGGTGGTGGAAGCCGGTGACCGTTACGGGAATG 4742
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||| |||||||||||||||
Db   4680 GTGGTGCGTCAGGTCAGGTCCTTCGGTCGGCGGTCGTGGCGGTGGAAGCTGGAGTGACCTGGAAGCTGGTACGGGAATG 4739

Qy   4743 GAACCTGACCTGACAGCAAAACTACTGACTTTACGACAACTGCCTTACACCCGCAGCC 4802
          |||||||||||||||||||||||||||||  ||| |||||||||||||||||||||||
Db   4740 GAACCTGACTTGACAGCAACTAACTACTGACTTTACGACTGCGCCTTACACCCGCAGCC 4799

Qy   4803 GTCCAGCTGACATTGGGAAGCCGCGGTGTGTTCTTTCGGGGCTGTCCCTCCGTTGCCCCGTTGAGGGATG 4862
          |||||||| ||| |||||||||||||||||||||||||||||||||| |||||||||||| ||||||||
Db   4800 GTCGGCGGCTGATATCGGAAGAGCCGGCCGGTGTTCTTCCTCTCGCTGGGCTGCCGCCCATTGAGGGATG 4859

Qy   4863 CATCCCGATGTTAGCTGGCACCCGGCCAAAAGTTCGCGGCGTCAACTGGCCCCTTCCTGGTGGGTGTT 4922
          || || |||||| ||||| |||||||||| |||||||||||||| |||||||| ||||| ||||| |||
Db   4860 CACCCTGATGTCAGCTGGGCACCCGGCCAAAAGTTCGCGGCGTCAACTGGCCCCTCTTGTGTGGGTGTGT 4919

Qy   4923 CAGCGGACCATGTGCCGGGAAACACTGTCTCCGGCCATCGGATGACCCCAGTGGGCA 4982
          ||||| ||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   4920 CAGCGGACCATGTGCCGGGAAACACTGTCTCCCGGCCATCGGATGACCCCAATGGGCA 4979

Qy   4983 GGTCTGAAGGCCCGAATCCTGTCCCACTCCTGCTGAGGTGGGGCAATGATTTACCATCT 5042
          |||| |||||||| |||||  ||||||||||  |||||||||||||||| ||||||||||
Db   4980 GGTCTGAAGGGCCCCAAATCCTGTCCCACTCTGCTGCTGAGGTGGGGCAATGATTTACCATCT 5039

Qy   5043 AAAGTGGCCGGCGCCATCACATCGTGGACGACCGGTCCTGCTCCGGTTGGCGGAGGGT 5102
          |||| ||||||| |||||||||||||  |||||||||| | |||||||||||| ||||||
Db   5040 AAAGTGGCCGGCGCCACCACACTAGTGGACGACCTGGTCCGCCGGTCGTGTGGCGGAGGGT 5099

Qy   5103 TACGTCCGGCTGCGATGGCGGGGACCCATCTTCGTGATGTGGCCTCGGCTATTGCGGGCCATG 5162
          |||||||||||| || |||||||||||||| | | ||| |||  ||||||||||||||||||
Db   5100 TACGTCCGGCTGCGACGCGGGGACCCATCTTGATGATGGTCTAGCTCTGGTCGGCTATGCGGGGAATG 5159

Qy   5163 ATCTATGCGTCATCACACCGGGTCTCTCGTGGTGTTTACAGACTGGGATGTGAAGGGGGT 5222
          || |||||||||||||||||||||||||||||||||| ||||||||||| |||||||||||
Db   5160 ATCTACGCGTCATCACACCGGGTCTCGCTCGCTGTAGTGTGACAGACTGGGATGTGAAGGGGGGT 5219

Qy   5223 GGCAGCCCCCTTTATCGGCATGGGGGAGACACCACGCCCAGCCGGTTGTGCAGGTCCCC 5282
          |||  ||||  |||||||||||||||  ||||||||||||||||| ||||||||||||||
Db   5220 GGCGCCCCCCCTTTATCGGCATGGGGGACACCACGCCCAGCCGGTCGGTGGTGCAGGTTCCT 5279

Qy   5283 CCGGTAGACCATCGCGGGGGGAGAGCTCGCGCCATGGATGCCAACACAGTGACAGAT 5342
          |||| ||||||||||  |||||||||||| ||  |||||||| ||||||||||||||
Db   5280 CCGGTAGACCATCGCGGGGGGGTGAATCAGCACCATCGGATGCGAAGACAGTGACAGAT 5339

Qy   5343 GCGGTGGCGGCCATCCAGTGGATTGGTCAGTTGGTCATGACCCGTCGATCGGGAGAA 5402
          ||||| || |||||||||| || ||| |||||| || ||||| ||||| |||||| |
Db   5340 GCGGTGGGCAGCCATCCAGTGGACTGGGTCAGTATCATGACTCGTCGATCGGGAGAGA 5399

Qy   5403 GTGTCGTCCTTGGCCCAGCTGAAGACGCGGCCCTACCAGCTACCACCAAGTGGCTT 5462
          |||||||||| |||||||  ||||||||| |||  ||||||| ||||||||||||||
Db   5400 GTGTTGTCCTTGGCTCAGCTGAAGGACGGGCCGAGCCCACTGTTCAATTGTTGACAAGCTCTTC 5459

Qy   5463 GCTGGCTGCTACACGGCCGCCGTCCCCACTGTTTCAATTGTTGACAAGCTCTTC 5522
          ||||||||||  ||||||| |||||||||||| |||||||||||| ||||||||
Db   5460 GCTGGCTGCTACACGGGACGCCGGTCCCCACTGTATCCATTGTGTTGACAAGCTCTTC 5519

Qy   5523 GCCGGGGGGCTGGGGCGGCGGTGGTAGGAGTAGTAGGAGTAGCTGCGGGCCAGTGGCG 5582
          |||||||||||||||||||||||||||| || |||||||||| | |||||||||||||
Db   5520 GCCGAGGGGGTGGGGCGGCGGTGTGGGGCGGTGTGGGTGGGTAGAGGTGCTGCGGCGGTGGGGCG 5579

Qy   5583 GCCTATGGGGCTTCTAGGAGCCCTTCATGGGGTTG 5642
          ||| |||||||||| ||||||||||||||||||||||
Db   5580 GCCTACGGGGCTTCAAGGAGCCCCGTGGCAGCCGCGGCGGCTTCTCTACTTGATGGGGTTG 5639

Qy   5643 GGGCTGGAGGCAACGCGCAAACCGCGAAACTCTGCCTCAGCAGCGGAGAGGACGC 5702
          |||||||||||||| | |||||||||||||||||||| | |||||||||||||||
Db   5640 GGGCGTGGAGGCAACGTGCTCAGACCGCGCGTGTCGTCCCTCTCCCTATTGGGGGCGTCTGGA 5699
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Qy  5703  ACCGCTCTGGGCACGCCTGTCGTGGGTTAACCATGGGGCGCCGTTCATGGGAAGTGCT  5762
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Db  5700  ACCGCCTGGGCGACTCCTGTCGTGGGCGTTGACCATGGCCGTTCATGGGAGGGGGGCC  5759

Qy  5763  AGCGTCTCCCCCTCCTTGGTCACCATTTTACTGGGGGCTGGGGGCGTGGGAGGGCGTG  5822
          |||||||||||||||||||| |||||||||||||||| |||||||||||||||||
Db  5760  AGTGTCTCCCCCTCCTTGGTCACCATTTTATTGGGGCGTCCGAGGTTGGGAGGGTGTT  5819

Qy  5823  GTGAATGCGGCTAGCGTTGTCTCGACTTTATGGCGGGAAACTATCATCAGAAGATCTG  5882
          | |||||||||||||| |||||  |||||| |||||||||||||||||||||
Db  5820  GTCAACGCGGCGAGCCCTAGTCTTTGACTTCTTCATGGCGGGGAAACTTTCATCAGAAGATCTG  5879

Qy  5883  TGGTATGCCATCCCAGTGCTAACCAGTCCGGGGGCAGGACTTGCGGGGATCGCCCTCCGGG  5942
          ||||||||||||| ||||| | |||||||| |||||||||||||||||||||||
Db  5880  TGGTATGCCATCCCGGTACTGACCAGCCCGGGGGCGGGCCTTGCGGGGATCGCTCTCCGGG  5939

Qy  5943  TTTGGTGTTGTACTCAGCTGCTAACAACTCTGGCACTACCACTTGGTTGAACCGTTGCTGCTGACT  6002
          ||||||||| |||||||||||||||||||||||||| ||||||||| | |||||||||||||||||
Db  5940  TTTGGTTTGTATTCAGCTGCTAACAACTCTGGCACTACCACTTGGTTGAACCGTTGCTGCTGACT  5999

Qy  6003  ACATTGCCAAGGTCCTACATGCATCCCTGACAGTTACTTTCAGCAGGCCGATTACTGTGAC  6062
          | |||||| |||||| | | |||| ||||||| ||||  |||||||||||||||||
Db  6000  ACGTTACCAAGGTCTTCATGTATCCCCGGACAGTTACTTTCAGCAGGCTGACTATTGCGAC  6059

Qy  6063  AAGGTCTCAGCTGTCTGCTCCGACACCGTTGGTCCCTCCACCGTTGCCCTGGTCAAC  6122
          |||||||||| |||| || ||||||||| || |||||||||||||| || ||||||||||||
Db  6060  AAGGTCTCAGCCGTCTGCCTCCGGCCTCGAGCCTCACCGCCACAGTGGTTGCCCTGGTCAAC  6119

Qy  6123  AGGGAGGCTAAGGTGGATGAGGTTCAGGTGGGTACTCTGGGACTTGTGGGAGTGGATC  6182
          |||||||||||||||||||||  ||||| |||| ||| ||||||||||||||||||||
Db  6120  AGGGAGGCTAAGGTGGATGAGGTACAGGTGGGGTATGTCTGGGACCTGTGGGAGTGGATC  6179

Qy  6183  ATGCGTCAAGTGCCCATGGTGATGAGCCAGACTTCGGGCCCCTCCGCCCCCTGGTGTCATTA  6242
          |||||||||| ||| ||||| | ||||||||||| |||||||||||||| |||||||||
Db  6180  ATGCGTCAAGTGCGCGTGGTCATGGCCAGACTTCAGGGCCCCTGCCCCGCGGTGGTGTCACTA  6239

Qy  6243  CCCTTATGGCACTGCGGGGGAGGGGTGGTCCGGAGAATGGTTGTTGGACGGCCATGTTGAG  6302
          |||| ||| ||||||||||||||||| || ||||||||| ||||||| |||||||||||||
Db  6240  CCCTTGTGCACTGCGGGGGAGGGGTGGTCCGGGAATGGTTGCTTGACGGTCATGTTGAG  6299

Qy  6303  AGTCGTTGTCTTTGTTGGTTGCGTGATCACCGGTGATGTGTTTGAAATGGGCAACTCAAAGAT  6362
          |||||| || |||||||||| ||||||||||| |||| | ||||||| ||||||||||||
Db  6300  AGTCGCGCTCTGTGTGGTTGCGTGATCACTGGTGACGTGTTTGAAATGGGCAACTCAAAGAA  6359

Qy  6363  CCAGTTACTGCTACCAAGCTGTGCAGGCATTATTGGATGATGGACAGTCCCTGTGAACATG  6422
          ||||||||||| |||||||||||||||| |||||||||||||||||||||| ||| |||||
Db  6360  CCAGTTACTGCTACCAAGCTGTGCCGGCCACTATTGGGGATGGTGTCCCTGTGAACATG  6419

Qy  6423  CTGGGCCTATGGCCAGAACGTCGCCTTTGCTCGGGCACACCCGAAGGTGGTACCATTC  6482
          ||||||||||||| || |||||||||| |||  |||||||||||||||||||||||
Db  6420  CTGGGTTACGGTGAAACGTCGCCTTCCGGCCTCTCCGACACCCGAAGGTTGTGCCCTTC  6479

Qy  6483  GGGACGGTCTGGGTGGGCTGAGGTGACCCTACCCACCGTTGTGATCAGGCGAACA  6542
          ||||||||||||||||| ||||||||||| |||| ||||||| |||| |||||||||
Db  6480  GGGACGGCTGGGGTGGGCTGAGGTGGTGTGACCACCCACCGGGTAATCGGGAGGACC  6539

Qy  6543  TCCGGCCTCAAACTGCCTGCGCCGACGAAATCCTGTCGCTGGTCGTGTTGTTGCTATTAC  6602
          ||||| ||||| | ||||| |||||||  |||||||| | |||||||| | ||||||||
Db  6540  TCCGGCCTATAAGCTGCTGCGCGGGACGCAAATCCTATCGGCTGCTGTGAGCTGCTACTAC  6599

Qy  6603  GTCGACGGGCATACCGGTCTCATGGGAACCGCGAGCGCGTGCCATGGTCTATGGC  6662
          |||| ||||| ||| |||||||||||||||||||||  ||| ||||||||||||||
Db  6600  GTCGACGGGCATTCCGGTCTCATGGGACGCGGGGCGCGTCTCGCCGCCCATGGTCTATGGC  6659

Qy  6663  CCTGGGCAAAGTGTCACCATTGACGGGGAACCGCTACACCCCTTCCGCATCAACTGCGGCTT  6722
          ||||| |||||||| ||||||||||||||||||||| |||||||||||| | ||||||| ||
Db  6660  CCTGGGCAAAGTGTTCCATTGACGGGGAGCGGCGCTACACCTGCCTCCATCAACTGCGGCTC  6719

Qy  6723  AGGAATGTCAGGAACTGACTGAGGTCCGCCCCTCGAGGTCATTGGGACCGGGACGGACT  6782
          |||||| || |||||||||||| | |||||||| |||||||||| ||||||||||||||
Db  6720  AGGAATGTGGCACCCCTCTGAGGTTCATTCAATGTCCATTGGGACGGACTGGGACGGAGACT  6779

Qy  6783  GAAGACTTCAGAGACTGACTGAGGCCGACCTGCCCGGCCGGCCCTCAGGCTATC  6842
          |||||| |||  ||||| || ||||||| |||||  | |||||||||
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Left column:

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Db  7860  CCCCCCCTGGACTTCCGGATAGCTGAAAAGCTCATCTTGGGAGACCCAGGCGCGGTAGCC  7919
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Qy  7923  AAGGCGGTGTTGGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAATTAGGGAG  7982
          |||||||||||||||||||||||||||||||||||| || |||||||||||| ||| |||
Db  7920  AAGGCGGTGTTGGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAGTTAAGGAG  7979

Qy  7983  ATGCTCAAACTGTGGGAATCAAAGAGACACCATGCGCCATCTGTGTGGACGCCACATGC  8042
                   |||| |||| || |||||||||||||||||||||||||||||||||||||
Db  7980  ATGCTCAAGCTATGGGAGTCTAAGAGAGACCCCTTGCGCCATCTGTGTGGACGCCACCTGC  8039

Qy  8043  TTCGACAGTAGCATAACTGAAGAGGACGTGCGCGTGGAGACAGAGCTTTATGCCCTGGCT  8102
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  8040  TTCGACAGTAGCATAACTGAAGAGGACGTGCGCTTTGGAGACAGAGCTATACGCTCTGGCC  8099

Qy  8103  TCAGACCATCCAGATAGGGTGCGTGCCCTGGGGAAATACTATGCTCTGCGACAATGGTA  8162
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Qy  8163  ACCCCCGAGGGGTGCCAGTGGGTTGAGAGGTATTGTAGATCCTCAGGGGTCTTGACCACC  8222
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Db  8160  ACCCCCGAGGGGTGCCCGTCCGGTGAGAGGTATTGCAGGGATCCTCGGGTGTCCTAACAACT  8219

Qy  8223  AGTGGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCCGCCTGTGAGAGGGTGGGG  8282
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Db  8220  AGCGCGAGCAACTGCTTGACCTGCTACATCAAGGTGAAAGCTGCCTGTGAGAGTGGGG  8279

Qy  8283  CTGAAAAATGTCTCGCTCCTCCATCGCTGGCCATGACTGTTGATCATATGCGAACGGCCT  8342
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Db  8280  CTGAAAAATGTCTCTCTTCTCATAGCCGGCGATGACTGCTTGATCATATGCTGATGATGCTGCCCA  8339

Qy  8343  GTGTGCGATCCTAGCGACGCTTTGGGCAGAGCCCTGGCCGAGCTACGGGTACGCATGCGAG  8402
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Db  8340  GTGTGCGACCCAAGCGACGCAGCGCTTGTGGGCAGAGCTATAGGGTACGCGGTGCGAG  8399

Qy  8403  CCTTCCTATCAAGCGGTGCCAGTGGGTCTGGGTCGTCCACTTGGCTAGCTGAGTGC  8462
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Db  8460  AATGCAGATGGGAAGCGCCATTTCTTCCTGACCACGGACTTTCCGGAGGCGCCGCTCGCGC  8519

Qy  8523  ATGTCGAGCGAGCTACAGTGACCCAATGGCTTCGGCCCATCGGTTACATCCTCCTATACCCT  8582
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Db  8520  GTATCCGAGTGAGTATATGCCCGGCGCTTCGGCCCATCGGTTCACATCCCTCCTTTATCCT  8579

Qy  8583  TGGCCATCCTATCACACGGTCGGGTCATCATCCTCACGTGCTCACCTGGCGTTTAGGGGT  8642
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Db  8580  TGGCACCCCATCACACGGTCGGGTGGCATCATCATCCTCTAAACGTGCTAACGTGCAATTCAGGGGT  8639

Qy  8643  GGTGGCACACCGTCTGATCCTGTGTGCAGGTACATGTAATTACTACAAGTTTCCA  8702
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Qy  8703  CTGGACAAACTGCCTAACATCATCCTGGCCCTCCACGGACCAGCAGCGTTGAGGGTTACC  8762
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Qy  8883  GGTTGGGCTGAGTTGGCTAGGGGCGTAGGGGTTCCCCCTTTCCCCCTTTCCCCCTCCG  8942
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Db  8880  GGTTGGGCTGAGTTGGCTGGCTAGGGGGTTCCCCGGTTCCCATCCGGTCATCATCCCCCT  8939

Qy  8943  GAGATTGCTGGTATCCCGGGGGGGGTATCCCGGGGGGGGTTCCCCTCTCTCCCCCCCATCAT  9002
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Db  8940  GAGATTGCTGGTATCCCGGGGGGGGTATCCCGGGGGGGGTTCCCCTCTCTCCCCCCCATATGT  8999
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RESULT 10

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LOCUS       AR065378                9392 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5849532.
ACCESSION   AR065378
VERSION     AR065378.1  GI:5995594
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 9392)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie., Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5849532-A 14 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1..9392
                     /organism="unknown"
BASE COUNT     1694 a   2551 c   2998 g   2148 t      1 others
ORIGIN
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Query Match   84.9%; Score 7979; DB 6; Length 9392;
Best Local Similarity   90.7%; Pred. No. 0;
Matches 8515; Conservative   1; Mismatches 876; Indels   1; Gaps   1;

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Qy     3  ACGTGGGGGGGTGATCCCCCCCCCCCCCCGGCACTGGGTGCAAGCCCCATAAACCGACGCCT   62
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Db     1  ACGTGGGGGAGTTGATCCCCCCCCCCCCCCGGCACTGGGTGCAAGCCCCAGAAACCGACGCCT   60

Qy    63  ATCTAAGTAGACGCAATGACTGGTGTAGTTGTAAATCCCGGTCATCCTGTAGCCACTATAGGTGGT  122
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    61  ATCTAAGTAGACGCAATGACTGGTGTAGTTGTAAATCCCGGTCATCCTGTAGCCACTATAGGTGGT  120

Qy   123  GTGGTGACAGGGTTGGTAGTTGGTGTAAATCCCGGTCACTTGGTAGCCACTATAGGTGGGT  182
          ||||| ||||| |||||||||||| |||||||||||||||||||| |||||||||||||||||
Db   121  GTGATGACAGGGTTGGTAGTTGGTGTAAATCCCGGTCACTTGGTAGCCACTATAGGTGGGT  180

Qy   183  CTTAAGAGAAGGTCAAGACTCCTCTGTGCTCCTGTTCTCTGTCCTGTCGGACCCGCCACAGT  242
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Db   181  CTTAAGAGAAGGTTAAGATTCCTCTGTGCTCCTGTCCTCTGTCGGCCGAGACCCGCCACAGT  240

Qy   243  GCTGGCCCTACCGGTGGGGTTCCCCCTTTTCCCCCTCTCTCGTTCGTTAAACCGAGCCCGT  302
          |||||||||||||||| |||| |||||||||||||||||||| |||||||||||||||||
Db   241  GTTGGCCCTACCGGTGGGAATAAGGGCCCAGTAAGGCCCAGCTCAGGCTCGTCGTTAAACCGAGCCCGT  300
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Qy   303  CACCCCACTGGGCAAACGACGCCCACGTACGGTTCCACGTCGCCCTTCAATGTCTCTCTTG  362
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Db   301  TACCCACCTGGGCAAACGACGCCCACGTACGGTTCCACGTCGCCCTTCAATGTCTCTCTTG  360

Qy   363  ACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAGTGGGGCGGGGTTATGGGAAG      422
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Db   361  ACCAATAGGCGTAGCCGGCGAGTTGACAAGGACCAGTGGGGCGGGGT-TGGAGAGG      419

Qy   423  GACCCCAAACCCTGCCCTTCCCGTGGGCCGGGAAATGCATGGGGCCACCCAGCTCCCG      482
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Db   420  GACTCCAAGTCCCGCCCTTCCCGTGGGCCGGGAAATGCATGGGGCCACCCAGCTCCCG      479

Qy   483  GCGGCCTGCAGCGCGGGGTAGCCCAAGATCCTTCGGGTGAGGCGGGTGGCATTTCTCTT    542
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Db   480  GCGGCCCTGCAGCGCGGGGTAGCCCAAGATCCTTCGGGTGAGGCGGGTGGCATTTCCTTT   539

Qy   543  TTCTATACCATCATGGACGAGTCCTTCTCCGTGGTTGAGGCCGGGGCCATTCTG        602
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Qy   603  GCCCCGGCCACCCAGCTTGTCGAGCGAATGGGCAATATTCCTCACAAATTGCTGTGCC    662
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Db   600  GCCCCGGCCACCCAGCTTGTCGAGCGAATGGGCAATATTCCTCACAAATTGTTGTGCC    659

Qy   663  CCGAAGACATCGGTTCTGCGCTGGAAGGCGATGCCTGGTGCCCTGGGGTGCCACGGTT    722
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Db   660  CCGAGGAGACATCGGTTCTGCGCTGGAAGGCGATGCCTGGTGCCCTGGGGTGCCACGATT  719

Qy   723  TGCACCGACCGTTGCTGCCACTGTATCAGGCGGGTTTGGCTGTCGGCCGCCTGGCAAGTCC  782
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   720  TGCACTGACCAATGCTGGCCACTGTATCAGGCGGGTTTGGCTGTCGGCCGCCTGGCAAGTCC  779

Qy   783  GCGGCCCAGCTCGTTGGGGAACTGGGGAGCCCTGTACGGCGGGCCCTATACGGGCCTTAC  842
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Db   780  GCGGGCCCAACTGGTTGGGGAGCTGGGGAGCGTACCGTGTACGGGCCCTGTCGGCCCTAT  839

Qy   843  GTAGCCGGGATCCTGGGCTGGGCGGAGTTTACTCCCGGGTCTGACAGTTGGTGTTGCG    902
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Db   840  GTGCTCGGGGATCCTGGGCTGGGTGTCGGGGTGTCCTAACGGTGGGAGTCGCG        899

Qy   903  TTGAGGGCCCGGGTCTACCTGATGGCCCAACCTGAAGTGTGCAGTAGAATGTGACGTTAAG  962
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   900  TTGACGCGGGGTCTACCCGCGTGCCTAACCTGACGTTGCAGTGTTGCAGTGTGAGCGTAAAG  959

Qy   963  TGGGGAAGTGAGTTTGGAGATGGACTGAGCAGTGGCCTCCAATTACTGGATTTTGGAA   1022
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   960  TGGGGAAGTGAGTTTGGAGATGGACTGAGCAGTGGCCTCCAACTACTGGATTCTGGAA   1019

Qy  1023  TACCTTTGGAAAGTCCCATTTGAATTTTGGAGAGGAGTGATGAGCCCTGACCCCCTCTGTTG 1082
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Db  1020  TACCTCTGGAAGGTCCCATTTGATTTTCTGGAGAGGGCGTGATAAGCCTGACCCCCTTGTTG 1079

Qy  1083  GTTTGGGGTGGCCGCCATTGCTTTTGCTGGAGCAACGGATTGTCATGGTTTCCTGCTGGTG  1142
          ||| ||||||||||||||||||| ||||||||| |||||||||||||||||| |||||||
Db  1080  GTTTGGTGGCCGCCATTGCTTTTGCTGCTGGAACGGATTGTCATGGTTTGACTTGTCGTGTG  1139

Qy  1143  ACGATGGCGGGGATGTTGCAAGGCGGATGTCACGGTTGCGCCCCTTGAC   1202
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Db  1140  ACGATGGCCGGATGTGTCCAAGGCGCAGACCTGCGCCGTTCGCGTTTTGAC   1199

Qy  1203  TACGGGTTGAAGTGGCAGTCATGGCTCTCCTGCAGGGCTCGCGATTCCCCACTGGG   1262
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Db  1200  TACGGGCTGAAGGTGTGCAGACACCGTTACGCTTCAGTGACTGAGTGCCAACGGCCCCTGG  1259

Qy  1263  TACGGGGTTGAAGGTGTGGCAGTCATGGCTCTTGTGTGACTGCGCCCCAACGGCCCCCTGG 1322
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Db  1260  GAGAAGGTGTGGGACCGTGGGAACGTTACGGTTGCAGTGCAACGGCCCGGGTTTGAC     1319

Qy  1323  GTTTGGGTCCCCGGGCCTTTGCCAAGCAATCGGCTGGGGTGGGGCGACCCCATTGAGC   1382
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Db  1320  GTTTGGGTTGGCCCAGCCCTTTGCCAGGCAATCGGCTGGGGTGGGGCTTATTGGAGC   1379
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Qy  1383  CACGGACAAAACCAGTGGCCCCATATCATGCCCCAATATGTCATATGGTCTGTGTCCGTA  1442
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Db  1380  CACGGGCAAAATCAGTGGCCCCTTTCATGCCCCAGTATGTCTATGGTCTCGTCGCTACAGTC 1439

Qy  1443  ACGTGCGTGTGGGGTTCCGTGTCTTGGTTTGCCTCGACCGGTCGTGATTCGAAGATC   1502
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Db  1440  ACTTCGTGTGGGGTTCCGTGTCTCGCTTCGTTCCTCCCACCAGTGGTCGCGACTCGAAGATA   1499

Qy  1503  GATGTGTGGAGTTTGTGCCGGTTGGATCGTGCCAGCTGCCACCATAGCCGCTCTAGGGTCA  1562
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Db  1500  GATGTGTGGAGTTTAGTGCCAGTTGGTCTGTGCCACCTGCCACCATAGCCGCCACTTGGATCA  1559

Qy  1563  TCGGATCGGCACACGGTGGTTGAGCTGTCCCAGTGGGAGTCCCGTGCGTAACGTGTATT  1622
          |||||||| | | |||||||||||||||||||||||||||||||||| |||||||||
Db  1560  TCGGATCGGCACACGGTGGTCTCCGGGCTTCCCAGTGGGAGTGGGGAATCCCGTGCACGTGTGTT  1619

Qy  1623  CTGAACCGTCGCGCTGCTTCATGTGCCACCTGTGTCGCGGACTGCTGGCCCGAAACCGGG   1682
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Db  1620  CTGGACCGTCGCGCCTGCTTCCTGCGCCACCTGTGTCGCGGACTGCTGGCCCGAGACCGGG   1679

Qy  1683  TCGGTTAGATTCCCTTTCATCGGTTGTGCCGCACGGGCCTCGGCTGCGACAAAGGACTTGGAA  1742
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Db  1680  TCGGTTAGGTTCCCATTCAATCGGTTGCGGAGTGTCCCACACCGGCCTCGGCTGCGACAAAGGACTTGGAA  1739

Qy  1743  GCTGTGCCCCTTCGTCAACAGGACAACTCCCTTCACCATAAGGGGCCCCCTTGGGCAACCAG  1802
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Db  1740  GCTGTGCCCCTTCGTCAACAGGACAACTCCCTTCACCATTAGGGGGCCCCTTGGGCAACCAG  1799

Qy  1803  GGGAGGAGGCAACCCGGTGCGGTCCGGTCGCCGTTGGCGTTCTACACCATGACCAAGATC  1862
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Qy  1863  CGGGATTCCCTGCATTGGTGAAATGCCACCACAGCCATAGAGCCTCCGACTGAAACG   1922
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Db  1860  CGAGATACCCTACATCTGGTGAGTGTCCCACCACAGCCATTGAGCCTCCCACCGGGACG   1919

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Db  1920  TTTGGGTTCTTCCCCGGACGCCGCCTCTCAACAACTGCATGCCGCTCTTGGGCACGGAAGTG  1979

Qy  1983  TCTGAGGCATTGGGCGGAGCTGGGGTTCTACGGGCCTCTTGGTTCCGCAGG   2042
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Db  1980  TCCGAGGCACTTGGGGGGGCCTGGGCCGCTGGGGGGTTCTATGAACCCCTGGTGCCGCAGG   2039

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Qy  2103  GGTAGACCTGACGGGTCATCACGGGTGGATGGGAGTGCACCTGCGAGGAGTGCGGCCAAC  2162
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Qy  2223  AAGCTGGCTGAGGCGACGGTTGGTCCTGCGTCTTGTGTCTTGGGTGGTGGTGGAAC   2282
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Qy  2343  GGCCCTGCCTTGTCATGGTGTTTGGGCCTTCCGGCGGGTGAAGTTTTTGCG      2402
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Qy  2403  AACCTGGTGTTGTTGTGTCCTTGGGTGCGGCCCTCAGCGCCGCCTCATGTTCCTCGTGTGTTGTGA  2462
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Db  3540  TGTTGGGTCATCAGATCCGACGGGCCCATGCCATGCTTGAGCAAGGTG                     3599
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Qy  3723  ACTGCGCGCGATTCACTAGGCCGTGACTCAAGTACCAACAGATGCCAAGACTACCACA          3782
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Db  3720  ACCGCGCACGGTTCACTAGGCCGTGACCCGGAGCCCAAGTGCCAAAACCACTACT            3779

Qy  3783  GAACCCCTCCGTGCCGGCAAAAGGAGTTTCAAGGAGGCCCGTTGTTTATGCCTACG          3842
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Db  3780  GAACCCCTCCGTGCCGGCAAAAGGAGTTTCAAAGAGGCCCGTTGTTTATGCCTACG          3839

Qy  3843  GGGGGCGGGAAAGAGCACCCGCGTACCGTGGAGTACGGCAACATGGGCCACAAGGTCTTG       3902
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Db  3840  GGAGCGGGAAAGAGCACTCGCGTACCGTTGGAGTACGGCACATAACCATGGGCCACAAGGTCTTA  3899

Qy  3903  ATCTTGAACCCGTCGTAGCTACCGTGAGGGCCATGGACATGGAGCGGCGGCTGGCG           3962
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Db  3900  ATCTTGAACCCCTCAGTGCCCAGTGGCCCATGCGCGGGCCCATGGGCCGTACCATGGAGCGGCGGCTGGCG  3959

Qy  3963  GGGAAACACCCCAGTATTACTGTGGCCATGACACCACTGCTTTCACAAGGATCACTGAC        4022
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Db  3960  GGTAAACATCCAAGTATATACTGTGGGCATGATACAACTGCTTTCACAAGGATCACTGAC       4019

Qy  4023  TCGCCCCTTACGTATTCCACTTACGGACGAAGGTTTTTGGCCAACCCTAGGCAGATGCTGAGG    4082
          || ||||||||||| |||||  |||||||||||||||||||||||||||||||||| |
Db  4020  TCCCCCCTGACGTATTCAACCTATGGGACGAAGGTTTTTGGCCAACCCTAGGCAGATGCTACGG  4079

Qy  4083  GGTGTGTCGGTGGTCATTTGTGACGACTGCCACAGTCATGACTCAACTGTGTTGTTGGGC       4142
          |||||| || ||| ||||||||||||| ||||| ||| ||| |||||||||| |
Db  4080  GGCGTTTCGGTGGTCATTTGTGACGACTGCCACAGTCATGGAATACCCTCGAGCGGATGCCGAAGG  4139

Qy  4143  ATTGGCGGTGTCAGGAGCTGCGCGAGGAGGATGCGGCCATTGGTGCTCTCACGCCCACCT      4202
          |||| |||||| ||||||||| |||||||||||| |||||||| | ||||||||||||||
Db  4140  ATTGGGAGAGTCCGGAGCTGCGCGAGCTGGGGTGCGGGCGTCCAACTAGTGCTCTTACGCCCACC   4199

Qy  4203  GCCACCCCTCCCGGATCCCCGATGACCCAGCACCATCAATCATTGAGACAAAACTGGAC        4262
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Db  4200  GCTACACCTCCCGGATCCCCATGACCCCTCCATATAGGGCTAAAATTGAGACAAAAATTGGAC    4259

Qy  4263  GTGGGAGAGATCCCCTTCTATTGCCAGTGCATTGGCATTACCTCTTGAGCGGATGCGGACGGAAGG  4322
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Db  4260  GTGGGCCAGATTCCCTTTTATGCGGTCATTGGCATGGAATACCCTCGAGCGGATGCGAACGGGAAGG  4319

Qy  4323  CATCTGTATTCTGCCACTCCAAGGCTGAGTGCGAGCGGCCTTGGGGCCAGTTTTCGGCT       4382
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Db  4320  CACCTGTGTTCTGCCATTCTCAAGGCTGAGTGCGAGCGGCCTTGCTGCCAGTTCTCCGCT       4379

Qy  4383  AGGGGGTGTAAATGCCATCGCCTATTACAGGGGGAAAGACAGTTCTATCATCAAAGATGGA      4442
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Db  4380  AGGGGGGTCAATGCCATTGCCTATTATAGGGGGTAAAGACAGTTCTATCATCAAGGATGGA      4439

Qy  4443  GACCTGGTGGTTGTGTCTACAGACGCACTATCCCACTGGGTACAACTTCGATTCT          4502
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Qy  4503  GTCACCCGATTGTGGGTTAGTGGTCAGGTCGTCAGGTCACCCTTGATCCCACCATT          4562
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Db  4500  CACCTGTGTTCTGCCATTCTCAAGGCTGATTGGAGTGCGGACCCTTGATCGTCCACCATT        4559

Qy  4563  ACCATCTCCCTGCCACGGTGCCGGTCGCCTGACTGTCGAACTGTCGATGCGGCGAGAGCGC      4622
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4560  ACCATCTCCCTGCCGACAGTGCCGTCGGCTGACTGTCGATGCGGTCGCAAAGACGAGGACGC    4619

Qy  4623  ACGGGTAGGGCAGGTCTGGGCGTCTGGACGCTACTACGGCGGGGTGCCAAGGCCCCCTGCTGGT   4682
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||| |||
Db  4620  ACGGGTAGGGCAGGTCTGGGCGTCTGGACGCTACTACGGCGGGGTGGGCAAAGCCCCTGCGGGT    4679
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Db  2460  AAGCTTGCTCGGGGAGCTTCCCGCTGGCCCTTGATGGGATTTCGGCGACCCGCGGG           2519
          |||||| ||||||||||||||||||| || ||||||||||||||||||||||||||
Qy  2523  CGCACCTTCTGTCGCGGGCCGAGTTCTGCTTCGAGTGTGGACACTTCG                   2582
          ||||||| ||||||||||| |||||||| |||||||||||||||||||
Db  2520  CGCACCTCAGTGCTCGGCGGCCGAGTTCTCGCTTCGAGTGTGGACACTTCG                2579

Qy  2583  GTGTTGGGCTGGTGGTGGCCAGCCGGTGGCCATAGCCGCTCCTGAGCTCAATG              2642
          ||||||||| || ||||||||| || || ||||| |||| ||||||||| |||
Db  2580  GTGTTGGGCTCGGTGGTGGCCAGTGGTAGCTTGGCCATTGCCTCCTGAGCTCGATG           2639

Qy  2643  AGCCGCAGGGGGTGGAAGCACAAGCCCGTGATCATATAGGACGTGTGTAAAGGGTACCAG       2702
          |||||||||| ||||||||||||| |||||||||||||||| ||||||||||||||||||
Db  2640  AGCCGCAGGGGGTGGAGGCACAAGACCGTGATCATAGGACGTGTGTAAGGGGTACCAG         2699

Qy  2703  GCTGTGCGCCAGAGGGTGTCGGCGGCCCTACCAAGCTTCTG                          2762
          |||||||| |||||||| ||||||||| |||||||||| ||
Db  2700  GCAATCCGTGCCAAAGGGTGAGGAGCCCGGGCTGGCGGCCGCTCGCCAAACCCCTG           2759

Qy  2763  ACGTTCGCCTGGTGCTTGGCCTCATACATTCGGCCGATGCTGTGATGAGTTGGTGGTG        2822
          |||||||||||||||| |||| |||||||||| ||||||||||||| ||||||||||||
Db  2760  ACCTTTGCCTGGTGCTTGGCCTCGTGCATCTGGCCAGATGCTGTGATGAGTTGGTGGTT       2819

Qy  2823  GCCTTGGTCTCCTCCTTCGGCCACTGTTCGACGCACTGGGCCCGTGGGGGAGCTTCCTG       2882
          ||||||||||| ||| ||||| |||||| ||||||||||| ||| ||||||||||||||
Db  2820  GCCTTGGTCTCCTTTCTCTTTTGCCGTGTTCGACGCGTGTGTGTTGGCCTTGGGGGAGGATCTTG   2879

Qy  2883  GTCTCCCGGCCCTCGTTACGGCGACTGGCACGGTCGTTGAGTGCTGTGTGATGGCGGGC        2942
          |||||||||||| || ||||||||||| || |||| |||||||| ||||| |||||||
Db  2880  GTGTCCCGGCCCTGCTTGGCGTTGGCTCGTCGTGTGGTTGAGTGCTGTGTGATGGCGGGT      2939

Qy  2943  GAGAAGGCCACCACCATCCGACTGGTCTCTCCAAGATGTGCAAGAGGGGCCTACCTGTTT       3002
          |||||||||||||||| || |||||||||| |||||||||||||| |||| ||||| |||
Db  2940  GAGAAGGCCACAACCCTCCGCGTGCTGTCTCCCAAGATGTGCGAGAGGAGCTTATTGTTC       2999

Qy  3003  GACCACATGGGCTCTTCTCTGCCGGCCGTGTTGTTGCTCAAGGGACCGGGACCGGCGGCT      3062
          |||||||||| || ||||| |||||||| ||||| ||||| |||||||||||||||||||
Db  3000  GATCATATGGGCTCTTTTTTCCGCGTGCTGTGTTGGAATGGGACGCGCCTCCGACCCAGCT      3059

Qy  3063  TTGGAGCCCTTGTCATTCACTAGGACGACGTGTCCGCATCATCAGAGATGCCGCGAGGACC     3122
          |||||||| | |||| |||| | ||||||||| |||| ||||||||||||| ||| |||||
Db  3060  CTTGAACCTGTGTTCTGCCATTCAACTGGATCCGTCCTCCATCATAACCGGATGCCGCGAGGACT   3119

Qy  3123  CTGTCCTGCGGACAGTGCGTCATGGGTTACCCGTGTAGCACGGCGCGCGTGATGAGGTT       3182
          |||||||||||||||||| | ||||||| | |||||||||||||||||||| ||||| ||
Db  3120  TTGTCCTGCGGGCAGTGCGTCATGGGTTACCCGTGTTGGGCCGTGTTGCGCCGTGATGAGGTT     3179

Qy  3183  CTCATCGGCGTGCTTCAGGATGTGAATCATTGGCCTCCCCGGGTTGCCTGCCGACTGCCACCA   3242
          |||||| |||||||||||||||||||||||| | || ||||||||||||||||||||| |||
Db  3180  CTCATCGGCGTGCTTCAGGATGTGAATCATTGGCCTCCCCGGGTTTGTTCCGACCGGCGCCT      3239

Qy  3243  TTGGAGCCCTTCGTGCGGAAAGGCTTCCTGGGGCTTCACGAAGGCAGCCTTGACAGGT        3302
          |||| |||| ||||||||||||||||||||| ||||| |||||||||||||||||||||
Db  3240  GTTGTCATCCTGTGTTCTGCCATTCGTGGGGGAAAGGCTGCCTTCGGGGTCACCAAAGGCAGCCTTGACAGGT  3299

Qy  3303  AGGGATCCTGACTTACATCCAGGGAACGTTCAGAATCCATGGGGCTTCCATGCCGCACGTTCACGAAGC  3362
          ||||||||||| ||||||||||||||||| ||||||||||||||||||||||||||||| |||||||
Db  3300  CGGGGATCCTGACTTACATCCAGGGAACGTCATGGGTTGGGGACGCGTTGGGGACGCGGACGTTACGGAAGC  3359

Qy  3363  ATGGGCCACATGTCTGAATGCCATCGCCTATTACAGGGGCTTCATCATCCCGAACC           3422
          ||||| |||| |||||||||||||||| ||||||||||||||||||||||||||||
Db  3360  ATGGGAACATGCTTGAACGCGTCTGTGTTCTGCCATTCGTGGGGGCTTCATCATCCCGAACC      3419

Qy  3423  GTTGTCATCCTGTGGGCCCGTGCGGTCAGCCAGTGCTGTCAGGTCACGGTGACGTCACG        3482
          |||||||| ||||||||||||| |||| |||||||||||| ||||| ||||||||||||
Db  3420  ATCGGCCACCACCGTGGGGGCCCGTGCGGTCGTTGAGTGCTGTGGAGTGCGGGTGACGATGTCACG     3479

Qy  3483  GTGTACCCGTTCCAGATGGGGCAACTTCGTTGCCACTTGCCAGGCGACGGTCC              3542
          |||||||||||||||| ||||| |||||| ||||||||| |||||||||||||
Db  3480  GTGTATCCCCGATGGGGGCGGTCAGTGCCGACTTGCCAGCGGTCGCCACCGGTGTTAACCTTGTACTTGTACTTGTACTTGTACTT  3539

Qy  3543  TGTTGGGTTATTAGATCCGACGGGCCATGCCATGCTTGTGCCAAGGGGGACAAGGTT          3602
          |||||| | ||| | |||| | ||| || || || || | || |||||||||||||||
Db  3540  TGTTGGGTCATCAGATCCGACGGGCCCATGCCATGCTTGAGCAAGGTG                   3599
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Qy 4683 GTGGTGTCGCTCAGGTCCTGCTCTGGTCTGGCGCTGGAAGCCGTGTGACCTGGTACGGAAATG 4742
          ||| ||||||||||||||| || | |||||||||||||||||||| ||||| ||||||||||
Db 4680 GTGGTGTCGCTCAGGTCCTGCTCTGGTCGGCGGTGGGAAGCTGGGAGCTGGGTACGGGAAATG 4739

Qy 4743 GAACCTGACCTGACAGCAAAACTACTGAGACTTTACGACAACTGCCCTTACACCGCAGCC 4802
          |||||||||| ||||| ||||||||||||||||||||||| |||||||||||||||||||
Db 4740 GAACCTGACTTGACAGCTAACCTACTGAGACTTTACGACACTGACCCTTACACCGCAGCC 4799

Qy 4803 GTCGCAGCTGACATTGGGAAGCCGCGGTGTCTTCTTTTCGGGGCTTCGCCCGTGAGGATG 4862
          |||| ||||| ||||||||||||||||||||||||||| | |||| ||||| |||||||||
Db 4800 GTCGGCGGCTGATATCGGAGAAGCCGCGGTGTTCTTCTCTCGGGCTCGCCCCATTGAGGATG 4859

Qy 4863 CATCCCGATGTTAGCTGGGCAAAAGTTCGCGCGTCAACTGCCCTTCGTGTGGGTGTT 4922
          ||| | ||||| |||||| ||||||||||||||||||| ||||| | |||||||||
Db 4860 CACCCTGATGTCAGCTGGGCAAAAGTTCGCGCGTCAACTGCCCCGTCGTGTGGGTGTT 4919

Qy 4923 CAGCGGACCCATGTGCCGCGGGAAAACACTGTCTCCCGGCCCATCGGATGACCCCCAGTTGGGCA 4982
          |||| ||||||||||| | ||||| ||||| |||||||||||||||| |||||||| |||||
Db 4920 CAGCGGACCCATTGTGTCGGGGAAAACAGTCTCTCCCGGCCCATCGGATGACCCCCAATTGGGCA 4979

Qy 4983 GGTCTGAAGGGCCCGAATCCTGTCCCACTCCTGCTCGAGGTGGGGCAATGATTTACCATCT 5042
          |||||||||||||||||||| |||||||||||||||| || || |||||||||||||||||
Db 4980 GGTCTGAAGGGCCCAAATCCTGTCCCACTCCTGCTCGAGGTGGGGCAATGATTTACCATCT 5039

Qy 5043 AAAGTTGGCCGGCCATCACATCGGACGACCTGGTCCGTAGGCTCCGGGGTTGCGGAGGGT 5102
          |||||||||||||||||||||||||||||| ||| |||||| ||||||||||||||||||
Db 5040 AAAGTTGGCCGGCCACCACCAGTGGACGACCTGGTCCGGAGCTCCGGTGTGCGGAGGGGT 5099

Qy 5103 TACGTCCGTGCGATGCGGACCCATCTTGATGGTGGCCTCGCTATTGGTGGGGGGCATG 5162
          ||||||||||| ||||| | | | |||||| || || |||| || | |||||||||
Db 5100 TACGTCCGCTGCGACGCTGGGCCGATCTTAGCTATGTATCGCGGGGGAATG 5159

Qy 5163 ATCTATGGCGTCATACACCGGGTCTCTCGTCGTGGTTACAGACTGGGATGTGAAGGGGGT 5222
          ||||| ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||
Db 5160 ATCTACGGCGTCATACACCGGGTCGCGGTGTGGTTGGTGCAGACTGGGATGTGAAGGGGGT 5219

Qy 5223 GGCAGCCCCCCCTTTATCGGCATGGAGACCACGCCCCAGCCCGTTGTCAGGTCCCC 5282
          |||||||||| |||||||||||||||||||||||||||||||||||||||| | |
Db 5220 GGCGCCCCCCCTTTATCGGCATGGAGACCACGCCCGGGTGTGAATCAGGTGTGGTTCCT 5279

Qy 5283 CCGGTAGACCATCGGCGGGGGGAGAGTCTGCGCCACCATCGCGCCAACAGTGACAGAT 5342
          ||||||||||||||||| ||| ||| |||||||||||||| | ||||||||||||||||
Db 5280 CCGGTAGACCATCGGCGGGGGTGAATCAGCAGCACCATCAGCACTATCATGACAGAT 5339

Qy 5343 GCGGTGGCGGCCATCCAGTTGGATTGCGATTGGTCAGTCAGTCATGACCCGTCCATCGGGGAA 5402
          |||||||| |||||||||||||||||||||||| | ||||| |||| |||||||||| | |||
Db 5340 GCGGTGGCGGCCATCCAGTTGGACTATCAGCAGCCGAGGCCTACAACGCGCCAAGTGGCTC 5399

Qy 5403 GTCGTGGCTGCTACACGGGACGCGGCGCGGCCGTCCCCACTGTTCAAGCACCACCAAGTGGCTT 5462
          || | ||||| |||| |||||||||||||||| ||||||||||||||| ||||||||||||
Db 5400 GTGTTGTCCTTGCTACACGGGGACGCGGCGCGGCCGTCCCCACTGTTCATGACTACTACCAAGTGGCTC 5459

Qy 5463 GCTGGCTGCTACACGGGAGACGCGGCGCGGCCGTCCCCACTGTTTCAATTGTTGCAAAGCTCTTC 5522
          |||||||||| ||| ||||||| |||| |||||| |||||| |||| || |||||||||| ||||
Db 5460 GCTGGCTGCTATACGGGAGACGCGGCGCGGCCGTCCCCACTGTATCCATTGTTGACAAGCTCTTC 5519

Qy 5523 GCCGGGGCTGGCGCGTGGTAGGCCATTGCCACAGTGTAATAGCTGCGCGGCCAGTGGCG 5582
          |||| ||||| |||||||| |||||| | ||||||| || ||| |||| ||||||||
Db 5520 GCCGAGGGGTTGGGCGGCTGTGGTGGCGGTGGATTGCTGCCACGGGCGTGGCCATGGGCG 5579

Qy 5583 GCCTATGGGGGTTCTAGGAGGCCGCCCTTCCATTGCTGCGTGCCGCGGCTTCATCGGGGTTG 5642
          ||||| ||||||| || |||||||||||||||||| ||| | |||||| ||||| || |||
Db 5580 GCCTACGGGGGTTCAAGGAGCCGCCCGTTGGCAGCGCCCGGCTTCCTCATCGATGGGGTTG 5639

Qy 5643 GGCGTCGGAGGCAACGCGCAAACCGCTAGCCTCCGTCGTCTCCTACTAGGGGCCGCTGGG 5702
          |||| || |||||||||||||||| || |||| ||| || ||||| | |||| ||| |
Db 5640 GGCGTTGGAGGCAACGCGCTCAGACGCGTCGTCTCGTTATTTGGGGGCTGCTGGA 5699

Qy 5703 ACCGGCCTCTGCAGACTCTGGGCTGTCGTGTGGGGCACGCCGTTCATGGGGAAGTGCT 5762
          ||| || ||| | |||||| ||||||||||||| || ||| |||||||||||| |||
Db 5700 ACCGGCCTTGGAGGCACTCGCTGGGGTCTGTGTGGGGCACTGGCCGTTCATGGGGGGGGGCC 5759

Qy 5763 AGGTCTCCCCTCCTTGGTCACCATTTTACTGGGGCGTGGGGGCTGGGAGGGCGTG 5822
          | ||||||||||||||||||||||| |||||| |||||| | |||||||||| |
Db 5760 AGTGTCTCCCCTCCTTGGTCACCATTTTATTGGGGCGTCGGAGGTTGGGAGGGTGTT 5819

Qy 5823 GTGAATGCGGCTAGCCTTGTCTTCGACTTATTGCGGGAAACTATCATCAGAAGATCTG 5882
          | || ||||||||||||||||||||| | |||||||||||||||||| ||||||||
Db 5820 GTCAACGCGGCGAGCCTAGTCTTCGACTTTCATCGGGGGAAACTTCATCAGAAGATCTG 5879

Qy 5883 TGGTATGCCATCCCAGTGCTAACCAGTCCGGGGGATCGCCCTTGCGGGGATCGCCCTCCGG 5942
          ||||||||| ||| | ||||| || || |||||||| |||| || ||||||| ||||||
Db 5880 TGGTATGCCATCCCGGTACTGACCAGCAGTCCGGGGGATCGCCCTTGCGGGGATCTCTCGG 5939

Qy 5943 TTGGTGTTGTGTACTCAGCTAACAACTCTGGCCACTTGGTTGACCGTCTGTGGTGTT 6002
          |||| ||| | || |||||||| || || |||||||||| || |||||||||||||||
Db 5940 TTGGTTTTGTGTATTCAGCTAACAACTCTGGCCACTTGGTTGACCGTCTGTGGTGTT 5999

Qy 6003 ACATTGCCAAGTTCCTCATGCATCCCTGACAGTTACTTTCAGCAGGCCGATTACTGTGAC 6062
          | ||| ||||| || |||||||| ||||||| | ||||||||||| | ||||||||||
Db 6000 ACGTTACCAAGGTCTTCATGTATCCCGGACAGTTACTTTCAGCAAGTTGACTATTGCGAC 6059

Qy 6063 AAGGTCTCAGCTGCTGCTCCGACGCTTGAGCCTCAACCTGGTTGCCCGTGGTCAAC 6122
          |||||||||||||||||| || |||||||| || |||||||| ||||| |||||||
Db 6060 AAGGTCTCAGCTGCTGCTCCGGCCTCCCGAGCCTCACCCGCACAGTTGCCCGTGGTCAAC 6119

Qy 6123 AGGGAGCCTAAGGTGGATGAGGTTCAGGTGGGTACGTCTGGGGACTTGTGGGAGATGGATC 6182
          ||||||||||||||||||||||||||| ||||| |||||| ||||||||||| ||||||
Db 6120 AGGGAGCCTAAGGTGGATGAGGTTCAGGTGGGTATGTCTGGGGAGTGGATGGATC 6179

Qy 6183 ATCGTCAAGTGCCGCATGGTGATGGTCCAGACTTCGGGCCGTTGCCCCGTGGTGTCATTA 6242
          ||||||||||| | ||||||||||| ||| |||| ||||||| || |||||||| |||
Db 6180 ATCGCCCAAGTGCCGCGTGTGTGTCATCAGGGGCCCTCGGTGTCGTGGGTGGTCACTA 6239

Qy 6243 CCCTTATGGCACTGCGGGGAGGGGTGTCCGGAGGAATGGTGTTGGACGGCCATGTTGAG 6302
          |||| ||| ||||| |||||| ||| ||||| ||||||||||| |||||||| |||
Db 6240 CCCTTGTGGCATTGCGGGGAGGGGTGGTCCGGGGAATGCTTGCTTGACGGTCATGTTGAG 6299

Qy 6303 AGTCGTTGTCTTTTGTGGTTGCGTGATCACCGGTGATGTTTGAATGGCAACTCAAAGAT 6362
          |||||| ||||| | || || || |||| ||||| || || ||||||| |||| |||||
Db 6300 AGTCGCTGTCCTGTGGCTGGCGTGGTCATCACTGGTGACGTTCTGAATGGGCAACTCAAAGAA 6359

Qy 6363 CCAGTTTACTCTACCAAGCTGTCGCAGGCATTATTGGAGCATTAGGGGACAGTCCCTGTGAACATG 6422
          ||||||||||||||| |||| ||||| |||| ||||||||| |||||||| |||||||||||||
Db 6360 CCAGTTTACTCTACCAAGCTGTTGCGCGTAGTCGGCACTATTGGATGGGGACTGTCCCTGTGAACATG 6419

Qy 6423 CTGGGCTATGGCATGGAGACACCCCGGAGGTGTGTGGGGAA 6482
          ||||||||||| |||| | | || ||||||||||||||
Db 6420 CTGGGTTACGGTGAAACCGCGGCTCTCCCGACACCCCGAAGGTGTGGTTACCATTAC 6479

Qy 6483 GGACGTCTGGGTGGGCTCAGGTGGTGCGCCAGCAAATCCTGTCGTGTTGTGATCAGGCGAACA 6542
          || |||||||||||||||||| |||||||||||||||| | | |||||| || ||| |||||
Db 6480 GGGACGTCTGGGTGGGCTGAGGTGGTGCGCCAGCAAATCCTATCGGCTGCTGCTGTGAGCCCTACTAC 6539

Qy 6543 TCCGCCTACAAACTGCTGCGCCGCAGGCCTACCGGCTACCACCAAGTGGCTCTATTAC 6602
          ||||| ||| |||||| | | |||||| |||| ||||| ||||||||||| |||| |
Db 6540 TCCGCCTATAAGCTGCTGCGCCGCAGGCCCAGCAAATCCTATCGGCTGCTGCTGTGAGCCCTACTAC 6599

Qy 6603 GTCGACGGGCATACCGGGTCTCATGGGACGCGGCGGCGCTGCCATGGTCTATGGC 6662
          ||||| ||| |||||||| |||||||||||||||||||||||| || || |||||
Db 6600 GTCGACGGGGCATTCCGGGTCTCATGGGACGCGGCGGACGCGGCGTCGTCCGCGCCATGGTCTATGGC 6659

Qy 6663 CCTGGGCAAAGTGTCACCATTGCCACCTACCCCTTCCGCATCAACTGCGCGCTT 6722
          |||||||||||||| |||| || |||||||||||||| ||||| || |||||
Db 6660 CCTGGGCAAAGTGTTACCATTGCCACCTACCCTTCCTCATCAACTGCGCGAGGCTC 6719

Qy 6723 AGGAAATGTGGCGCGCCCCTCTGGAGTGTCATCCGAGTGCTCATTGGACGGAGACT 6782
          |||| |||||| || || |||||||||||||| |||||||| |||| ||||| |||
Db 6720 AGGAATGTGGCACCCCTCTGGAGTGTTCATCCGAGTGTCCATTGGGACGGAGACT 6779

Qy 6783 GAAGACTCAGAACTGACTGAGGCCCGGCTGCTCCAGCCCTCAGGCTATC 6842
          ||||| |||||| |||| |||||||| |||| || ||| || ||||| |
Db 6780 GAAGACTCAGAACTGACTGAGGCCGATCTGCCGCCGCTGCTCTCCAAGCGATC 6839

Qy 6843 GAGAATGCTGCCGAGAATTCTTGAACCTCACATAGATGTCATCATGGAAGATTGCAGTACA 6902

Db 7920 AAGGCGGTGTTGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAGTTAAGGAG 7979
         |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Qy 7983 ATGCTCAAACTGTGGAATCAAAGAGACACCATGCGCCATCTGTGTGGACGCCACATGC 8042
         ||||||| || | ||||||||||||||| |||||||| |||| ||||||||||||| |||
Db 7980 ATGCTCAAGCTATGGGAGTCTAAGAAGACCCCCTTGCGCCATCTGTGTGGACGCCACCTGC 8039

Qy 8043 TTCGACAGTAGCATAACTGAAGAGGACGTGCGCGTTGGAGACAGAGCTTTATGCCCTGGCT 8102
         ||||||||||||||||||||||||||||||||| |||||||||||||||| || |||||||
Db 8040 TTCGACAGTAGCATAACTGAAGAGGACGTGCGCGTTGGAGACAGAGCTATACGCCTGGCC 8099

Qy 8103 TCAGACCATCCAGAATGGGTGCGTGCCCTGGGGAAATACTATGCCTCTGGCACAATGGTA 8162
         || ||||||||||||||||||||||||||||||| ||||||||||||||| || |||||
Db 8100 TCTGACCATCCAGAATGGGTGCGGGCACTTGGGAAATACTATGCCTCAGGCACCATGGTC 8159

Qy 8163 ACCCCCGAGGGGGTGCCAGTGGGTGAGAGTGTTAGATCCTCAGGGGTCTTGACCACC 8222
         |||| | ||||||||| |||||||||||||||| |||||| ||| |||||||| || |
Db 8160 ACCCCCGAGGGGGTGCCCGTGGGTGAGAGTATTGCAGATCCTCGGGGTGTCCTAACAACT 8219

Qy 8223 AGTGCGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCGCGCCTGTGAGAGGGTGGGG 8282
         || |||||||||||||||||||||||||||||||||||||| ||||||||||| |||||
Db 8220 AGCGCGCAACTGCTTGACCTGCTACATCAAGGTGAAAGCGCCTGTGAGAGAGGGTGGGG 8279

Qy 8283 CTGAAAAATGTCTCGCTCCTCATCGCTGGCGATGACTGTTTGATCATATGCGAACGGCCT 8342
         |||||||||||||||||||||||||||||||||||| |||||||||||||||| |||| |
Db 8280 CTGAAAAATGTCTCTCTTCTCATAGCCGGCGATGACTGCTTGATCATATGTGAGCGCCCA 8339

Qy 8343 GTGTCGCATCCTAGCGACGCCCTTTGGCAGAGCCCTGGCGAGCTACGGGTACGCATGCGAG 8402
         |||||||||| |||| ||||||||||||||||||||| |||||||| |||||||||||||
Db 8340 GTGTCGCACCCTAGCGACGCTTTGGGCAGAGCCCTAGCGAGCTATGGGTACGCGTGCGAG 8399

Qy 8403 CCTTCGTATCATGCATCACTGACATCACTGGCTAGCTGAGTGC 8462
         || | ||||||| ||||||||||||||||| |||||||||||||
Db 8400 CCCTCATATCATGCATCACTGACATCACTGGCTTGCTTGCTGAGTGC 8459

Qy 8463 AATGCAGATGGGAAACGCCATTCTTCCTGACCACGGACTTTCGGAGGCCCCTCCGCTCGC 8522
         |||||||||||||| ||||||| ||||||||||||||| ||||||||| ||||| |||| |
Db 8460 AATGCAGATGGGAAGCGCCATTCTTCCTGACCACGGACTTTCCGGAGGCCCGCTCCGCGC 8519

Qy 8523 ATGTCGAGCGAGTACAGTGACCCAATGCTTCGGCCACCAAGGTGTAT 8582
         |||||||||||| ||| |||||||||||||| |||||||| || ||| |
Db 8520 ATGTCGAGTGAGTATAGTGACCCGGATGCTTCGGCCATCCTCCTTTATCCT 8579

Qy 8583 TGGCATCCTATCACACGGTGGGTCATCATCCCTCACGTGCTCACCTGCGCTCCAAGTGCCCCT 8642
         ||| | ||||||| |||||||||||||||||||||||||| |||||| ||| |||||||||||
Db 8580 TGGCACCCCATCACACGGTGGGTCATCATCCCTCACGTGTGTCAACGTGGCCATTCAGGGGT 8639

Qy 8643 GGTGGCACACCGTCTGATCCTGTGTGGTGCCAAGGTACATGGGTACTACAAGTTTCCA 8702
         ||| || || ||||||||| |||||||| ||||||| |||||| |||| |||||||||||
Db 8640 GGAGGCACACCGTCTGATCCTGTGTGCCAAGGTGCATGGTGTAACTACTACAAGTTTCCA 8699

Qy 8703 CTGGACAAACTGCCTAACATCATGGGCGCCCTCCACGACCAGCGCGTTGAGGGTTACC 8762
         ||||||||||||||| |||||||||| || | |||||||||||||||||| ||||||||
Db 8700 CTGGACAAACTGCCTAACATCATCGGGCATCGTGCCCTCCACGACCAGCGCGTTGAGGGTTACC 8759

Qy 8763 GCAGACACAACTAAGACAAAAATGGAGGCTCGGCAAGGTGCTGAGCGACCTCAAGCTCCCT 8822
         |||||||||||| |||| ||||||||||||||||| ||||| |||||||| |||| |||||||
Db 8760 GCAGACACAACTAAAACAAAAGATGAGGCTCGGCAAGGTGCTGAGCGACCTCAAGCTCCCT 8819

Qy 8823 GGCCTAGCAGTCCACCGAAGAAGGCCAGGGCAGTTGCGAACACGATGCTCCGGTCCGCGC 8882
         ||||||||| |||||||| ||||||| |||||||||| ||||| |||||||||||| ||||
Db 8820 GGCCTAGCAGTCCACCGGAGAAGGCCGGGCGGGGCCATTGCGAACACGATGCTCCGCGC 8879

Qy 8883 GGTTGGGCTGCAGTTGGCTAGGGGCCTGTTGTGCGTCCAGGCCTGCAAGTGCCGTTACC 8942
         ||||||||||||| |||||||||||||||||| | |||||| ||| |||||||| ||||||
Db 8880 GGTTGGGCTGCAGTTGGCTGGCATCCAGGGGCTTGTTGTGCATCCAGGCTTTCCTCCCCCT 8939

Qy 8943 GAGATTGCTGTCGTATCCCGGGGTTCCCCCTTTCCCCCTATATGGGGTGGTTCAT 9002
         |||||||||||||| ||||| ||| ||| | | ||||| |||||||||||||| ||
Db 8940 GAGATTGCTGTCGTATCCCGGGGTTCCCCTCTCCCCCTATATGGGGTGGTGGTTACAT 8999

Qy 9003 CAATTGGATTCACAAGCCAGAAGTCGCTGGCGTGGTTCTTAGCCCTGCTC 9062
         |||||||||||||||||||||||||| |||||||||||| |||||||||||
Db 9000 CAATTGGATTCACAAGCCAGAAGTCGCTGGCGTGGTTCTTAGCCCTGCTC 9059

Db 6840 GAGAATGCTGCGAGGATTCTTGAACCGCACAATTGATGTCATCATGGAGGACTGCAGTACA 6899
         ||||||||||||||||||||||||||| | ||||||||||||||||||| ||||||||||
Qy 6903 CCTCTCTTGTGGAGTAGCCGAGATGCCTCTGTGGGGAGAAGACATACCCGCACT 6962
         ||||||||||||||||||||||||||||| ||||||| |||||| ||||| |||
Db 6900 CCTCTCTTGTGTAGTAGCCGAGATGCCTGTATGGGGAGAAGACATCCCCGTACT 6959

Qy 6963 CCATCGCCAGCACTTATCTCGGTTACTGACAGCCCAGATGAGAAGCACCCCGTCGGTG 7022
         ||||||||| |||||||||||||||| || ||||| ||||||||||||||||| ||||||
Db 6960 CCATCGCCAGCACTTATCTCGGTTACTGAGACAGCTCAGATGAGAAGCACCCCGTGGTG 7019

Qy 7023 TCTTCCTCGCAGGAGGATCACCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCGAG 7082
         || || ||||||||||||||||||| ||||| |||||||||||| | ||| |||||||||
Db 7020 TCTTCCTCGCAGGAGGATCACCCGTCCTCTCATCTGACTCATTCGAGGTGTCATCCAAGAGTCCGAG 7079

Qy 7083 ACAGCCGAAGGGGAGGAAAGCGTCTTCAACGTGGCTCTTCCGCTACTAAAAGCCTTGTTT 7142
         ||||||||||||||||||||||||||| ||||| |||| |||| || |||||| |||| ||
Db 7080 ACAGCCGAAGGGGAGGAAAGTGTCTTCAACGTGGCTCTTCCGTATTAAAAGCCTTATTT 7139

Qy 7143 CCACAGACGATCCCACAAGAAAGCTTACCCGTTAAGATGTCATGCTGTTGAGAAGAGC 7202
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Db 7140 CCACAGAGGACGACGGACCAGGAAGCTTACCGTTCGTGTCCTGCCTTGAAAAGAC 7199

Qy 7203 GTAACACGCTTCTTTCATTGGGATTGACGGTCGCAAGCGTCGTGTGTGAGATG 7262
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Db 7200 GTCACGCGCTTTTTCTCATTGGGTTGACGGTGCGATGTTGCTAGCCTGTGTGAGATG 7259

Qy 7263 GAAATCCAGAACCATACAGCCTATTGTGACAAGTGCGCACTCCGCTTGAATTGCAGGTT 7322
         ||||||||||||||||||||||| || |||||||||| ||||| |||||||||||||||||
Db 7260 GAAATCCAGAACCATACAGCTTATTGTGACCAGTGCGCACTCCGCTCCGCTTGAATTGCAGGTT 7319

Qy 7323 GGGTGCTTGGTGGGCAATGTTGGTGAGAAGAGTTGACAAGTGTGAGGCTAGGCAAGAG 7382
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Qy 7383 ACCTTGGCTTCCTCTCTCTTACATTTGGCTCTGCCTGGGTGCTGCCCACTGACGAGGCCACTCCGGCC 7442
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Qy 7503 GTCACCAACCGGCAACAATGTTGGGAGAAGAGTTGACAAGGTTACCTTCTGGCGTGCCCCT 7562
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Qy 7683 ATGGGCTGGGGATCTGGAAAGCTTATTCTGGGGAAGACCTGCGCGGGGAAGATGGCT 7742
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Db 7680 ATGGGCTGGGGATCTGGAAAGCTTGGAAAGCTCATCTTTGGGACCAGGCGGGGAAGATGGCC 7739

Qy 7743 GTCCATGACAGTCCAGGAGATACTTGAAAGGAGGACGCGCCAGTCCGTTTTACTCTTACTGTG 7802
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Qy 7923 AAGGCGGTGTTGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAGTTAGGGAG 7982
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Db 7920 AAGGCGGTGTTGGGGGGGCCTACGCCTTCCAGTACACCCCAAATCAGCGAGTTAAGGAG 7979

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NFIPPPRWLLLDFVFLLYLMKLAEARLVPLILLLWWVNQLAVLGLPAVEAAVAGI
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BASE COUNT     1694 a     2551 c     2998 g     2148 t      1 others
ORIGIN

Query Match
Best Local Similarity   84.9%;        Score 7979;   DB 14;   Length 9392;
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Matches 8515;  Conservative     1;  Mismatches   876;  Indels    1;  Gaps    1;
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Qy    3 ACGTGGGGGGTTGATCCCCCCCCCCCCGCACTGGGTCAAGCCCCATAAACCGACGCCT  62
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Qy  123 GTGGTGACAGGGTTGGTAGTCGTAAATCCCGTGCCTCGGCGGGCCGAGACCCGCGCACAGT 182
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Qy  243 GCTGGCCTACCGGTGTGAATAAGGGCCCACGACGTCGTCGGCCTCGTTAAACCGAGCCCGT 302
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Qy  303 CACCCACTGGGCAAACGACGCCCACGGTCACGTCGCCCTTCAATGTCTCTCTTG 352
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Qy 9123 ATACCGGAGGAGGTTCCCCGCCCTCCCCCCCAGGGGTCTCCCCGCTGGGTAAAAAGGG 9182
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Qy 9183 CCCGGCCTTCGGGAGGCATGGTGGTTACTAACCCCCTGGCCAGGTCAAAGCCTGATGGTGC 9242
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Qy 9243 TAATGCACTGCCACTTCGGTGGCGGTCGCTCGCTACCTTATAGCGTAATCCGTGACTACGGC 9302
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RESULT 11
HGU44402
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DEFINITION  Hepatitis G virus, complete genome.
ACCESSION   U44402
VERSION     U44402.1  GI:1167560
KEYWORDS    .
SOURCE      Hepatitis G virus
  ORGANISM  Hepatitis G virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            GBV-C/HGV group.
REFERENCE   1  (bases 1 to 9392)
  AUTHORS   Linnen,J., Wages,J., Zhang-Keck,Z.-Y., Fry,K.E., Krawczynski,K.,
            Alter,H., Koonin,E., Gallagher,M., Alter,M., Hadziyannis,S.,
            Karayiannis,P., Fung,K., Nakatsuji,Y., Shih,W.-K., Young,L.,
            Piatak,M.Jr., Hoover,C., Fernandez,J., Chen,S., Zou,J.-C.,
            Morris,T., Hyams,K.C., Ismay,S., Lifson,J.D., Hess,G.,
            Foung,S.K.H., Thomas,H., Bradley,D., Margolis,H. and Kim,J.P.
  TITLE     Molecular cloning and disease association of hepatitis G virus: a
            transfusion-transmissible agent
  JOURNAL   Science 271 (5248), 505-508 (1996)
  MEDLINE   96152370
REFERENCE   2  (bases 1 to 9392)
  AUTHORS   Linnen,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JAN-1996) Jeff Linnen, Genelabs Technologies, Inc.,
            505 Penobscot Dr., Redwood City, CA 94063, USA
COMMENT     Corresponding author for this submission is Jungsuh P. Kim.
FEATURES             Location/Qualifiers
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                     /db_xref="GI:1167561"
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                     RIVMVFLLVTMAGMSQGAPASVLGSRPFDYGLTWQTCSCRANGSRFSTGEKVWDRGNV
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Nucleotide sequence alignment (Qy vs. Db). Left-column alignment blocks (positions ~363–1502) and right-column alignment blocks (positions ~1440–2582).

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Db   2520 CGCACCTCAGTGCTCGGGGCCGAGTTCTGCTTCGATGCTACATTCGAGTGGACACTTCG 2579

Qy   2583 GTGTTGGGCTGGCTGGGTGGCCAGCGTCGGTGGCCATAGCGTCCTGAGCTCAATG 2642
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Db   2580 GTGTTGGGCTGGGTGGCCAGCGTGGGCCATTGCGCTCCTGAGCTCCGATG 2639

Qy   2643 AGCGCAGGGGGGTGGAAGCACAAAGCCGTGAGTCTATAGGACGTGGTGTAAAGGGTACCAG 2702
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Qy   2703 GCTGTGGCCAGAGGGTGGTGCGGAGGGCGTGGAGCCCCTCGGGGAGGGCGCGTCTACCAAGCTTCTG 2762
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Qy   2823 GCCTTGTCCTCCTCTTCGGCCTCTGTTCGACCCACTGGGCCCTGGACTGGAGGAGCTCCTG 2882
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Qy   3063 TTGGAGCCCTTGCATTCACTTACTAGGACGGACTGTCGCATCATCAGATGCCGCGAGGACC 3122
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Qy   3363 ATGGGCACATGTCGAATGGCCTGCTTGTTCACAACTTTCCATGGGGCTTCATCCCGGAACC 3422
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Db   3360 ATGGGAACATGTGACGTTGAACGGCCTGCTTGTTCACAACCTTTCCATGGGGCTTCATCCCGGAACC 3419

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Db   3840 GGAGCGGGAAAGAGCACTCCGTTGGAGTACGGATACGGCGATAACATGGGCCACAAGGTCTTA 3899

Qy   3903 ATCTTGAACCCGTCGGTAGCTACCGTGAGGGGCCCATACATGAGCGGCTGGCG 3962
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Qy   3963 GGGAAACACCCCAGTATTTACTGTGCGGCCATGACACCACTGCTTCACAAGGATCACTGAC 4022
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Qy   4503 GTCACCGATTGTGGGTTAGTGGTTGAGGGTGCGGAGGTCGTCGAGGTGACCCTTGATCCCACCATT 4562
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Db   4500 GTCACCGACTGTGTCGTGGATTAGTGGTTGAGGGTGAGGTCGTCGAGGTGACCCTTGATCCCACCATT 4559

Qy   4563 ACCATCTCCCTGCCACACGGTGCCCCGCGTCCGCCTCAGCCGGACGGAGGACGACGC 4622
          |||||||||||||||||||||||||||||
Db   4560 ACCATCTCCCTGCCGCACAGTGCCGCCTGCGTCGGCTGAGCAAAGACGAGGAGCGACGC 4619

Qy   4623 ACGGGTAGGGCAGGTCTGGGGGACGCTCTGGGGTCGGCGGCAAGGCCCCCTGCTGGT 4682
          ||||| ||||||||||||||||||||||||||
Db   4620 ACGGGTAGGGCAGGTCTGCGACGGCTGCTACTACCGGGGTGGGCAAAGCCCCCTGCGGGGT 4679

Qy   4683 GTGGTGCGCTCAGGTGCGCTCGTCTGCTTCCGTGTCTGCTGTTCACGGTACGGAATG 4742
          |||||||||||||||||||||||||||||
Db   4680 GTGGTGCGCTCAGTGCGCTCGTCTGCTTCCGTGTCTGCTGTTCGGAGTGACCTGGTACGGAATG 4739
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Qy  4743  GAACCTGACCTGACAGCAAACCTACTGAGACTTTACGACAACTGCCCTTACACCCGCAGCC  4802
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  4740  GAACCTGACCTGACAGCTAACCTACTGAGACTTTACGACGCTGCCCTTACACCCGCAGCC  4799

Qy  4803  GTCGCAGCTGACATTGGGAAGCCGCGGTGTTCTTTTCGGGGCTTGCCCCGTTGAGGATG  4862
          |||||||||||| |||||||||||||||| || | ||||||||||||||||||||||||
Db  4800  GTCGCGGCTGATATCGGAGAGAGACCCGGCGCGGGTTCTTGGGGCTCGCCCCATTGAGGATG  4859

Qy  4863  CATCCCGATGTTAGCTGGCCAAAAGTTCGCGCGGTCAACTGGCCTTCCTTCGTGTGGGTGTT  4922
          || |||||||| |||||||||||||||||||||||| | |||||||||||||| |||||
Db  4860  CACCCTGATGTCAGCTGGCCAAAAGTTCGCGCGGTCAACTGGCCTTCCTTCGTGTGGGTGTT  4919

Qy  4923  CAGCGGACCATGTGCCGGGAAACACTGTCTCCGGCCATCGATGACCCCAGTGGGCA  4982
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||| |||||
Db  4920  CAGCGGACCATGTGTCGGGAAACACTGTCTCCCGGCCATCGATGACCCCAGTGGGCA  4979

Qy  4983  GGTCTGAAGGGCCCGAATCCTGTCCCACTCCTGCTGTGAGGTGGGCCAATGATTTACCATCT  5042
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  4980  GGTCTGAAGGGCCCAAATCCTGTCCCACTCCTGCTGTGAGGTGGGCAATGATTTACCATCT  5039

Qy  5043  AAAGTTGCCCGGCCACCATCACATCTGACGACCTGGTCCGTAGGCTGGCGGCCTTCGGGGGTT  5102
          |||||||||||||||||||||| || ||||||||||||| | ||||| |||||||||||
Db  5040  AAAGTTGCCCGGCCACCATAGTGACGACCTGGTCCGGGGTATCTGGGAGTCGGGGGT  5099

Qy  5103  TACGTCCGTCCGATCGGGACCATCTTGATGGTGGGCGCTATTGCGGCATGGCATG  5162
          |||||||||||||||||| | || |||||||||||| |||||||||||||||||
Db  5100  TACGTCCGTCCGCTGCGACGGTCGGGGCCGATCTTGATGCTGTCGCCGATCTTGATGCTGTCATGT  5159

Qy  5163  ATCTATGCGTCATACACCCGGGTCTCTCGTTGGTGGTTACAGACTGGGATGTGAAGGGGGT  5222
          ||||||||||||||| ||||||| || ||||||||| |||||||||||||||||||||||
Db  5160  ATCTACGCGTCATACACCCGGGTCTCGCGCTGGTGGTGACAGACTGGGATGTGAAGGGGGT  5219

Qy  5223  GGCAGCCCCCTTTATCGGCATGGAGACCAGGCCACGCCCCAGCCGGTGTGTCAGGTCCCC  5282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  5220  GGCGCCCCCTTTATCGGCATGGAGACCAGGCCACGCCCCAGCCGGTGGTGCAGGTGCAGGTTCCT  5279

Qy  5283  CCGGTAGACCATGGCCGGCGGGGAGTCTGCCGGTGGCCAACAGTGACAGAT  5342
          |||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  5280  CCGGTAGACCATGGCCGGCGGGGGAGTCTGCCGGTGAATCAGCACAGTGACAGAT  5339

Qy  5343  GCGGTGGCGCGGCCATCCAGTTGGTGATTGGTCAGTCAGTCGATGGCGGAA  5402
          |||||||||||||||| |  ||||||||||||||| |||||||||||||||
Db  5340  GCGGTGGCGCGGCCATCCAGTTGGTGATTGCCACAGTTGTAATAGCTCGTCGATCCGAGAA  5399

Qy  5403  GTCGTGTCCTTGGCCCCAGGCTAAGACGGCCGAGGCCGACTACCAGCTGGCTT  5462
          ||||| |||||||||||||||||||||||||||| ||| |||||||||||
Db  5400  GTCGTGTCCTTGGCCTCAGGCTAAGACGGCCGAGCCGACTACCAGCAACGGCCAAGTGGCTC  5459

Qy  5463  GCTGGCTGCTACACGGGGACGCGGCCGTCCGCTTAGCCTCCATTGGGCCCTCATGGGGGCCTT  5522
          ||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db  5460  GCTGGCTGCTACACGGGGACGCGGCCGTCCGCTTAGCCTCCATTGGGGGCTTGCCCGCTGGC  5519

Qy  5523  GCCGGGGGCGGCGGCGGGCGGTGGGTAGCCCGGCTGCCACAGTGTAATAGCTCGGCCAGTGGCG  5582
          ||||||| |||||||||||||||| ||||||||||||||| |||| |||||||||||||
Db  5520  GCCGGGGGAGGAGGTGGGCGGTGTGGGTGCCCGGCTGCCACAGTCGCCACAGCTGATGGCG  5579

Qy  5583  GCCTATGGGGCTTCAGGAGCCCTCCATTGGCCTCCCATGGGGCTTGACGGCCGCTT  5642
          ||||||||||| ||||||||||||||| |||||||||| |||||||||||||||
Db  5580  GCCTACGGGGGCTTCAAGGAGCCCTCCATTGGCCTCTGATGGGGTTGACGGGCTC  5639

Qy  5643  GCTGGCTGCTAGCCTTAGCCTCCCGCGTAGCCTCCTAGTGGGGCCTATGGCCCCTGGG  5702
          |||||| ||||||||||| |||||| ||||||| ||||||||||| | |||||||
Db  5640  GCTGGCTGTTGGAGGCAACGCTCAGGCGGGGCGTCTCCTATTGGGGGCTGCTGGA  5699

Qy  5703  ACCGCTCTGGGCACCGCCCTGTCGTGGGTTAACCATGCGGGCCGTTCATGGGAAGTGCT  5762
          |||||||||| |||||| |||| | |||||||||| | |||||||||||||| |||||||
Db  5700  ACCGCTGGGCCACTCCTCTGTCGTGGGTTGCGTTGCTGACCAGTGGCCGTTGCTGGGGGCC  5759

Qy  5763  AGGTCTCCCCCTCTTGCTTTACTGGGGCGTAGGGGCGGGTG  5822
          ||||| ||||||||| |||||||| |||||||||||||||| ||
Db  5760  AGTGTCTCCCCCTTGGTCACCATTTATTGGGGGCTGCGAGGTTGGGAGGGTGTT  5819

Qy  5823  GTGAATGCGGCTAGCCTTGTCTTCTTGCGACTTATGCGGGGAAACTATCATCAGAGAGATCTG  5882
          ||||||||||||||||||||||||||||||||||||||||| ||
Db  5820  GTCAACGCGGCGCAGCCTGACTTCAGTCTTTGACTTCATCGGGGATGCCCTCGGG  5879
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Qy  5883  TGGTATGCCATCCCAGTGCTAACCAGTCGGTGCCCGTTGCCCCGTTGAGGATG  5942
          ||||||||||||||||||||| || ||||||||||||||||||||| |||||
Db  5880  TGGTATGCCATCCCGTGCTACTGACCAGTCCAGCCCGTTGCGGGATCGCTCTCGGG  5939

Qy  5943  TTGGTTGGTTGTACTCAGCTAGCCTGGCACTCAGTTACTTCAGCAGGTTACTTCAGCAGGTTACTACTGTGAC  6002
          |||||| || ||| | |||||||||||||||| ||||||||||||||||
Db  5940  TTGGTTTGTATTCAGCTAGCCTGGCACTCAGTTACTTCAGCAGGTTACTTCGACTATTGCGAC  5999

Qy  6003  ACATTGCCAAGTCCTCATGCATCCCTGACAGTTACTTTCAGCAGGTTACTACTGTGAC  6062
          || |||||||||||||| || |||||||||||||||||||||||| |||||||
Db  6000  ACGTTACCAAGGTCTTCATGTATCCCGACAGTTACTTTCAGCAAGTTACTATTGCCAC  6059

Qy  6063  AAGGTCTCAGCGTGTCGCGACGCTTGAGCCTGGGGCTCACTGCACCGTGGTTGCCCTGGTCAAC  6122
          |||||||||||||||||||||||||| | |||||||||||||||||||||||||
Db  6060  AAGGTCTCAGCGTGTCGCGACGCTGAGCCCTGGGTATCTGGGAGTCGGGGTGCGGTCAAC  6119

Qy  6123  AGGGAGCCTAAGGTTCAGGTGGATGAGGTCCGGGACTCTGTGGGACTGTGTGGGAGTGATC  6182
          |||||||||||||||| |||||||||||||||||||||| |||||||||||||||||
Db  6120  AGGGAGCCTAAGGTTCAGGTGGATGAGGTACAGCGGTATCTCGGGGAGTCGGGGAGTGATC  6179

Qy  6183  ATGCGGTCAAGTGCGCATGGATGGTGGTCCGGAGAATGGTTCTTGTTGGACGGCCATGTCATTA  6242
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  6180  ATGCGGCCAAGTGCGCATGGACGTCATGGCCCAGATCAGGCCCCTCGCCCCGTGTGTCACTA  6239

Qy  6243  CCCTTATGGCACTGCGGGGAGGGGTGGTCCGGAGAATGGTTGTTGACGGCCATGTTGAG  6302
          ||||| |||||||| ||||||||||||||| || || ||||||||||||||||||||||
Db  6240  CCCTTGTGGCCATTGCGGGGAGGGGTGTGCCGTGCCGATCGGGGAATGGTTGCTTGACGGTTCATGTTGAG  6299

Qy  6303  AGTCGTTGTCTTTGTGTTGCGTGATCACCCGTGATGTTTTTGAATGGCCAACTCAAAGAT  6362
          ||||||||||||||||||||||||||||||||||| | |||||||||||||||||||
Db  6300  AGTCGCTTGTCGTCTCGATCCGTGATCAGTCACTGTCTGAATGGGGTCTCGAATGGCAACTCAAAGAA  6359

Qy  6363  CCAGTTTACTCTACCAAGCTGTGCAGCATTATTGGATGGGACAGTCCCTGTGAACATG  6422
          |||||||||||||||||||||| ||||||||| ||||||||||||| |||||||||
Db  6360  CCAGTTTACTCTACCAAGCTGTGCCGCACTGTCTATCGGCTGTCCCTGAACATG  6419

Qy  6423  CTGGGCTATGGCGAGACGTCGCCCTTGCTCGCGCCTCAGACACCCGAAGGTGGTACCATTC  6482
          ||| ||||||| || || |||||||| |||| | |||| ||||||||| ||| |||
Db  6420  CTGGGCTACGGTGAAACGTCGGCCTCTCCTCCCGAAGCGTTGTGCCCTTCGCCCCG  6479

Qy  6483  GGGACGTCTGGGCTGGGTGAGGTGGTGGTTCGATCAGGGGACCCTACCCAGTTGATCAGGCCGAACA  6542
          ||||||||||||||||| |||||||||||| || |||||||||||||||| || ||| |||||
Db  6480  GGGACGTCTGGGCTGGGTGAGGTGGTGCTGGGGACCTACCCACGTGGTGTAATCAGGAGGACC  6539

Qy  6543  TCCGCCTACAAAACTGCTGCGCGCCAGCAAATCCTGTCGCGCTGCTGTTGCTGAGCCCTATTAC  6602
          ||||||||| |  |||||| ||||||||||| |||| ||||| |||| ||| ||| || ||
Db  6540  TCCGCCTATAGCGGCCCGTTCCGCAGCAAATCCTAGTGTCTGTGTGTAGCCCTACTAC  6599

Qy  6603  GTCGACGGCATACCGGTCTCATGGGACGCCTCATGGCCATAGTAGCTGCGCGCCGCTCTATGGCC  6662
          ||||||||||| |||| ||||||||||||||||| |||||||||||||||||||||||| |||
Db  6600  GTCGACGGCATTCCGGTCTCATGGGACGCGATCGCCTGCGCCCGCCGCCCATGGTCTATGGC  6659

Qy  6663  CCTGGCAAAGTGTCACCATTGACGGGGAACGCTACACCCCTTCCGCATCAACTGCCGCTT  6722
          |||||||||| |||||||||||||| | | |||| || |||||||| |||| |||||||||
Db  6660  CCTGGCAAAGTGTTACCATTGACGGGGAGGCGCTACACCCTTGCCCTCATCAACTGAGGCTC  6719

Qy  6723  AGGAATGTGGCCGCCCCTGAGGTGTCATCCGAGGTGTCCATTGACATTGGGGACGGAGACT  6782
          |||||| ||| || ||| ||||| || ||||||||| |||||| ||||||||||||||||
Db  6720  AGGAATGTGGCACGCCCCTCGAGGTGTCCATTGACATTGGGGACGGAGACT  6779

Qy  6783  GAAGACTCAGAACTGACTGAGGCCGACCTGCCGCCGCTTCAGGCTATC  6842
          |||||||| |||||| ||||||| || ||| ||||| |||||||| |
Db  6780  GAAGACTCAGAACTGACTGAGGCGATCGCCGCTGCTTCTCCAAGCGATC  6839

Qy  6843  GAGAATGCTGCCGAGAATTCTTCACATAGATGTCATCATCGAAGATTGCAGTACA  6902
          |||||||||| |||||| || ||| || || || || |||| |||||||| |||
Db  6840  GAGAATGCTGCCGAGGATTCTTGAACCCACATTGATCGTCATGATGGGACTGCAGTACA  6899

Qy  6903  CCCTCTCTTTGTGGGAGTAGCCGAGAATGCCGAGAGATGCCGTGTGGGGAGAACATACCCCGCCACT  6962
          ||||||| | ||||||||||||||||||||||||| |||||||||||| ||||| ||
Db  6900  ...
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Db  6900  CCCTCTCTTTGGTAGTAGCCGAGAGATGCCTGTATGGGAGAAGACATCCCCGTACT  6959

Qy  6963  CCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCCCAGATGAGAAGACCCGCGGTG  7022
          |||||||||||||| |||| |||||||||||||||||||||||  |||||||||||||
Db  6960  CCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCTCAGATGAGAAGACCCGGCGGTG  7019

Qy  7023  TCTTCCTCGCAGGAGGATACCCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCGAG  7082
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Db  7020  TCCTCCTCGCAGGAGGATACCCCGTCTCTGACTCATTCGAGGTCATCCAAGAGTCCGAG  7079

Qy  7083  ACAGCCGAAGGGGAGGAAAGCGTCTTCAACGTGGCTCTTTCCGTACTAAAAGCCTTGTTT  7142
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Db  7080  ACAGCCGAAGGGGAGGAAAGCGTCTTCAACGTGGCTCTTTCCGTATTAAAAGCCTTATTT  7139

Qy  7143  CCACAGGCGATGCCAAGAGAAGCTTACCGTTAAGATGTCATGCTGTGTTGAAGAAGAGC  7202
          |||||||||||||| ||||||||||||||||||||||||||||||| |||||||||||
Db  7140  CCACAGAGCGACGCGCACCAGGAAGCTTACCGTTCAAGATGTCGTGCTGCTTGAAAAGAGC  7199

Qy  7203  GTAACACGCTTCTTTTCATTGGATTGACGGTCGCTGACGTGGCAAGCCTGTGTGAGATG  7262
          ||| |||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  7200  GTCACGCGCTTTTTCATTGGGATTGGCGTGGCTGACGTGGCTAGCCTGTGTGAGATG  7259

Qy  7263  GAAATCCAGAACCATACAGCCTATTGTGACAAGGTCCGCACTCCGCTTGAATTGCAGGTT  7322
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Db  7260  GAAATCCAGAACCATACAGCCTATTGTGACAAGGTGCGCACTCCGCTTGAATTGCAGGTT  7319

Qy  7323  GGGTGCTTGGTTGGGCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGCTGTAGGCAAGAG  7382
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7320  GGGTGCTTGGTTGGGCAATGAACTTACCTTTGAATGTGACAAGTGTGAGGCTGTAGGCAAGAG  7379

Qy  7383  ACCTTGGCTTCCTTCTTGTGTTGGTCTGGGGTGCCACTGACGAGGGCCACTCCCGGCC  7442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7380  ACCTTGGCTTCCTTCTTGTGTTGGTCTGGGGTGCCACTGACGAGGGCCACTCCCGGCC  7439

Qy  7443  AAGCCCCTGTGGTGAGGCCGGTTGCCGTGTGCTGGGCCGACACCACCAAGGTGTAT  7502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7440  AAGCCCTCCGTGTGGTGAGGCCGTGGCCGTGTCTTGTTGTAGTGGCCGACACTACTAAGGTGTAT  7499

Qy  7503  GTCACCAACCCGGACAATGTTGGGAGAAGATGTGACCAAGGTTACCTTCTGGCCTGCCCCT  7562
          |||||||||| |||||||||||||||| ||||||||||||||||||||||||||||||||
Db  7500  GTTACCAATCCAGACAATGTGGGACCAGGTGGGACCAAGGTGACCTTCTGGCCTGCTCCT  7559

Qy  7563  AGGGTTCATGACAAATTCCTCGGACTCCATAGAGCGCGCTAAGAGGCGCACTCAAGCC  7622
          ||||||||||||||| ||||||||||||||||||| ||||||||||||||||||||||
Db  7560  AGGGTTCATGATAAGTACCTCGGACTCTATTGAGCGCGTCTAAGAGGGCCGTCAAGCC  7619

Qy  7623  TGCCTAAGCATGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACCATGCTGCC  7682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7620  TGCCTAAGCATGGTTACACTTATGAGGAGGCAATAAGGACTGTAAGGCCACCATGCTGCC  7679

Qy  7683  ATGGGCTGGGGATCTAAGGTGTCGGTCAAGAGATGGGCT  7742
          ||||||||||||||||||||||||||||||||||||||
Db  7680  ATGGGCTGGGGATCTAAGGTGTCGGTTAAGGACTTAGCACCCCGCGGGGAAGATGGCC  7739

Qy  7743  GTCCATGACCGGCTCCAGGAGATACTTGAAGGGACGCAGCTCCCCTTTACTCTTACTGTG  7802
          ||||||||||||||||||||||| ||||||||||||||||||||||| || ||||||||
Db  7740  GTCCATGACCGGCTTCCAGGATAGCTCATCTTGGGACACCCCGTCCCCTTTACTCTTACTGTG  7799

Qy  7803  AAAAGGAAGTGTTCTTCAAAGACCGAAAGAAGGAAGAAGGCCCCGCCCCGCCTCATTGTTTC  7862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7800  AAAAGGAAGTGTTCTTCAAAGACCGAAAGAAGGAGGAAGGCCCCGCCCCGCCTCATTGTTTC  7859

Qy  7863  CCCCCTGGACTTCGGAGATAGCTGAAAAGCTTATTCTGGGAGACCTGGACGGGTAGCC  7922
          |||||||||||| || ||||||||||||| ||||||||||||||||||||||||||||
Db  7860  CCCCCTCGGACTTCGGGATAGCTGAAAAGCTCATCTTGGGAGACCCCGGGTAGCC  7919

Qy  7923  AAGGCGTTGTTCGGGGGGCCTTCAGTACACCCCAAATCAGCGAATTAGGGAG  7982
          |||||||||||||||||||||| |||||||||||| |||| |||||||||
Db  7920  AAGGCCGTGTTCGGGGGGGCCTTCCAGTACACCCCAAATCAGCGAGTTAAGGAG  7979

Qy  7983  ATGCTCAAAATGTGGGAATCAAAGAAGACACAGCGCCATCTGTGTGGACGGCCACATGC  8042
          |||| |||||| | |||||||||||||||||||||||||||||||||||||||| ||
Db  7980  ATGCTCAAGCTATGGGAGTCTAAGAGAGACCCCGTGTGTGGACGGCCACCTTGC  8039
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Qy  8043  TTCGACAGTAGCATAACTGAAGAGGACGTGGCGTGGAGACAGAGCTTTATGCCCTGGCT  8102
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Db  8040  TTCGACAGTAGCATAACTGAAGAGGACGTGGCTTGGAGACAGAGCTATACGCCTCTGGCC  8099

Qy  8103  TCAGACCATCCAGAATGGGTGCGTGCGTCCCTGGGAAATACTATGCCTCTGGCACAAATGGTA  8162
          | ||||||||||||||||||||||| ||||||| |||||||||||||||||| ||| |||
Db  8100  TCTGACCATCCAGAATGGGTGCGCGCCACTTGGGAAATACTATGCCTCTTGAGCGCACCATGGTC  8159

Qy  8163  ACCCCGAGGGGTGCCAGTGGGTGAGAGTATTGTAGATCCTCAGGGGTCTTGACCACC  8222
          |||| || ||||||||||||||||||||||||| ||| |||||||| ||||||
Db  8160  ACCCCGAAGGGGTGCCCGTCGGTGAGAGTATTGCAGATCCTCGGGGTCCTAACAACT  8219

Qy  8223  AGTGGCGCAACTGCTTGACTTGCTATATCAAGGTGAAAGCCGCCTGTGAGAGGGTGGGG  8282
          || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8220  AGCCGGCAGCAACTGCTTGACCTGCTACATCCAAGGTGAAAGCTGCCTGTGAGAGTGGGG  8279

Qy  8283  CTGAAAAATGTCTCGCTCCTCATCATCGCTGGCGATGACTGCTGTTGATCATATGCGAACGGCCT  8342
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||||
Db  8280  CTGAAAAATGTCTCGCTCCTCATAGCCGGCGATGACTGCTGTTGATCATATGTGAGGCGGCCA  8339

Qy  8343  GTGTGCGATCCTAGCGACGCGTTTGGGCAGAGCCCTGGCAGAGCCGGGTACGCATGCGAG  8402
          |||||| || ||||| |||||||||||||||| ||||||| |||||||||||| |||||
Db  8340  GTGTGCGACCCAAGCGACGCGTTTGGGCAGAGCCCTAGCGAGTATGGGTACGCCTGCGAG  8399

Qy  8403  CCTTCGTATCATCACTGGACACGGCCCCCCTTCTCGCTCCTGACCACGGACCTTCCGGAGTGC  8462
          | | |||| ||| |||||||||||| ||||| ||||| ||||||||||||||||||||||||
Db  8400  CCCTCATATCATCATGCACATCATGGCACGCGCCCTCTGCGCTCGCTGCCCACTGGCTGCTGGAGTGC  8459

Qy  8463  AATGCAGATGGGAAAGCCATTCTTCCTGACACGGACGACTTTCCGGAGGGCCCCGCTCGCC  8522
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  8460  AATGCAGATGGGAAAGCCATTTCTTCCTGACACGGACGACTTCTTCCGGAGGGCCGCTCGCC  8519

Qy  8523  ATGTCGAGCGAGTACAGTGACCCAATGCTTCGGCCCATCGGTTACATCCTCCTATACCCT  8582
          ||||||||||||||||||| ||||||||||||||||||||||| |||| || |||||||
Db  8520  ATGTCGAGTGAGTATAGTGACCCAATCATCATCGGCCCATGGGTTACATCCTCCTTTATCCT  8579

Qy  8583  TGGCATCCTATCACACGGTGGGTCATCATCCCGCTCACGTGCTCACGTTTAGGGGT  8642
          | |||| ||||||||||||||||| ||||||||| |||||||||||||||| ||||
Db  8580  TGGCACCCATCACACGGTGGGTCATCATCCCATGTCTCAACGTCGCCATTCAGGGGT  8639

Qy  8643  GGTGGCCACCGTCTGATCCTGTGTGCCAGTGACATGGTACATGGTAATTACACAAGTTCCA  8702
          | ||||||||| |||||| ||||||||||||| ||||| ||||||||||||||||||||||
Db  8640  GGAGGCCACACCGTCTGATCCTGTTGGTGCATGGTACATGGTAACTACTACAAGTTTCCA  8699

Qy  8703  CTGGACAAACTGCCTAACATCATCCGTGCCCTCACGGACTGTAAGCCACCATGCTGCC  8762
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Db  8700  CTGGACAAACTGCCTAACATCATCCGTGCCCTCACGACCCATAAGGACCTTGCTGGGTACC  8759

Qy  8763  GCAGACAACTAAGACAAAAATGAGGAGCGTGACGACTCAAGCTCCCT  8822
          |||||||||||||||||||||||||||||||||||||| ||||||||
Db  8760  GCAGACACAACTAAACAACAAAGATGAGGAGCGTGAAGGTTCTGAGCGACCTCAAGCTCCCT  8819

Qy  8823  GGCCTAGCAGTCCACCGGAAGAAAGGCCGCGGCATTGCAACCGCGTATCCTTCCGCTCCGCGC  8882
          |||||||||| ||||||| |||||||||| ||||||  |||||||| ||||||||||||
Db  8820  GGCTTAGCAGTTCCACCGGGAACCGGGGCGTTGCAAACCACGCCGTTGCGAACCCATGCTCCGCGCC  8879

Qy  8883  GGTTGGGCTGAGTTGGCTAGGGGTGGGCGTGTTGTGGGGCTTCCCCCTCCG  8942
          |||||||||||||||||||||||||| |||||||||||| |||||||||||
Db  8880  GGTTGGGCTGAGTTGGCTGGCATCCCGAGTTGTGTGGGGCCTTCCTCCTCCCCCT  8939

Qy  8943  GAGATTGCTGGTATCCCGGGGGTTTCCCCCTTTCCCTCTCCGCGGTTCAT  9002
          |||||| |||||||||||||||| ||||||||||||||||| ||||||||
Db  8940  GAGATTGCTGGTATCCCGGGGGTTTCCCCTCTCCCTATATGGGGTGTACAT  8999

Qy  9003  CAATTGGATTTCACAAGCCAGAGAGTCCGGAATTAGGGAGCCTGCTCG  9062
          |||||||||||||||||||||| |||||||||||||||||| |||||||
Db  9000  CAATTGGATTTCACAAGCCAGAGAGTCCTGGCGGTTCTTAGCCCTGCTCG  9059

Qy  9063  ATGCTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGGCGCCACATGCGACTGATC  9122
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  9060  ATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTTGCGGTGAAGGTCTGGTGACTGATC  9119
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BASE COUNT     1665 a     2582 c     2992 g     2112 t
ORIGIN

Query Match              84.5%;  Score 7936.8;  DB 14;  Length 9351;
Best Local Similarity   90.6%;  Pred. No. 0;
Matches 8474;  Conservative    0;  Mismatches 877;  Indels    1;  Gaps    1;

Qy     23  CCCCCCGGCACTGGGTGCAAGCCCCATAAACCGACGCCTATCTAAGTAGACGCAATGAC     82
           |||||||||||||||||||||||||| |||||||||||||||| |||||||||||||||
Db      1  CCCCCCGGCACTGGGTGCAAGCCCCAGAAACCGACGCCTATCTAGTAGACGCAATGAC     60

Qy     83  TCGGGGCCGACTCGGCGACCGGCACCGGCCAAAAGGTGGTGATGGGTGGTGACAGGGTTGGTAGG    142
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  TCGGGGCCGACTCGGCGACCGGCACCGGCCAAAAGGTGGTGATGGGTGGTGACAGGGTTGGTAGG    120

Qy    143  TCGTAAATCCCGGTCATCCTGGTAGCCACTATAGGTGGGTCTTAAGAGAGAGGTCAAGACT    202
           ||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||| |
Db    121  TCGTAAATCCCGGTCACCTTGGTAGCCACTATAGGTGGGTCTTAAGAGAGAGGTTAAGATT    180

Qy    203  CCTCTTGTGCCGCGGAGACCGGCACGTCGCCGAGTGCTGCCCTACCGGTGTGAA    262
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||
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Qy    263  TAAGGGCCGACGTCAGGCTCGTCGTTAAACCGACCGAGCCCGTCACCCACCTGGCAAACGAC    322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TAAGGGCCGACGTCAGGCTCGTCGTTAAACCGACCGAGCCCGTCACCCACCTGGCAAACGAC    300

Qy    323  GCCCACGTACGGTCCACGTCGCCCTTCAATGTCTCCTTGACCAATAGGTTATCCGGCG    382
           |||||||||||||||||||||||||||||| |||| |||| ||||||||||| ||||||
Db    301  GCCCACGTACGGTCCACGTCGCCCTTCAATGCCCTTCTTGGCCAATAGGTTAACCGGCG    360

Qy    383  AGTTGACAAGGACCAGTGGGGCCGGGGTTATGGGAAGGACCCCAAACCCTGCCCTTC    442
           ||||| ||||||||||||||||||||||  ||| || |||||| ||| |||||||||||
Db    361  AGTTGGCAAGGACCAGTGGGGCCGGGGGCT-TGGAGAGGACTCCAAGTCCTCAAGTCCTGCCCTTC    419
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Qy   9123  ATCACTGGAGGAGGTTCCGCCGCCTCCCGCGCCCCCAGGGGTCTCCCGCTGGGTAAAAGGG   9182
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Db   9120  ATCACCGGAGGAGGTTCCGCCGCCTCCCGCGCCCCCAGGGGTCTCCCGCTGGGTAAAAGGG   9179

Qy   9183  CCCGGCCCTGGGAGGCATGGTGGTTACTAAACCCCTGGCAGGGTCAAAGCCTGATGGTGC   9242
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Db   9180  CCCGGCCCTGGGAGGCATGGTGGTTACTAAACCCCTGGCAGGGTCAAAGCCTGATGGTGC   9239

Qy   9243  TAATGCACTGCCACTTCGGTCGGCGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC   9302
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9240  TAATGCACTGCCACTTCGGTCGGCGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGC   9299

Qy   9303  TGCTCGCAGAGCCCTCCCCGGATGGGGCACAGTGCACTGTGATCTGAAGGGTGCACCCC   9362
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||| |
Db   9300  TGCTCGCAGAGCCCTCCCCGGACGTGGGCACAGTGCACTGTGATCTGAAGGGTGCACCCG   9359

Qy   9363  GGTAAGAGCTCGGCGCCAAAGGGCCGGGTTCTACT   9395
           ||| |||||||||||||| |||||||||||||||||
Db   9360  GGGAAGAGCTCGGCGCCGAAGGGCCGGGTTCTACT   9392
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RESULT 12
AF031827
LOCUS       AF031827      9351 bp  ss-RNA     linear   VRL 22-DEC-1999
DEFINITION  Hepatitis G virus strain HGV-T55875 polyprotein gene, complete cds.
ACCESSION   AF031827
VERSION     AF031827.1  GI:3004900
KEYWORDS    .
SOURCE      Hepatitis G virus.
  ORGANISM  Hepatitis G virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            GBV-C/HGV group.
REFERENCE   1  (bases 1 to 9351)
  AUTHORS   Bukh,J., Kim,J.P., Govindarajan,S., Apgar,C.L., Foung,S.K.,
            Wages,J. Jr., Yun,A.J., Shapiro,M., Emerson,S.U. and Purcell,R.H.
  TITLE     Experimental infection of chimpanzees with hepatitis G virus and
            genetic analysis of the virus
  JOURNAL   J. Infect. Dis. 177 (4), 855-862 (1998)
  MEDLINE   98194579
   PUBMED   9534956
REFERENCE   2  (bases 1 to 9351)
  AUTHORS   Bukh,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-OCT-1997) Hepatitis Viruses Section, LID, NIAID,
            National Institutes of Health, 7 Center Drive 0740, Building 7,
            Room 201, Bethesda, MD 20892-0740, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:45255"
                     /note="isolated from a blood donor from the US; consensus
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                     LTWQSCSCRANGSRIPTGEKVWDRGNVTLLCDCPNGPWVWLPALCQAVGWGDPITHWG
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                     ASVVAWAIALLSSMSAGGWRHKAVIYRTWCKGYQAVRQRVVRSPLGEGRPTPLTFAW
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Db          |||||  ||||||||||||||||||||||  ||  |||||||||||||||||||||||
       1500 AGTTGGCTCTGCCACCTGCACCCAGTCCGCACCATAGCCGCGATCCGGTCATCGGACGCGTCGGT 1559

Qy     1583 TGAGCTCTCCAGTGGGGAGTCCCGTGCTAACGTGTATTCTGACACTGGCAGT 1642
            |||||||||||||||||  |||||||||||||||||||||||||||||||||
Db     1560 TGAGCTCTCCAGTGGGGATCCCGTGCGTATTCTGACGCTCGGCCTCGGCCCTC 1619

Qy     1643 ATGTGGCACCTGTGTGCGGGACTGCTGGCCCGAAACCGGTCGGTTAGATTCCCTTTCCA 1702
            ||||||||||||||||||| ||||||  |||| ||||||||||||||||||||
Db     1620 TTGCGCGCACCTGTGTAGGGACTGCTGGCCCGAGACTGGGTCAGTCAGGTTCCATTCCA 1679

Qy     1703 TCGGTGCGGCACGGGGCCTCGCGCTGTGCCCTGACAAAGGACTTGGAGCTGTGCCCTTCGTCGTCAACAG 1762
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Qy     1763 GACAACTCCCTTCACCATAAGGGGCCCCTGGCAACCAGGGAGAGGCAACCCGTGCG 1822
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Db     1740 GACAACTCCCTTCACCATCAGGGGCCCCTGGGAAACCAGGGGCGAGGTAACCCGTGCG 1799

Qy     1823 GTCGCCCCTGGGTTTTGGGTCCTACACCATGACCAAGATCCGGATTCCCTGCATTTGGT 1882
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Qy     1883 GAAATGTCCACACAGCCATAGAGCTCCCCACTGAACGTTCGGGTTCTTCCCCGAGT 1942
            |||||||||||||| |||||||||||||||||||||||||| |||||||||||||
Db     1860 GAAATGTCCACACCCCAGCCATTGAGCCTCCCACCCGGACGTTTGGGTTCTTCCCCGGAC 1919

Qy     1943 CCCGCCCATTAACAACTGCATGCCCGCTAGGCACGGAAGTGTCTGAGGCATTGGGCGGAGC 2002
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Db     1920 GCCGCCCCTTAACAACTGCATGCGCTCTTAGGCACAGAGTGTCTGAGGCACTCGGTGGGGC 1979

Qy     2003 TGGGCTTACGGGGGGGTTCACGGGGGTTCACGGGGGTTCTCGGTGATGGGACG 2062
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Qy     2063 CCGAAATCCGGTTCGCCCGGGGTACGGCATGCCGACCTGTCCTCTGACGCGGTTCAT 2122
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Qy     2123 ACACGTTCCAGGGGCCACCTGCAGGAGGTGGATGCGGGCAACTTCATCCCTCCCACGCTG 2182
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Db     2100 ACATGTTCAGGGGCCACCACCACAGGAGGTAGATGCTGTGGTCATCCCTCCTCGTTG 2159

Qy     2183 GTTGCTCTTGGAGTTTGTATTTGTCCTGCTCTGATGAAGCTGGCTGAGGCACGGTT 2242
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Db     2160 GTTGCTCTTGGACTTTGTGTTGTCCTGTTATACCTGGCTGAGAAGCTGGCTGAGGCACGGTT 2219

Qy     2243 GGTCCGTGATCTTGCTTCTGCTGTGGTGGTGGTGAACCAGTTGGCGGTTCTAGGACT 2302
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Db     2220 GGTCCCGTAATCTTACTACTGCTGTGGTGGTGAACCAGTTAGCAGTTCCTAGGGCT 2279

Qy     2303 GGCGGCTGTGGACGCGTGCCGTGGGGGTGAAGTTTTCGGGCCCTGCCTTGTCATGGTG 2362
            |||||||||||||| ||||||||||||||| || |||||||||||||||||||||||
Db     2280 GCCGGCTGTGGAGCGCGTGCCAGCTGGTGAGTGTTTTCGGGCCCTGCCTTGTCCTGGTG 2339

Qy     2363 TTTGGGCCTTCCCACTGTCAGTATGATACTAGGTTCTAGCAAACCTGTGTTTACTTTCG 2422
            ||| ||||| ||||||||||||||||||||||||| |||||||||||||| |||||
Db     2340 CCTGGGGCTCCCGGTCGTCAGTAGTCAGTATGATACTAGGTTTAGCCAACCTGTGTGTTACTTTAG 2399

Qy     2423 GTGGATGGGCCCTCAGCGCCTCAGCGCCTCATGTTCCTCGGGAAGCTCGCTCGGGGAGCTTT 2482
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Db     2400 ATGGCTGGGACCCCAACGCCTGATGTTCCTTGTGTGTGTGGGAGTCTCGGGGAGCTTT 2459

Qy     2483 CCCGCTGGCACTTTTGATGGGGATTTCGGCGACCCGCGGCGGCCACCTCGTGCTCGGGGGC 2542
            |||||||||||||||||||||  |||||||||||| ||||||||||||||||||||||
Db     2460 CCCGCTGGCTCTTCTGTGATGGGGATTTCGTGATGGGGCGACCCGCCACCTCGTGCTCGGGGGC 2519

Qy     2543 CGAGTTCTGCTTCGATGTCACATTCGAGGTGGACACTTCGGTGTTGGGGTGGTGGC 2602
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Db     2520 CGAGTTCTGCTTCGATGCTACATTCGAAGATCGATGTGGACACTTCGGTGTTGGGGTGGTGGC 2579

Qy     2603 CAGCGTGGTTGGTGCTGCTTGGGCCCATAGCGCCTCCTGCAGCTCAATGAGCGCCTGGAAGCA 2662
            ||| ||||||||||||||||||||||||||||||||||||||||| |||||
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Qy      443 CCGGTGGGCCGGGAAATGCATGGGCACCCAGTCCGCGGCGCGGCCTCCGCGGGGTAG 502
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      420 CCGGTGGGCCGGGAAATGCATGGGCACCCAGTCCGCGGCCTCCGCGGGGTAG 479

Qy      503 CCCAAGAATCCTTCGGGTGGCATTCTCTTTTCTATACCATCATGGCAGT 562
            |||||||||||||||||||||||||||| ||||||||||||||||||||
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Qy      563 CCTTCTGCTCCTTCTCGTGGTTGAGGCCGGGGCCGGGGCCATTCTGGCCCGGCCACCACGCTTG 622
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Db      540 CCTTCTGCTCCTTCTCGTGGTTGAGGCCGGGGCCATTTTTGGCCGGGCCACCACGCTTG 599

Qy      623 TCGAGGCAATGGGCAATATTCCTCACAAATTGTGTGCCCGGAAGACATCGGGTTCTG 682
            |||||| ||||||  ||||||||||||||||||||||||||||||||||||||
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Qy      683 CCTGGAAGGCGATGCGTCGGTGCCGTTTGCACCGACCGTTGCTGCGCC 742
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Db      660 CCTGGAAGGCGGATGCGTCCGGTGCCGTGTACAATTGCACTGACCGCTGGGCC 719

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Qy      803 ACTGGGAGCCTGTACGGGCCCTTGTCTCGGCTTACGTAGCCGGGATCCTGGGTCT 862
            |||| ||||||||||||||||||||||||||||||||| ||| |||| |||||||
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Qy      863 GGGCGGAGGTTTACTCCGGGGTCCTGACAGTTGTGTCGTTGAGGCGCCGGGGTCTACCT 922
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Qy      923 GATGCCCAACCTGAAGTGTGCAGTAGAATGTGACGTTAAGTGGGAAGTGGAGTTTTGGAG 982
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Qy      983 ATGGACTGAGCAGTTGGCCTCCAATTACTGGATTTTGGAATACCTTTGGAAAGTCCCATT 1042
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Qy     1043 TGAATTTTGGAGAGGAGTGATGAGCCTGACCCCCTCGTTTGGTTGGTGGCCCATTGCT 1102
            || | |||||||||||||||| ||||||| |||||||||||||| |||||||||||||
Db     1020 TGATTTCTGGAGAGGTGTGATGAGCCTGACTGCCTTGTTTGCCTTGCTTGCCCTGCT 1079

Qy     1103 TTTGCTGCAACGGATTGTCATGGTTGCTCGTGTGGACGATGGCGGGATGTTGCA 1162
            |||||| |||||||||||||||||||||||||||||||||| |||||||||||
Db     1080 GCTGCTTGCAGCAACGGTTGTCATGGTCTTGGTGACGATGGCGATGTGGCCA 1139

Qy     1163 AGGCGCCCCCGCCTCCGTTTGGGGTCCGCCCCCATTGAGACTACGGGTTCAGTTGGCAGTC 1222
            ||||||||||||| |||||| |||||||| || |||||||||||||||||||||||||
Db     1140 AGGCGCCCCCGCCCCCGTTTGGGTGATCCCCATTACCCCATTTGACTACAGTTGGCAGTC 1199

Qy     1223 ATGCTCCTGCAGGGCTCAATATGTCATGGGGCTAACGGGTGTGATTCCGCGTATTCCAGAGG 1282
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Db     1200 CTGCTCCTTGCAGGGCTCAACGGCTCGCGTATTCCGCGTATTCCGACCCGTGG 1259

Qy     1283 GAATGTCACGCTCTTGTGACTGCCCCAACGGCCCCTGGGTTGGGTCCGGCCTTTTG 1342
            |||||||| ||||||||||||| ||||||||||||| ||| |||||||||||||
Db     1260 GAACGTCACACTCTTGTGCCTGCACTGCCCCAACGGCCCCTGGGTCGGGTCCCCAGCTCTCTG 1319

Qy     1343 CCAAGGCGGTTGGGTGGGGCGACCCCCATCACCCATTGAGAGCCACGGACAAAACCAGTGCC 1402
            |||  ||||||||| |||||| |||| ||||||||||||| |||||||||||| |||
Db     1320 CCAACAGTGGGCGTGGGGCGATCCCATACCCATTGGGCGTCAAAATCGGTGGCC 1379

Qy     1403 CCTATCATGCCCCCCAATATGTCTCGTGTTCCGTAACGTCGTGTGGGGTTCCGT 1462
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Db     1380 CCTTTCATTGCCCCCAGTGTCTATGGGTCTCGTGTTCAGTCACTTGCTTCTGC 1439

Qy     1463 GTCTTGGTTTGCCTCGACCGCGTCGTCGTTGATTCGAAGATCGATGTGGGAGTTTGGTGTCC 1522
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Qy     1523 GGTTGGATCTGCCAGCTGCCACCATAGCCGCCTCTAGGGTCATCGGACGCGTCGGT 1582
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Qy  3743  GCCGTGACTCAAGTACCAAACAGATGCCAAGACTACCACAGAGACCCCCTCCGTGTGCCGGC  3802
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Qy  3803  AAAAGGAGTTTTCAAGGAGGCCCGTGTTTATGCCTTACGGGGCGGGAAAGAGCACCCG       3862
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Qy  3863  CGTACCGTTGGAGTACGGCCAACATGGGCCACAAGGTCTTGATCTTGAACCCGTCGTAGC     3922
          |||  || |||||||| |||||||||||||||||||| ||||| |||||||||  ||| ||
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Qy  3923  TACCGTGAGGGCCATGGGCCCATACATGGAGCGGCGTCGGCGGGGAAACACCCCAGTATTTA   3982
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Db  3900  TACTGTGCGGGCCATGGGCCGTCCGTACATGGAACCGCTGCGGGGAAAACATCCAAGCATATA  3959

Qy  3983  CTGTGGCCATGACACCACTGCTTTCACAAGGATCACTGCCCCTTACGGTATTCCAC         4042
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Qy  4043  TTACGGAAGGTTTTGGCCAACCCTAGGCAGATGCTGAGATGCTGCGGGGTGTCGTCATTTG   4102
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Qy  4103  TGACGAGTGCCACAGTCATGACTCAACTGTGTTGGGGCCCTTGTGTCAGGGGACT          4162
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Qy  4163  GGCGCGAGGATGTGGAGTGCAATTGGTGCTCCACGACGTGCGCT                    4222
          |||||| | ||| |||||| |||||||| ||||| | ||| | |
Db  4140  GGCGCGTGGATGTGGAGTGCAACTTGTGCTCTTACGCCACTGTCTACTCTCCTTGGATCCCC  4199

Qy  4223  GATGACCCAGCACCATCAATCATTGAGACAAAACTGGACGTGGAGAGATCCCCTCTA       4282
          ||||| | |||||||||||||||||||||||| ||||| |||||||| || |||||||||
Db  4200  GATGACCCAGCACCATCAATCATTGAGACAAAACTGGACGTGGAGAGATCCCCTCTA       4259

Qy  4283  TGGGCATGGCATACCTTCTTGACGACTGCGGATGCGGAAGGCATCTCGTATTCTGCCACTC  4342
          ||||||| |||||||||||||||||||||| || ||||||||||||| || ||||||||| |
Db  4260  TGGGCATGGTATCCCCTTGACGACTGCGGATGCGGAAGGCATCTCGTATTCTGCCATTC     4319

Qy  4343  CAAGGCTGAGTGCGAGCGCCTTGGCGGGGTAAATGCCATCGC                      4402
          ||||||||||| ||||||||||||| || ||||| ||||| ||
Db  4320  TAAGGCTGAGTGCCAGCGCCTTGGTCAGTTTTCCGCTCAATGCCATCGC               4379

Qy  4403  CTATTACAGGGGGAAAGACAGTTCTATCATCAAAGATGGGTGTGTGCTAC              4462
          ||||||||||||||||||||||||||||| ||||| |||||| |||| |||
Db  4380  TTATTACAGGGGGAAGGACAGTTCAATCATCAAAGACGGACTAGTGTGTGCTAC          4439

Qy  4463  AGACGACTATCCACTGGTACACTGGGAACTTCGATTCTGTCACTGATTGTGGGTTAGT       4522
          |||||||||||||||| | |||||||||||||||||||||| | ||||||||||||| |
Db  4440  AGACGACTACTCACTGGGTACACTGGGAACTTCGATTCTGTCACCGACTGTGGGTTGGT      4499

Qy  4523  GGTGAGGAGGTCGTCAGGGTGACCCTGATCCCACCATTCTCCTCCGCGCACGGT          4582
          |||||||||||||||||||||||||||||||||| || ||||| ||||||||||||
Db  4500  GGTGAGGAGGTCGTTGAGGTGACCCTTGATCCCACCATTACAATCTCCCGCGACAGT       4559

Qy  4583  GCCCGGCTCGGCTGACTGTGATGCAGCGGCGGCCACGGCAGGTCTGG                 4642
          |||||||||||| |||||| | | ||||| ||| | |||| |||||||
Db  4560  GCCCGGCCGTCGCTGAATGTCATGATGCAGAGAGCGAGGACGCACGGTAGGCAGGTCCGG    4619

Qy  4643  GCGCTACTACGCGGGGTCGCCAAGGCAGGTCGGTGGTGGTGTGGGCCTAGCTCCTGT       4702
          |||| ||||| ||||| || ||||||||||||| ||| || |||||||| |||||||||
Db  4620  GCGCTACTACTGCGGGGTTGGTGGAGGTCGGGTTGGTGTGGTGGTGGGCCTAGCTCCTGT    4679

Qy  4703  CTGGTCGCGGTGGAAGCCGGTGTGACCTGAGCAAAGGGCACGTTACGGAATGGAATCCCAA  4762
          |||||||||||||| ||||||||||||| | | ||| |||||||| || |||||||| |||
Db  4680  CTGGTCGCGGTGGAAGCCGGTGTGACCTGAGAGAGGGGCACGTTACGGAATGGAACCTAA    4739

Qy  4763  CCTACTGAGACTTTACGACAACTGCCCCTTACACCGCCGTCGCAGCTGACATTGGGGA      4822
          |||||||||||||||||| ||||| |||||||| |||||||||||||| ||||||||||||
Db  4740  CCTATTGAGACTTTACGACGACTGCCCCTTACACCGCCGTCGCAGCTGACATTGGGAGA     4799
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Db  2580  CAGTGTGGTAGCTTGGGCCATAGCGCTCCTGAGCTCGATGAGCGCAGGGGGGTGAGGCA     2639

Qy  2663  CAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCAGCTGTCGCCCAGAGGGTGGT    2722
          || |||| ||||||| |||||| |||| || ||||| ||||| || |||||||||||||
Db  2640  CAAAGCCGTGATCTATAGGACGTGGTGTAAGGGGTACCAGAGAGTGGT               2699

Qy  2723  GCGGAGCCCCCTCGGGAGGGGGCGTCCTACCAAGCTTCTGACGTTCGCCTTGGTGTTGGC   2782
          | |||||| ||||||||||||| ||| ||||| |||| || |||||||||||||||||||
Db  2700  GAGGAGCCCCCTCGGGAGGGGGCCGTCCACCAAACCTTTGACCTTCGCTTGGTGCTGGC    2759

Qy  2783  CTCATACATCTGGCCGGATGCTGCTGATGATGTGGTGGTCCTCCTTCGG             2842
          ||||||||||| ||||| || || || ||| || |||| || ||| |||
Db  2760  CTCATACATCTGGCCGGACGCGCGTGATGATGTGGTCGTTCGTTTGTCTTTGG          2819

Qy  2843  CCTGTTCGACGACTGGCCCTGAGGAGCGTCCTGCTCTCCCGGCCCTCGTTACG          2902
          ||| | ||||||| | |||||| || |||| || |||||||| ||||| | |||
Db  2820  CCTGTTCGACGCGTTGGACTGGCTTGGACGGAGTCTTGGTGTCCCGGCCCTCGTTTACG    2879

Qy  2903  GCGACTGGCACGGGTGGTTGAGTACGTGCTGGGCCGAGAAGGCCACCACCATCCG        2962
          | ||||| |  | |||||| |||||||| ||| ||||| | |||| || |||| ||
Db  2880  CCGCTTGGCCGCGGGTGGTTGAGTGCGTGCTGGGCGAGCCACCACCAACCGTTCG       2939

Qy  2963  ACTGGTCTCCAAGATGTGCCAAGAGAGGGCCTACCTGTTTGACCACATGGGCTCTTCTC   3022
          |||| ||| |||||||||| |||| ||||| || || | |||| |  |||||| |||||
Db  2940  GCTGGTCTCCAAGATGCGCGAGAGGGGCCTACTTGTTCGGTCGTTGTCATCACATGGGCTCTTTTC  2999

Qy  3023  GCGCCGCTGTCAAGGAGCGCGTTGTGGAATGGACGCGCCTTGGACGCCCTTGTCATTCAC   3082
          ||||||||||||||||||| ||||| |||||||||||||||||| || |||||||||||||
Db  3000  GCGCCGCTGTCAAGGAGCGCGTTGTGGAGTGGACGCGCCTTGGAACCCTGGTGTCTTCCAC   3059

Qy  3083  TAGGACGGACTGTGCGCATCAGAGATGCCGCGGAGGACGCCGTGCTGCGT             3142
          |||||||||| ||| ||||||| | |||| || ||  | |||| ||||||||
Db  3060  TAGGACGGACTGTGCGCATAAGAGATGCGCGCGGAGGACGCCGTGCTGCGT            3119

Qy  3143  CATGGGTTTACCCGTGTAGCACGGCGCCGCGGTTCATCGGCGTCTTTCAGGA           3202
          ||||| |||||||||| ||||| ||||| |||| ||||||||||| ||||||
Db  3120  CATGGGCTTGCCCGTGTTGCCGTCACAAAGGCCTCCTTGCCTTTATCGGCGTCTTTCAGGA  3179

Qy  3203  TGTGAATCATTTCCCGGTTGCTCCCCGGATTGCTTCATCCGCCGTCGGTGCGG          3262
          || |||||| ||||| | ||| ||||| |||| | | |||||||| || |||||
Db  3180  TGTGAACCATCTGCTTCCCCGGATTGCTTCCAACTGCTTCATCCGCCGTCGGTGCGG      3239

Qy  3263  AAAGGGCTTCCTCGGGGTCACGGAGGCAGCCTTGACAGTGTAGGGATCCTGACTTACATCC  3322
          || |||||| | ||||||||||| |||| || || || ||| | | ||||||||| ||||
Db  3240  TAAGGGCTTTCGTGGGGTCACAAAAGGGTCGGGGACCGTCGCCTGCCTTGACGTGACTTACATCC  3299

Qy  3323  AGGAACGTCATGGTGTTGGGGGACCGGCTACGTCACGACAATGGCACATGTCTGAATGG    3382
          ||| |||| || |||||||| |||||| |||| |||||| ||  ||| ||| ||||| |||
Db  3300  AGGAACGTCATTGTGTTGGGGGACCGGCTACGTCGCCGGGCAACATGGGAACATGTCTAAACGG  3359

Qy  3383  CCTGTTGTTCACAACTTTCCATGGGCGCTTCCATGGGCGCGCCCGTGGGGGC           3442
          |||| | ||||||| |||||||||||| ||||||||||||||||| ||||||||
Db  3360  CCTGCTTTTCACGACTTTCCATGGGCGCTTCCATGGGCGACGCCGTGGGGGC          3419

Qy  3443  CCTTAATCCCAGGTGGTGTTCAGCCAGTGTCAGCTGATGACGCTCAGGTGCCCGATGG     3502
          |||||||||||||||  | |||||||| |||||  | || || || ||||| ||||||
Db  3420  CCTTAATCCCAGGTGGTGTTCGGCCAGTGTCGGCTGACGTCACCGTCTACCCGGATGG     3479

Qy  3503  GGCAACTTCGTTGACGAGTCCACTTGCCGAGTCCTGTTGGGTTATTAGATCCGA        3562
          |||| ||||| ||||| || |||||  || || | |||| || |||| | |||| |
Db  3480  AGCCACTTCGTTGACGAGCTGCCACTTGCCGAGTCCTGTTGGGTTCATCAGGTCCGA     3539

Qy  3563  CGGGGCTTTGTTGCCATGGCTTGAGCAAGGGACAAGGTTGAGCTGATGGCCATGGA      3622
          ||| || ||| | || |||| || |||| ||| |||| || ||| ||||||||||||
Db  3540  CGGGGCTTTGTTGCCATGGCTTGAGTGTCGGGACAAGGTGAGCTGATGGCCATGGA      3599

Qy  3623  GGTCTCTGACTTCCGTGGTTCTGCGGCAAAAGGGCACGGCACGCAGT                3682
          |||| ||||||| ||||||||| || |||| ||||| |||||||||||
Db  3600  GGTCTCTGATTTCCGTGGTTCTGCGGCGACCGTCTCTGTGCCGCGGCACGCCACTAGT     3659

Qy  3683  AAGAATGCTCCGTGTCAGTGCTTCCACCTCGGCCAGGGGTTACTGCGGAGTTCACTACG    3742
          || ||||||| ||||| ||||| |||| |||||||||| ||||| | || ||  | ||| |
Db  3660  AGGAATGCTCCGTGTTCATTGTGCTTCATTCCCGGTGGCAGGGGATGACCGGTTCGGTTCACTAG  3719
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Qy  4823 AGCCGCGGTGTCTTTCGGGCTTGCCCCGTGAGGATGCATCCGATGTTAGCTGGGC 4882
         ||||||| ||  ||| |||||||||||||||||||||||||||| |||||||||||
Db  4800 AGCCGCGTGTTTTTCTCCGGCGCTGCCCCGTTGAGGATGCACCCCGATGTCAGCTGGGC 4859

Qy  4883 AAAAGTTCGCGGCGTCAACTGGCCCTTCCTGGTGTTCAGCGGACCATGTGCCGGGA 4942
         ||||||||||||||||| |||||||||||| |||||| ||||||||||||||||||
Db  4860 AAAAGTGCGCGGCGTCAACTGGCCCTTCCTGGTGTGTTCAGCGGACCATGTGCCGGGA 4919

Qy  4943 AACACTGTCTCCCGGCCCATCGATGACCCCAGTGGGCAGTCTGAAGGGCCCGAATCC 5002
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4920 AACACTGTCTCCCGGTCATCGGATGACCCCAATGGGCAGTCTGAAGGGCCCGAATCC 4979

Qy  5003 TGTCCACTCCTGCTGAGGTGGGCAATGATTACCATCTAAAGTGGCCGGCCATCACAT 5062
         |||||| ||||||||||||||||||||||||||||| |||||||||||||||||||
Db  4980 TGTCCCGCTGCTGAGGTGGGCAACGATTTGCCATCTAAGGTGGCCGGCCATCACAT 5039

Qy  5063 CGTGGACGACCTGTCTCCGTAGGCTCGGGCTGGCCGAGGTTACGTCCCGCTGCGATGCGGG 5122
         |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  5040 AGTGGACGACCTGTCTCCGAGACTCGGGCTGTGGGCGAAGGTTATGTCCCGCTGCGATGCTGG 5099

Qy  5123 ACCCATCTTGATGGTGGCCTCCTATTGCGGGGGCATGATCTATGCGTCATACACCGG 5182
         || ||||||| || |||||||||||| |||||||||| |||||||||||||||||||
Db  5100 GCCCATCTTGATGCTTGCCTCGCTCTGGGGGATGATCTATGCGTCTTACACCGG 5159

Qy  5183 GTCTCTCGTGGTGGTTACAGACTGGGATTGTGAAGGGGGTGGCAGCCCCCTTTATCGGCA 5242
         ||| || |||||||| ||||||||||| |||||||||||||||||||| |||||||||||
Db  5160 GTCCCTAGTGGTGGTCGACAGACTGGGATGTGAAGGGGGTGGCAGCCCCCTCTTTATCGGCA 5219

Qy  5243 TGGAGACCAGGCCACGCCCCAGCCGGTTGTGCAGGTCCCCGTAGACCATGGCCGGG 5302
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  5220 TGGTGACCAGGCCACGCCCCACAGCCGGTGTGCAGGTACCCCGTAGACCATCGGCCGGG 5279

Qy  5303 GGGAGAGTCGCCGCCATCGGATGCGGCCAACAGAGTGACAGATGCCGGCCGGCCATCCAGT 5362
         |||||||||| || |||||||||||||||| ||||||||||||||||||||||||||||||
Db  5280 GGGAGAGTCGACCATCCGGATCCGGCCAACAGTGACAGATGCGCGGTGGCAGCCATCAGGT 5339

Qy  5363 GGATTGCGATTGGTCAGTCATGACCGTCTGATCGGGGAAGTGCTGTTCCTTGGCCAGGC 5422
         ||| |||||||||| ||| ||||||||| |||| ||||||| ||||||| |||||||||
Db  5340 GGACTGTGATTGGTCAGTTCTCTGCCATCGGATCGGAGAAGTACTCGTTCCTTGGCCAGGC 5399

Qy  5423 TAAGACGGCCGAGCCTACCGCAGCTACCACCAGTGGCTTGCTGGCTCTACACGGGGAC 5482
         ||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||||
Db  5400 TAAGACGGCCGAGCCTACCGCACACGCGCCACCCCAGTGGCTTGCTGGCTCTACACGGGGAC 5459

Qy  5483 GCGGGCCCCCCACTGTTCAATTGTGACAAGCTCTTCGCCCGGGGGCTGGCCGCGGT 5542
         |||||||||||||||||||||||||| ||||||||| || ||||||||| |||||||
Db  5460 GCGGGCCCCGTCCCCACTGTATCCATTGTGACAGCTCTCCGCCGTCTCGGAGGTGGGCCGCCGT 5519

Qy  5543 GGTAGGCCATTGCCACAGTGTAATAGCTGCGGGCCAGTGGGGCTTCATGGGCTTCTAGGAG 5602
         ||||||||||||||||||| |||||||||| |||||||| |||| |||| ||||||||||
Db  5520 GGTGGGCCATTGCCACAGTGTAATAGCTGCGGGCCGTGCTGCTGGTTCTTACGGGCTTCAAGGAG 5579

Qy  5603 CCCTCCATTGGCTGCTGCCGCGTCCTACCTCATGGGGCTGGGCGCTGGAGGCAAACGCGCA 5662
         ||||||||||||||||||||| ||||||||||||||||||||||||| ||||||||||||
Db  5580 CCCCCGGTCGCTGGCTGCCGCGTCCTACCTCTGTGGGGGCTGGGCCTGCGGCAACGCACGCTCA 5639

Qy  5663 AACCCAGCTTAGCCTCCCGCTCCTACTAGGGCCGCTGGCACGCGCCTGT 5722
         |||||| |||| | ||||||||||||| || ||| ||||||||||||||
Db  5640 GACGCGACTGGGCCGCGGCCTCCTACTGGGCTCCTGGGCACTCCCCGT 5699

Qy  5723 CGTGGGGTTAACCATGGCCGGCGTTCATGGGAAGTGCTAGCGTCTCCCCCTTGT 5782
         |||||| |||||||||||| |||| ||||||||||| ||||||||||||||||||
Db  5700 CGTGGGGTTTAACCATGGCCGGCGTTCATGGGAGGGCGTGGCCTATCCCCCTGT 5759

Qy  5783 CACCATTTTTACTGGGGGATCGTGTGGGGGAAATCGTGAATCGTGCCATCCAGTGCT 5842
         ||| |||||||||||||||| || |||||||||||||||||||||||||||||||||
Db  5760 CACCATCTTACTGGGGGATCGTGTGTGGGGAGGGGTCGTCAACGCGGCAGCCTTGT 5819

Qy  5843 CTTCGACTTTATGCGGGGAAACTATCATCGAGAAGATCGTGTATGCCATCCAGTGCT 5902
         ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  5820 CTTCGACTTTCATGCGGGGAAACTTGTGTGATGCAGAAGATCGTGTATGCCATCCATCCCGGTGCT 5879

Qy  5903 AACCAGTCCGGGGCAGGACTTGCCGCGGGATCGCCCCTCGGGTGTTGTACTCAGCTAA 5962
         |||||||||||||||||||||||||||||||| ||||||||||| || ||||||||||
Db  5880 GACCAGCCCAGGGCGGCGGCCTCGCCCTTGGGGGATCGCCCCTTAGGGTTGTTTGTACTCAGCTAA 5939

Qy  5963 CAACTTCGGCACTACCACTTGGTTGAACCGTCTGCTGCTGCTGACTACATTGCCAAGTCCTCATG 6022
         ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  5940 CAACTTCGGCACTACCACTTGGTTGAACCGTCTGACCACGTCTTGACCAAGTCTTCATG 5999

Qy  6023 CATCCCTGACAGTTACTTTCAGCAGGCCGATTACTGTGACAAGGTCTCAGCTGTGCTCCG 6082
         ||||||||||||||| |||||||||||| ||||||||||||||| |||||||||||||||
Db  6000 CATCCCTGACAGTTACTTTCAACAGCCGTGACTACTGCGACAAGGTCTCCCCGTGCTCCG 6059

Qy  6083 ACGCTTGAGCCTCACTCGACCGTGTTGCCCTGGTTGCCTCAACAGGAGCCTAAGGTGATGA 6142
         ||| |||||||| || ||||| ||||||||||| ||| ||||||||||||| ||||||||
Db  6060 TCGCCTGAGCCTCACTAGAACGGTGTCGCCCTGGTTGCTCAACAGGAGCCCAAAGTGGATGA 6119

Qy  6143 GGTTCAGGTGGGTACGTCTCGGGACTTGTGGGAGTGGATCATGCGTCAAGTGCGCATGGT 6202
         ||||||| ||| | ||||| |||||||| |||||||| ||||| |||||| ||||||||
Db  6120 GGTTCAGGTTGGATACGTCGTGGGACTTGTGGAGTGGATCATGCGGCAGTGTACGGCATGGT 6179

Qy  6203 GATGGCCAGACTTGGGGCCCTCTGCCCCGTGGTGTCATTACCCTTATGGCACTGCGGGGGA 6262
         ||||||||||||||||||||||||| |||||| ||| ||||| ||| |||||||||||||
Db  6180 CATGGCCAGACTTAGGGCCCTGCCCCGTCGGTGTGTCATTACCTTTATGGCACTGCTGGGGGA 6239

Qy  6263 GGGGTGTCCGGAGAATGGTTGTTGGATGGACGGCCATGTGGTGTGTCGTTGCTGTTGGTTG 6322
         |||||||||||||||||||||||||||| |||||||| || |||||| |||| ||||||||
Db  6240 GGGGTGTCCGGAGAATGGCTGTTAGATGGGCATTAGGGATTGAGAGTGTTGAGAGAGCTGTTGGTTG 6299

Qy  6323 CGTGATCACCCGTGATGTTTTGAATGGGCAACTCAAAGATCCAGTTACTCTACCAAGCT 6382
         ||||||||||| ||||| || ||||| ||||||| |||| ||||||||||||||||||||
Db  6300 CGTGATCACAGGCGACGACTGTCTAAATGGGCAACTCAAAGAGCCAGTTTACTCTACCAAAGCT 6359

Qy  6383 GTGAGGCATTATTGGATGGGAGCAGTCCCTGTGAACATCTGGGCTATGGCGAGACGTC 6442
         |||||||| ||||||||||||| || ||||| ||||||||||||||||||||||||||
Db  6360 GTGCCCGGCACTATTGGATGGGAACTGTTCCAGTGACGATGCTGGGTGGTACGTGAAACATC 6419

Qy  6443 GCCTTTGCTCGCTGCCCGAGAAGTGGTACACCCCCCACGTTCGGTCGTGGGGGCTGA 6502
         ||| || | |||||| |||||| |||| |||||||||||||| ||| ||||||||||
Db  6420 GCCCCTCCTGGCCTCCGACACCCCAAAAGGTCGTACCTTTTGGACGTCTGGGCTGA 6479

Qy  6503 GGTGGTGGTGACCCCCGTGTTGATCGGAACATCGTGTGAACATCCGGCTACAAACTGCTGCG 6562
         ||| |||||||||||||  ||| |||||| ||| ||||| ||| ||||||||| ||||||||
Db  6480 GGTGTGGTGACCCCCGTGTTGATCGTGTGATCGTGATCAGGAGACTCCGCCTACCAAGTTGCTGCG 6539

Qy  6563 CCAGCAAATCCGTGCGTGTTGCTGAGCCCTATTACGTGCGACGGCATACCGGTCTC 6622
         ||||||||| || || |||||||| |||| | ||| ||||||||| |||||||||||
Db  6540 CCAGCAAATCCTATCGCTGCTGTGTAGCTGCAGCCCTATGTTGACTATGTTCGCCGGCATCCGGCTCTC 6599

Qy  6623 ATGGACGACGCCGACGGCCGCCGAGCCCTGCCATGTCTATGGCCTGGGCAAAGTGTCACCAT 6682
         ||||||||||||||||||| |||||||||||||||| || ||||||||||||||||||||||
Db  6600 GTGGGACGGCGGACGCCCGTGCAGCTGCCCGTCTCATGTCCCAGGCAAAGTGTTACCAT 6659

Qy  6683 TGAACCTCACATAGATGTCATCATGGAAGATTGCAGTGCAGAATGTGGGCCCCCTGA 6742
         ||||||||||||| ||||||| ||||| |||| ||||||| ||||||||||||||||
Db  6660 TGAGCGGGAACGCTACACCCTCGTGTCATGTGGGGGAGAAGACTGTGGGCCCCCTGA 6719

Qy  6743 GGTGTCATCCGAGTGTGTCATTGACATTGACATCGAAGACTGAAGACTCAGAACTGA 6802
         |||||||| || |||||| ||||| ||| | ||||||||| ||||||||||||||||
Db  6720 GGTTTCATCCGAGGTATCCATTGACATTGACATCGAAGACTGAAGACTCAGAACTGA 6779

Qy  6803 GGGCGACCTGCCGCGCCGTGCCAGCTGCGGCCCCTCAGCGTATCGCGAAATGCTGCGAGAATTCT 6862
         ||| ||||||| ||| || |||||| || || ||||||| ||||||||| ||||||||||||||
Db  6780 GGCCGATTTGCCGCGACCAGCTGCAGCCCCTCCAGCGTATTGAGAATGCTGCGCGAGAATTCT 6839

Qy  6863 TGAACCTCACATAGAGTCATCATGGAAGATTGCAGTTGCAGTGCACCCTCTTCTTGTGGGAGTAG 6922
         ||||||| ||| || |||||| ||| ||||| |||| ||||||||||||| ||| ||||||||||
Db  6840 TGAGCCACACATTGATGTCATCATGGAAGATGCTAGTACACCCTCTTCTTGTGGTAGTAG 6899

Qy  6923 CCGAGAGATGCCTGTGTGTGGGGAAGACGTATACCCCGCACACACTCCATCCGGCCACTTATCTC 6982
         |||||||||||| || |||||||||||||| || ||||||||||||||||||||||||||||||
Db  6900 CCGAGAGATGCCGTGTGTGTGGGGAAGAAGCGTCCCCCCACACTGCCCCACTCCATCCCAGCCACTTATCTC 6959

Qy  6983 GGTTACTGAGAGCACCCGTCGCCCTCCGGGTCGTTCCTCGCAGGAGGATAC 7042
         |||||||||||||  || |||||||||||||||||||||||||||||||||
Db  6960
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Db   6960 GGTTACTGAGAGCAGCTCAGATGAGAAGACCCCGTCGGTGTCCTCTTCGCAGGAGGATAC 7019

Qy   7043 CCCGTCTTCTGACTCATTCGAGGTCATCCAAGAGTCCGAGACAGCCGAAGGGGAGGAAAG 7102
          |||||| |||||||||||||| |||||||||||||| |||||||||||||||||||| |
Db   7020 CCCGTCCTCTGACTCATTCGAAGTCATCCAAGAGTCTGAGACAGCCGAAGGGGAGGACAA 7079

Qy   7103 CGTCTTCAACGTGGCTCTTTCCGTACTAAAAGCCTTGTTTCCACAGAGCGATGCCACAAG 7162
          ||||||||||||||| |||||||||||||||||||| ||||||||||| |||||||| ||
Db   7080 CGTCTTCAACGTGGCCCTTTCCGTACTAAAAGCCTTATTTCCACAGAGTGATGCCACTAG 7139

Qy   7163 AAAGCTTACCGTTAAGATGTCATGCTGTGTTGAGAAGAGCGTAACACGCTTCTTTTCATT 7222
           |||||||| || |||||||||||||| |||||||||||||| || ||||||||||||||
Db   7140 GAAGCTTACTGTCAAGATGTCATGCTGCGTTGAGAAGAGCGTCACGCGCTTCTTTTCATT 7199

Qy   7223 GGGATTGACGGTCGCTGACGTGGCAAGCCTGTGTGAGATGGAAATCCAGAACCATACAGC 7282
          ||| |||||||| || |||||||| |||||||||||||||||||||||||||||||||||
Db   7200 GGGGTTGACGGTTGCCGACGTGGCTAGCCTGTGTGAGATGGAAATCCAGAACCATACAGC 7259

Qy   7283 CTATTGTGACAAGGTGCGCACTCCGCTTGAATTGCAGGTTGGGTGCTTGGTGGGCAATGA 7342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7260 CTATTGTGACAAGGTGCGCACTCCGCTTGAATTGCAGGTTGGGTGCTTGGTGGGCAATGA 7319

Qy   7343 ACTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAGAGACCTTGGCTTCCTTCTCTTA 7402
          |||||||||||||||||||||||||||||| ||||||||||| |||||||||||||| ||
Db   7320 ACTTACCTTTGAATGTGACAAGTGTGAGGCCAGGCAAGAGACTTTGGCTTCCTTCTCCTA 7379

Qy   7403 CATTTGGTCTGGGGTGCCACTGACGAGGGCCACTCCGGCCAAGCCCCCTGTGGTGAGGCC 7462
          ||| ||||| |||||||| ||||| |||||||| |||||||| || ||||||||||||||
Db   7380 CATCTGGTCCGGGGTGCCGCTGACTAGGGCCACGCCGGCCAAACCACCTGTGGTGAGGCC 7439

Qy   7463 GGTTGGCTCCTTGCTGGTGGCCGACACCACCAAGGTGTATGTCACCAACCCGGACAATGT 7522
          ||| ||||| ||| ||||||||||||| ||||||||||| || |||||||||||||||||
Db   7440 GGTAGGCTCTTTGTTGGTGGCCGACACTACCAAGGTGTACGTGACCAACCCGGACAATGT 7499

Qy   7523 TGGGAGAAGAGTTGACAAGGTTACCTTCTGGCGTGCCCCTAGGGTTCATGACAAATTCCT 7582
           ||||| ||||| |||||||| ||||||||||| || |||||||| |||||||| |||||
Db   7500 GGGGAGGAGAGTGGACAAGGTGACCTTCTGGCGCGCTCCTAGGGTCCATGACAAGTTCCT 7559

Qy   7583 CGTGGACTCCATAGAGCGCGCTAAGAGGGCAGCTCAAGCCTGCCTAAGCATGGGTTACAC 7642
          |||||| || || ||||| || | |||||| |||||||||||||||||||||||||||||
Db   7560 CGTGGATTCAATCGAGCGGGCCAGGAGGGCTGCTCAAGCCTGCCTAAGCATGGGTTACAC 7619

Qy   7643 TTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCCATGGGCTGGGGATCTAAGGT 7702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7620 TTATGAGGAGGCAATAAGGACTGTAAGGCCACATGCTGCCATGGGCTGGGGATCTAAGGT 7679

Qy   7703 GTCGGTCAAGGACCTCGCCACCCCTGCGGGGAAGATGGCTGTCCATGACCGGCTCCAGGA 7762
          |||||| |||||| | ||||||||||||||||||||||| || |||||||| ||||||||
Db   7680 GTCGGTGAAGGACTTGGCCACCCCTGCGGGGAAGATGGCCGTTCATGACCGACTCCAGGA 7739

Qy   7763 GATACTTGAAGGGACGCCAGTCCCCTTTACTCTTACTGTGAAAAAGGAAGTGTTCTTCAA 7822
          |||||||||||||||||||||||||||||| ||||||||||||||||| |||||||||||
Db   7740 GATACTTGAAGGGACGCCAGTCCCCTTTACCCTTACTGTGAAAAAGGAGGTGTTCTTCAA 7799

Qy   7823 AGACCGAAAGGAAGAGAAGGCCCCCCGCCTCATTGTGTTCCCCCCCCTGGACTTCCGGAT 7882
          |||||| ||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   7800 AGACCGCAAGGAGGAGAAGGCCCCCCGCCTCATTGTGTTCCCCCCCCTGGACTTCCGGAT 7859

Qy   7883 AGCTGAAAAGCTTATTCTGGGAGACCCTGGACGGGTAGCCAAGGCGGTGTTGGGGGGGGC 7942
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Db   7860 AGCTGAAAAGCTCATCCTGGGGGACCCGGGCCGGGTAGCCAAAGCGGTGTTGGGGGGGGC 7919

Qy   7943 CTACGCCTTCCAGTACACCCCAAATCAGCGAATTAGGGAGATGCTCAAACTGTGGGAATC 8002
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Qy   8003 AAAGAAGACACCATGCGCCATCTGTGTGGACGCCACATGCTTCGACAGTAGCATAACTGA 8062
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RESULT 13
AF031828
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DEFINITION  Hepatitis G virus strain HGV-1517 polyprotein gene, complete cds.
ACCESSION   AF031828
VERSION     AF031828.1  GI:3004902
KEYWORDS    .
SOURCE      Hepatitis G virus.
  ORGANISM  Hepatitis G virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE   1  (bases 1 to 9351)
  AUTHORS   Bukh,J., Kim,J.P., Govindarajan,S., Apgar,C.L., Foung,S.K.,
            Wages,J. Jr., Yun,A.J., Shapiro,M., Emerson,S.U. and Purcell,R.H.
  TITLE     Experimental infection of chimpanzees with hepatitis G virus and
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  JOURNAL   J. Infect. Dis. 177 (4), 855-862 (1998)
  MEDLINE   98194579
  PUBMED    9534956
REFERENCE   2  (bases 1 to 9351)
  AUTHORS   Bukh,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-OCT-1997) Hepatitis Viruses Section, LID, NIAID,
            National Institutes of Health, 7 Center Drive 0740, Building 7,
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Best Local Similarity   90.6%;
Matches  8474;   Conservative    0;   Mismatches  877;   Indels    1;   Gaps    1;

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Qy      83 TCGGCGCCGACTCGGCGACCGGCCAAAAGTGGTGGATGGGTCGTGTGACAGGGTTGGTAGG    142
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Qy    1583 TGAGCTCTCCGAGTGGGAGTCCCGTGCGTAACGTGTAATTCTGATACGGTCGGCCTGCTTC    1642
           |||||||||||||||| |||||||||||||||||||||||||| |||||||||||||
Db    1560 TGAGCTCTCCGAGTGGGGAGTCCCACTCGTCGTATTCTGGACGTGTATTCGGAGCTGCCCTC    1619

Qy    1643 ATGTGGCACCTGTGCGCGGGACTGCTGGCCCGGAAACCGGGTCGGTTAGATTCCCTTTCCA    1702
           |||||||||||||| ||||||||||||||||| |||| ||||||||| |||||||||||||
Db    1620 TTGCGGCACCTGTGTGAGGGACTGTTGGCCCGGAGACTGGGTCAGGTTCATTCCA        1679

Qy    1703 TCGGTGCGGCACGGGCCTCGGCTGACAAAGGACTTGGAAGCTGTGCCCTTCGTCAACAG    1762
           ||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||||
Db    1680 TCGGTGCGGCACGGGCCTCGGCTGACAAAGGACTTGGAAGCTGTGCCCTTCGTCAATAG    1739

Qy    1763 GACAACTCCCTCACCAGCCATAGAGCTTCGGACGTTCGGGTGCG    1822
           ||||||||||||||||||||| ||||| ||||||||||||||||
Db    1740 GACAACTCCCTTCACCAGCCATTGAGCCTCCACCAGGGCGAGGTAACCCAGGTGCG    1799

Qy    1823 GTCGGCCCTGGGTTTGGGTCCTCTACACCATGACCAAGATCCCTGCATTTGGT    1882
           ||||||||| |||||||| | ||||||||||||||| |||| ||||||||||||
Db    1800 GTCACCCTTGGGTTTGGGTCCTCTACACCATGACCAAGATCCGACACCCTACATCTGGT    1859

Qy    1883 GAAATGTCCCACCAGCCATAGAGACCTTCGGAACGTTCGGGTTCTTCCCCGGAGT    1942
           ||||||||||||||||||||| |||||||||||| |||||| |||||||||||
Db    1860 GAAATGTCCCCAGCCATTGAGCCCGGACCGGGACGTTTGGGTTCTTCCCGGGGAC    1919

Qy    1943 CCCGCCCATTAACAACTGCGATGCCGCGGAAGCTGTGAGGCACGGAAGCATTGGCGGGAGC    2002
           |||| |||||| ||| |||||||| |||| ||||||||||||||| |||||||||||||||
Db    1920 GCCGCCCTTAACAACTGCCATGTCTTAGGCACAGAGGTGTCTGAGGCACTCGGTGGGGC    1979

Qy    2003 TGGGCTTACGGGGGTTCTCGGTTCGCGAGCTGATGGGACG    2062
           || ||||||||||||||| ||| ||||||||| ||||||||
Db    1980 TGGTCTCACGGGGGTTCTATGAACCCCTGGTGCGCAGCTGATGTGGAGCTGATGGGACG    2039

Qy    2063 CCGAAATCCGGTTGCCCGGGTACGGCATGGGTACCGTCCTCGTGTACGCTGACGGGTTCAT    2122
           |||||||||||||| |||||||||||||||| || |||||||||||||||||||| |||
Db    2040 CCGCAATCCGGTTTGCCCGGGGTTTGCATGGGTCATGCGTCCTCCTCCCGGGTCGACCTGACGCGGGTTTAT    2099

Qy    2123 ACACGTCCAGGGACACCTGCAGGAGGTGGATGCGGCACCTTCATCCCTCCTCCACGCTG    2182
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Db   2100  ||||  |||||  |||||   ||||||||||||||||||||||  |||||||||||||||  ||  ||
           ACATGTTCAGGGCACCTACAGGAGGTAGATGCTGGCAACTTCATCCCTCCTCCGTTG         2159

Qy   2183  GTTGCTCCTTGGATTTGTATTTGTCCTGCTCGTGGTGGTCCGTGGTGGTGCTTCACGTT     2242
           ||||||||||||  |||||  || | ||||||||||| |||||||||||||||||||||
Db   2160  GTTGCTCCTTGGACTTTGTTGTCCTGTTATACCTGGTGGTGCTTGGTGGTGCTGAGGCACCGTT  2219

Qy   2243  GGTCCCCGTTGATCTTGCTTCTGCTCGTCCGTGGCGGTGAAGTTTTTGCGGGTGGTCTAGGACT  2302
           ||||||||||||||| |||||||  ||||| ||||||||||||||| |||||||||||||||||
Db   2220  GGTCCCGCTAATCTTACTACTGCTCGTGTGTGGCGGTGAACCAGTTAGCAGTCCTAGGGCT     2279

Qy   2303  GCCGGCTGTGGACGCGTCCGTGGCGGGTGAAGTTTTTGCGGGCCCTGCCTTGTCATGGTG      2362
           ||||||||||||||||||   |||||||||||||||||||||||||| ||||||||||||||
Db   2280  GCCGGCTGTGGACGCCGCCGTAGCTGGTGAGCGGTGTTTGCGGGCCCTGCCTTGTCCTGTG    2339

Qy   2363  TTTGGGCCTTCCCACTGTCAGTATGATACTAGGTCTAGCAAACCTGGTGTTGTTACTTTCG    2422
           |||||||||||||||||| ||||||||||||||||||||||| | |||||||||||||||||
Db   2340  CCTTAGGGCTCCCGTAGTCAGTATGATACTAGGTTTAGCCAACCTGGTGTTGTTACTTTAG    2399

Qy   2423  GTGGATGGCCCTCAGCGCCTCATGTTCCTCGTGTTGGAAGCTCGCTCGCTGGGGAGCTTT    2482
           | ||||||||||||||||||| ||||||||||||||||||||||||||| |||||||||||
Db   2400  ATGGCTGGGGACCCCAAACGCCTGATGTTCCTTGTCTGCTGTGCTCGCTCGCGGGGAGCTTT  2459

Qy   2483  CCCGCTGGCACTTTGATGGGGATTTCGGGCGACCCCGGGCGGCCCACCCTGTGCTCCGGGGC  2542
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460  CCCGCTGGCACTTTGATGGGGATTTCGGGCGACCCCGGGCGGCCCACCCTGTGCTCCGGGGC  2519

Qy   2543  CGAGTTCTGCTTGCTCGTGATGTCACATTGGACACTTCGGTGTTGGGCTGGTGGTTCGGC    2602
           ||||||||||||||||||| ||| ||||| |||||||||||||||||||||||||||||||
Db   2520  CGAGTTCTGCTTCGATGCTACATTCGAGGTGGACACTTCGGTGTTGGGCTGGTGGTTGGC    2579

Qy   2603  CAGCGTGGTGGTCCGTGGCGGCCCATAGCGCTCCTGAGCTCAATGAGCGCAGGGGGTGGAAGCA  2662
           |||||||||||||||||| |||||||||||||||||||||||| |||| ||||||||||||||
Db   2580  CAGCGTGTAGCTTGGGCCGCCCATAGCGCTCCTGAGCTCGATGAGCGCCGATGAGCGGCGGCA  2639

Qy   2663  CAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCAGGCTGTGCTGCCCAGAGGGTGGT    2722
           ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   2640  CAAAGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCAGGCGGTGCTGCCCAGAGAGTGGT    2699

Qy   2723  GCGGAGCCCCTCGGGGAGGGGCGTCGTTGATGGGCGGCGAGAAGGCCACCACCGGCTTGGC    2782
           || |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   2700  GAGGAGCCCCTCCGGGAGGGGCGTCGTTGATGGGCGGCGAGAGGCCGAGCCGAGCCGTTGGC    2759

Qy   2783  CTCATACATCTGCCGATGCTGTGATGATGGTGGTCGGGCGTCCTCCTCTTCGG           2842
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760  CTCATACATCTGCCGACGCTGTGATGATGGTCGGTGCTCCTTGGTTACTCTTTGG         2819

Qy   2843  CCTGTTCGACGGACGACTGCGGCTGGGCCCGGAGAGCTCGTGCTGCTGCCCCTCGTTACG     2902
           |||||||||||||||||||||  |||  ||||||||||| ||||||||||||||||||||||
Db   2820  CCTGTTCGACGCGTTGGGCGTTGGGCTTTGGGAGAGATCTTGGTGTCCCGGCCCTCGTTACG   2879

Qy   2903  GCGACTGCACGGGTGGTTGAGTGCTGATGGCGGCGAGAAGGCCACCACCATCCG          2962
           |||||||||||||||||||||| |||  |||||||||||||||||||||||||||
Db   2880  CCGCTTGGCGCGGGGCCCCTGGTGGTGTGATGGCGGCGAGCCACCACCACCGTTCG        2939

Qy   2963  ACTGGTCTCCAAGATGTGCCGCAAGAGGGGCCTACCTGTTTGACCACATGGGCTCTTTCTC    3022
           |||||||||||||||||||||| || |||||||||||||||||||||||||||||||||||
Db   2940  GCTGGTCTCCAAGATGTGCCGAGAGGGGCCTACTGTTTTCGATCACATGGGCTCTTTTTC    2999

Qy   3023  GCGCGTGTCAAGGAGACGCCTTGTTGGAATGGGACGCGGGCCCTTTGGGCCCTTGTCATTCAC   3082
           ||||||||||||||||||||||||  |||  |||||||||||  ||||||||||||||||||
Db   3000  GCGCGTGTCAAGGAGACGCCTGCTGGGAGTGGCGGGCGCGGGGCCCTTGGGGCCCTTGTCTTTCAC  3059

Qy   3083  TAGGACGACTGTCGCATCATCAGAGATGCCCGAGAAGGCCACCATGCGT              3142
           |||||||||||||||||||||| ||||||||||||||||||||||||||
Db   3060  TAGGACGACTGTCGCATCATCAGAGATGCCCGAGAAGGCCACCACCGGT               3119

Qy   3143  CATGGGTTACCCGTGGTAGCACGGCCCGGTGATGAGGTTCATCGGCGTCTTTCAGGA       3202
           |||||||  |||||||||||||||||| ||||||||||||| ||||||||||||||||
Db   3120  CATGGGCGTTGCCCGTTGGTAGCCGCCGCCCGGTGATGAGGTTCTTATCGGCGTCTTTCAGGA   3179

Qy   3203  TGTGAATCATTTGCTTGTGTCCCGACTGACGTTGTCCCAGTTGTGTCATCCGTCGCGG       3262
           ||||||| ||| ||| |||||||||| |||||||||||||||||||||||||| ||||||||
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Db   3180  TGTGAACCATCTGCCTCCCGATTCGTTCCAACTGCGCCCAGTTGTCATCCGGCCGTGCGG      3239

Qy   3263  AAAGGGGCTTCCTGGGGTCAGGAAGGCAGCCTTGACAGCCTTAGGGATCCTTGACTTACATCC   3322
           |||| ||| || ||||||||||  ||||| ||||||||||||||||||||||||||||||||
Db   3240  TAAGGGCTTTCTCGGGAGTCACAAAGGCTGCCTTGACGGGTCGGGACCCTGACTTACACTCC   3299

Qy   3323  AGGGAACGTCATGGTGTTGGGACGGCTACGTCACGAAGCATGGCACATGCTCGAATGG      3382
           |||||||||||||||||||||||||||||| |||||| ||||| ||||||||||||||
Db   3300  AGGGAACGTCATGGTGTTGGGACGGCTACGTCCGGAGCATGGGAACATGCCTAAACGG     3359

Qy   3383  CCTGCTGTTCACAACTTTCCATGGGCTTCATCCCGAACCATGCCACCGCGCCGGTGGGGGC    3442
           ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   3360  CCTGCTGTTCACGACGTTTCCCATGGGCTTCTTCCCGAACCATCGCGCCACGGTGGGGGC   3419

Qy   3443  CCTTAATCCCAGGTGGTGTCAGCCAGTCGATGAGGTCACGGTGTACCCGCTTCCAGATGG     3502
           |||||||||||||||| || ||||| ||||||| ||||||||||||||| |||||||||||
Db   3420  CCTTAATCCCAGGTGGTGTCGGCGCAGCGATGACGACGGTCACCGGTCTACCCGGTGCCGATGG   3479

Qy   3503  GGCAACTTCGTTGACGCCCTGCACTTGCCAGGCGAGTCCTGTTGGGTTATTAGATCCGA     3562
           |||||||| ||||| ||||||| ||||| ||||| |||||| ||| ||| |||||| ||||
Db   3480  AGCCACTTCGTTGACGCCCTGCACTTGCCAGGCTGAGTCCTGTTGGGTCATCAGTCCGA    3539

Qy   3563  CGGGGCTTTGTGCCATGGCTGAGCAAGGGGGACAAGGTTGAGCTGGATGTGGGCCATGGA     3622
           |||||||||| ||||||||||||||||||||||||||||||||| |||||| ||||||||||
Db   3540  CGGGGCGCTATGTGTCATGGCTGAGCAAGGGGGACAAGGTGAGCGTGAGACGTGGGCCATGGA    3599

Qy   3623  GGTCTCGACTTGCTCGTGGTTCGTCTCCTTGGCGACACTCCGGCACAAAGGGCACGCAGT    3682
           |||||||||||||||| || ||||||| ||||||||| ||||| ||||||||||||||||
Db   3600  GGTCTCTGATTTCCGTGGCTCGTCCGTCCTCCTGTGGCTACTGTCCCAACCGGGCACGCAGT   3659

Qy   3683  AAGAATGCTCGTGTCAGTGCTCCACTCTGCGCGGCGCAGGGTTACTGCGGCCGATTCACTAG   3742
           | |||||||||||| ||||||| | |||||||||||||||| |||  | |||||||||||||
Db   3660  AGGAATGCTCGTGTCGTGCTCCCTCATTCCCGGGCCAGGGTGACCGGTCCGGTCATCACTAG   3719

Qy   3743  GCCGTGGACTCAAGTACCAACAGATACCAAGACTACCACAGAACCCCTCCGGTGCCGGC    3802
           ||||||||||||||||||||||||||| |||| ||||| ||||| ||||||||||||||
Db   3720  GCCGTGGACCCAAGTACCAACAGATGTCCGTACATGGGTCCGTGGCCAACCCCGGTGCCAGC   3779

Qy   3803  AAAAGGAGTTTCAAGGAGGCCCCGTTGTTTATGCCTTCACAAGGATCACTGCCTATTCCAC    3862
           | ||||||||||||||||||| |||  |||| |||| |||||||||||||||||||| ||||
Db   3780  AAAGGGAGTTTTCAAGGAGGCCTCGTTTGTTTATGCCACAACGGGGGGGAAGAGCACACCCG   3839

Qy   3863  CGTACCGTTGGAGTACGGCAACATGGGCCACAAGTTCTTGATCTGAACCGTCGGTAGC     3922
           |||  ||||||||| |||||||||||||||||| ||| | ||| | |||||||||||||
Db   3840  CGTCCCCTTGGAGTACGGCAACATGGGCCACAAGTCCTGATTTTGAACCCTCGGTCGC     3899

Qy   3923  TACCGTGAGGGCCCATCATGAGCGGCGGCGGAAAACACCCCAGTATTTA              3982
           |||  ||||||  ||||| |||||| ||||||||  |||||||||||||
Db   3900  TACTGTGCGGCCGCATGGGTCGTACATGGAACGGGGGGAAACATCCAAGCATATA        3959

Qy   3983  CTGTGGCCATGACACCACTGCTTTCACAAGGATCACTGCGACTGGGCCCCCTTTACGTATTCCAC  4042
           |||||||||||||||||||| |||||| |||| |||||||||||||||||||||||||||||||
Db   3960  CTGTGGCCATGACACCACTGCTTTTACAAGGATCACCTGCTCACGATTGGGCCGATTATTCAAC  4019

Qy   4043  TTACGGAAGGTTTTTGGCCAACATGGGCCCAACCCATGGGCTCTTTCTC              4102
           | |  | ||||| ||| ||  |||| ||||||| |||||||||||||||
Db   4020  CTATGGGAGGTTCTTAGCCAACCCATATGGCCCAACCCATGAGTCGGTCATTTG         4079

Qy   4103  TGACGAGTGCCACAGTCATGACTTCAACTGTGTTGTTGGGCGTGTCAGGGAGCT          4162
           ||| ||||| ||||||||||  ||||||||| | | |||||| ||||||||||
Db   4080  TGACGAGTGCCACAGTCATGACTTCACCGTGTTGCTGGGGATTGGGAGAGTT          4139

Qy   4163  GGGCCGAGGATGTGGAGTGCAATTGGTGTGCTTCTACGCCCACCCCCCGGATCCCC       4222
           ||| ||||||| | ||| || | | ||||| |||  |  |||||| ||||||||||
Db   4140  GGCGCCGTGATGTGGAGTGCAACTTGTCAACTGCTACTCCTGATCCGGATCCCC         4199

Qy   4223  GATGACCCAGCACCCATCAATCATTGAGACAAAACTGGACATGGGAGAGATCCCCTTCTA    4282
           |||||||||||||||| ||||||| ||||| |||||||| |||||||||||||||||||
Db   4200  GATGACCCAGCACCCATCATCCATAATTGAGACCAAACTGGGATATGTGGGTGAGATCCCCTTCTA  4259

Qy   4283  TGGGCATGCGATACCTCTTGAGCGGATGATGGGAAGGCATCTCGTATTCTGTATTCTGCCACTC   4342
           ||||| |||||||||||| ||||| ||| |||||| ||||| | | ||| |||||||||||||
Db   4260  TGGGCATGCTGTATCCCCTCGAGCCGGATGATGCCGGATGCCGGACTGGAGGCATCTCGTATTCTGTATTC  4319
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Qy   4343  CAAGGCTGAGTGCGAGCGCTGGGCGGCCAGTGTTTCGGCTAGGGGGGTAAATGCCATCGC  4402
           ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   4320  TAAGGCTGAGTGCGAGCGCTGGGCGGCCAGTGTTTCGGCTAGGGGGGTCAATGCCATCGC  4379

Qy   4403  CTATTACAGGGGGAAAGACAGTTCTATCATCAAAGATGAGACCTGGTGGTGTGCTAC     4462
           ||||||||||||||| ||||||||| ||||||||   ||||||||| |||  ||| |||
Db   4380  TTATTACAGGGGGAAGGACAGTTCAATCATCAAGACGCCACTTAGTGTGTGTGCTAC     4439

Qy   4463  AGACGCACTATCCACTGGGTACACTGGGAACTTCGATTCGTCACCGATTGTGGGTTAGT  4522
           |||||||||||| ||||||||||||||||||| | ||| |||||||| |||||||||||
Db   4440  AGACGCACTATCCACTGGGTACACCGGGAACTTCGATTCGTCACCGACTGTGGGTTGGT  4499

Qy   4523  GGTGAGGAGGTCGTCGAGCTTGATCCCACCATTACCATCTCCCTGCCACCGGT        4582
           |||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   4500  GGTGAGGAGGTCGTCGAGCTTGATCCCACCATTACAATCTCCCTGCCGACAGT        4559

Qy   4583  GCCCGCGTCGCGTGAACGTGTCGATGCAGCGGCGGAGGACGACGCAGGTCTGG        4642
           ||||||||||||||||||||||||| |||  | |||||||||||||||||||||
Db   4560  GCCCCGCGTCGCGCTGGATGCAGAGACGACGAGGACCGCACGGTAGGAGGCAGTCGCCGG   4619

Qy   4643  GCGCTACTACGCGCGGGGTCGGCAAGGCCCTGCTCGGTGTGTCGCGCTCAGTCCTGT    4702
           ||||| ||||||||||| ||| |||||||||||||||||||| |||| |||||||||
Db   4620  GCGCTACTACTGGGGGGTGGGGCAAAGCCCCGTGTCGCGGCGGTGCGCGGTCCCTGT    4679

Qy   4703  CTGGTCGGCGGTGGGAAGCCGGTGTGACCTGTACGGGAATGGAACCTGACCTGACAGCAAA  4762
           ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   4680  CTGGTCGGCGGTGGGGAGTGACCTGTACGGGAATGGAACCTGACCTGACAGCTAA    4739

Qy   4763  CCTACTGAGACTTTACGACAACTGCCCTTACCACCCCGCAGCCTGACAGATGGGGA    4822
           |||| ||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   4740  CCTATTGAGACTTTACGACACTGCCCTTACACACCCGCAGCCGTGACAGATTGGAGA    4799

Qy   4823  AGCCGCGGTGTCTTTTCGCGGCGTCAACTGGGGATCATCCCGATGGTTAGCTGGGGC  4882
           ||||||||||  |  | |||||||| ||||| ||||||||||||||||||||||||
Db   4800  AGCCGCGGTGTTTTTTCTCCGGGCGTCAACTCGCCCCCGATGTCAGCTGGGGC    4859

Qy   4883  AAAAGTTCGCGGCGTCAACTGGCCCTTCTCGTTGGTGTTCAGCCGGACCATGTCCGGGGA   4942
           |||||||||||||||||||||  ||  ||||||| ||||||||||||| |||||||||||
Db   4860  AAAAGTGCGCGGCGTCAACTGGGCGCGTCCTCTGTGGTGTTCAGCCGGACCATGTGCGGGGA   4919

Qy   4943  AACACTGTCTCCCGGCCATCGGATGACCCCAATGGGGCAGTCTGAAGGGCCCGAATCC     5002
           |||||||||||||||||||||||  |||||||||||||||||||| ||||||||||||
Db   4920  AACACTGTCTCCATCGGATGACCCCAATGGGGCAGGTCTGAAGGGCCCGAATCC     4979

Qy   5003  TGTCCCACTCCTGCTCGAGGTGGGCAATGATTACCATCTAAAGTGGCCCGGCCATCACAT   5062
           |||||||||||||||||||||| |||||||||  ||  | |||  ||||||||||||||
Db   4980  TGTCCCCGCTGCTCGAGGTGGGGCAACGATTTGCCATCTAAAGGTGCCGGCCATCACAT   5039

Qy   5063  CGTTGGACGACCTGGTCTCCGTAGGGCTCGGCGGAGGGTTACGTCCGCTGCGATGCGGG   5122
           ||| ||||| ||||||||||||| |||||||| |||||||| |||| ||||||||||||
Db   5040  AGTTGGACGACCTGGTCTCCGTGTCCGGAGGGTTATGTCCGGTGCGATGCGGG    5099

Qy   5123  ACCCAGTCTTGATGGTGGGCGGCTATTGCCGCCGTCATCGATCATCGTCATACCACCGGT   5182
           ||||||||| |||||||| |||||||||| |||||||||| |||  | ||||||||||||
Db   5100  GCCGATCTTGATGGTGGGGGGCTATTGCCGCCGTCATCGATCATCGTCTTCACCACCGGT   5159

Qy   5183  GTCTCTCGTGGTGGTTACAGACTGGAGTGAAGTGGGGCCAGCCCCCCCTCTTTTATCGGCA   5242
           || |||||||||||||| |||||||||||| ||||||||||||||  ||||||||||||||
Db   5160  GTCTCCCGTGCTGCTGAGGTGTGGGGATGTGGAAGGTGTGGGGCGGCCCCCTCTTTTATCGGCA   5219

Qy   5243  CGTGGACGACCTGGTCGTAGGGTTGTTGCAGAGGGTTACGTCCCCGGTAGACCATCGGCGG   5302
           |||||||| ||||||||| |||||||| |||||||||||| |||| |||||||||||||||
Db   5220  TGGAGACGACCTGGTCGTAGGGGTTGTCAGAGGGTTACGTCCCGGTAGACCATCGGCGG   5279

Qy   5303  ACCCAGTCTTGATGGTGGGCGGCTATTGCCGCCGTCATGACCCGGCCGGCCATCCAGGT   5362
           ||||||||||||||||||||||||| |||||||||| ||||||||||||||||||||||
Db   5280  GGGAGTCTTGATGGTGGGGGGCTATTGCCGCCGTCATGACCCGGCCGGCCATCCAGGT   5339

Qy   5363  GGGAGTTGCGATTGGTCAGTTGATGACTCTGTCGGGAAGTGCTGTCGTCCTTGGCCCAGGC   5422
           || |||||||| ||||||||||| |||||||||  | ||||| ||||||||||||||||||
Db   5340  GGACTGCGATTGGTGATTGGTCAGTTGATGACTCGGATCGGAGAGTACGTGTCCTTGGCTCAGGC   5399
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Qy   5423  TAAGACGGCCGAGGCCTACGCAGCAGCTACCACCAAGTGCTTGCTGCCTACACGGGGAC  5482
           |||| ||||||||||||||||||||||||| |||  |||||||||||||||||||||||
Db   5400  TAAGACGGCCGAGGCCTACACAGCGACCGCCAAGTGCTTGCTGCCTACACGGGGAC  5459

Qy   5483  GCGGGCCGTCCCCACTGTTCAATTGTTGACAAGCTCTTCGCCGGGGCTGGCGGCCGGT   5542
           |||||||| |||||||||||| ||||||  ||||| |||||||||||||||||||||||
Db   5460  GCGGGGCCGTCCCCACTGTTCCATCCTATCCGTTGCACAGCTCTTCGCCGGAGGGTGGCGGCCGCGT   5519

Qy   5543  GGTAGGCCAATTGCCACAGTGTAATAGCTGCGGCGCAGTGCGGCCTATGGGCGTTCTAGGAG   5602
           ||  ||||||||||||||| || ||  ||||||| |||||||||||||| |||||||||||
Db   5520  GGTGGGCCAATTGCCACAGTGCTAATAGCTGCGGCCGTGGCTGGCCTTCACGGGCGTTCAAGGAG   5579

Qy   5603  CCCTCCATTGGCTGCTGCGCGTCCTGCCGTCTCCACCATTACCATCTCCCTGCCACGCGCA   5662
           ||| || |||||  ||||| | |||||||||||| |||||||||||||||||||||||||
Db   5580  CCCGGCCGTTGGGCTGCCAGCCCTCCTGATGGGGTGGGCGTCGGGGCGTTGGGGCGGGGGCAACGCCTCA   5639

Qy   5663  AACCCGCTTAGCCTCCGCTCTTCCTACTAGGGCGTCTGGGACCGCTCTCGGGCACGCCTGT   5722
           ||||| |  ||| |||| || |  ||| ||||| ||||||  |||||  |||||| |||||
Db   5640  GACGCGACTGGCGTCGCGTCCGCTGCACTGGGTCTGTGCTGCTGGGACTGCCTTGGGCACTCCCGT   5699

Qy   5723  CGTGGGGTTAACCATGCGGCGGCGTCAGTGGACGTGCTAGCGTCTCCGTCCCCCTCCTTGGT   5782
           ||| ||||| || |  |||| || || |||| |||| |||||  |  |||||| ||| |||
Db   5700  CGTGGGGTTTAACCATGCGGGGGGCGTTCATGGGCGTTCATCGCGGCCAGCGTATCCCCTCCCTGGT   5759

Qy   5783  CACCATTTTACTGGGGGCGTGGGGGCTGTGGAGGGCGTGAATGCGGCGTAGCCTTGT   5842
           |||||||||||||| |||||||||| |||| ||||| |||||||| | |||||||||
Db   5760  CACCATCTTACTGGGGGCGTGGGGCGTGTGGAGGTTGGGAGGGCGTCGTCAACGGCGGCAGCCTTGT   5819

Qy   5843  CTTCGACTTTATGGCGGGGGAAACATATCATCAGAAGATCTGGTGATGTCCATGCTGCT   5902
           ||| ||||| || |  |||||| |||| |||||| ||  |||| |||  |||||||||
Db   5820  CTTCGACTTCATGGCGGGGGAAACTTTCATCAGAAGAAATCGTGTGTGTTTCATCCCGGTGCT   5879

Qy   5903  AACCAGTCCGGGGGCAGGACTTGCGGGGATCGCCCCGTCCGGGGATGACTCAGCTAA   5962
           |||||  ||||||||||||| | | |   ||||| ||||||  ||||| ||||||||
Db   5880  GACCAGCCCAGGGGCGGGACTTTCAACCTAGGGTTCGCCCCGTCCGGGGATGACCTAGCTAA   5939

Qy   5963  CAACTCTGGCACTACCACTTGGTTCAGCAGGCCGATTACTGACTACGTCCTCATG   6022
           |||||||| | | | |||||  || ||||||   | |||  ||| |||| |||||
Db   5940  CAACTCTGGCACTACCACTTGGTTCAGCAGGTCTCGTTCGTGACCACGTCCTCATG   5999

Qy   6023  CATCCCGACAGTTACTTTCAGCAGGCCGATTGCTGACAAGGTCTCAGCTGTGTCTCCG   6082
           |||||||| |||| || ||||| |||||||||||| ||||| | ||||  ||||||||
Db   6000  CATCCCGACAGTTGGATACGTCTGTGGGACTGTGGATCATGCGCAAGAGTCTCCGCCGTGCTCCG   6059

Qy   6083  ACGCTTGAGCCTCACTCGCACCGTGGTTGCCCTGGTCAACAGGAGCCTAAGGTGGATGA   6142
           ||| ||| ||| |||||| ||| | || ||||| ||| | |||||||||  ||||||||
Db   6060  TCGCCTGAGCCTCACTCAGACGTGGTTCGCCCCTGGTCAACAGGAGCCCAAAGTCGGATGA   6119

Qy   6143  GGTTCAGGTGGGGTACGGTCTGGGACTTGTGGGAGTTGGATCATGCGCCAAGGCT   6202
           |||||||| | | ||||||| |||||| |||  ||| |||||||||||||||||||
Db   6120  GGTTCAGGTTGGATACGGTCTGGGATCTGTGGATCATGCGCCAGGTACGCGCCATGGT   6179

Qy   6203  GATGGCCAGACTTCGGGCCCTCTGCCCCTATTGGCACTGCCGGGGA     6262
           ||| |||||||| ||||||||||||||||  |||||| | |||||||
Db   6180  CATGGCCAGACTTAGGGCCCTCTGCCCCTTTTTATGGCACTGTGGGGA     6239

Qy   6263  GGGTGGTCCGGAGAATGGTTGTTGCGACGGCCATGTTGAGAGTCGTTGTCTTGTGTTG   6322
           |||| |||||||||| ||||||| ||||||| |||| |||| |||||| |||||||||||
Db   6240  GGGGTGGTCCGGAGAATGGTCGTTAGAGACGTGGTCATGGCTGCATGGTTGAGAGCCCGTGCCTTTGTTGTGTTG   6299

Qy   6323  CGTGATCACCGGTGATCGTTTTTGAATGGGCAACTCAGCTTTACTCTACCAAGCT   6382
           ||||| | ||||||| || |  |||| ||||||||| | |||||||||||||||||
Db   6300  GGTGATCACAGGCGACGTCCTAAATGGGCAACTCAAAGAGCCAGTTTACTCTTACCAAGCT   6359

Qy   6383  CGTTGCTCCCCTCAGACAGCCCCGGAGTGCTCCCGGTATGGGGCTATGGGACGTC   6442
           || ||||| ||  |||| |||||||||| | ||||| ||||| ||||||| |||||
Db   6360  GTGATCACAGGCCGCCACTATTGGATGGGAACTGTTCCAGTGGGAACTGTTCCAGTGTACCATGGGAAACATC   6419

Qy   6443  GTGCAGGCATTATTGATGATGGGGACAGTCCCTGTGAACATCTGGGCTATGCGAGACGTC   6502
           ||||||||| || |||||||||||||||| ||| ||||||||||| ||| |||||||||
Db   6420  GCCCTCCTGCTCCTCAGACACCCCGACACCCCCAAGGTCGTACCTTTTTGGACGTCTGGCTGGGGTGA   6479

Qy   6503  GGTGGTGTGGACCCCTACCCACGTTGTGATCAGGCGAACATCCGCCACACTGCTGCG    6562
           ||||| |||||| |||||||||| ||||||||| ||||||  || |||||||||||||
Db   6480  GGTGGTGTGGACCCCTACCCACGTTGTGATCAGGCGGAACATCCGCCACAAACTGCTGCG    6562
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Qy   6480 |||||||||||||||||| | ||||||||| ||||||||| |||||||||||| 6539
          GGTGGTGTGAGACCCTACCCATGGTGATCAGGAGGACTTCCGCCTACAAGTTGCTGCG

Db   6480 |||||||||||||||||| | ||||||||| ||||||||| |||||||||||| 6539

Qy   6540 CCACCAAATCCTGCGGCGTCGTGTTGCTAGCCCTATTACGTCGACGGCGTCTC 6599
Db   6540 CCAGCAAATCCTCATCGGCTGCTGCTGAGCCCTACTACTGTTGACGGCATCCCGGTCTC 6599

Qy   6600 ATGGGACCGGACGCGCGGAGCGCCTGCCATGGTCTATGGCCGCTGGGCAAAGTGTCACCAT 6682
Db   6600 GTGGGACCGGACGCCCGTGCGCCTGCCATGGTGTATGGCCGGGACAAAGTGTTACCAT 6659

Qy   6683 TGACGGGGAACGCTACACCCTTCCGCATCAACTGCGGCTTAGGAATGTGGCGCCCCTGA 6742
Db   6660 TGACGGGGAACGCTACACCCTGCGGCTTAGGAATGTGGCGCCCCTGA 6719

Qy   6743 GGTGTCATTCCGAGGTGTCCATTGACATTGGGACGGAGACTCAGAACTGACTGA 6802
Db   6720 GGTTCATTCCGAGGTGTATCCATTGACATTGGGACGGAGACTCAGAACTGACTGA 6779

Qy   6803 GGCCGACCTGCGCCGCGGCCGGCGTGCAGCCCTTCAGGCTATCGGAGAATGCTGCGAGAATTCT 6862
Db   6780 GGCCGATTTGCCGCGCCAGCCGTCGCCAGCCCTCCAGGCTATTGAGAATGCTGCGAGAATTCT 6839

Qy   6863 TGAACCTTCACATAGATGCATGGAGAGATTGCAGTATGCACCCTCTCTTTGTTGGGAGTAG 6922
Db   6840 TGAGCCCACCACATTGATGTGCATCGGGACTGTGAGTACACCCTCTCTTTTGGTGTAGTAG 6899

Qy   6923 CCGAGAGATGCCTGTGTGGGAGAAGACATACCCCGCACTCCATCGGCCAGCCACTTATCTC 6982
Db   6900 CCGAGAGATGCCTGTGTGGGAGAAGACGTCCCCCGCACTCCATCGGCCAGCCACTTATCTC 6959

Qy   6983 GGTTACTGAGAGCAGCCCAGATGAGAAGACCCCCGTGTCTTCCTCGCAGGAGGATAC 7042
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Qy   7043 CCCGTCTTCTGCTACTCATCGAGGTCATCCAAGAGTCCGAGACAGCCGGAAG 7102
Db   7020 CCCGTTCCTTCAATTGCATCCAGAGTCTGAGACAGCTCCAAGAGGGGAGGAGGACAA 7079

Qy   7103 CGTCTTCAACGTGGCTCTTTCCGTACTAAAAGCCTTGTTTCCAGAGAGCGATGCCACAAG 7162
Db   7080 CGTCTTCAACGTGGCCCTTTCCGTACTAAAAGCCTTATTTCCAGAGAGTGATGCCACTAG 7139

Qy   7163 AAAGCTTACCGGTTAAGATGTCATGCGTGTTGAGAAGCGTAACACGCTTCTTTTCATT 7222
Db   7140 GAAGCTTACTGTCAAGATGTCATGCGTGTTGAGAAGCGTCACGCGCTTCTTTTCATT 7199

Qy   7223 GGGATTGACGGTCGCTGACAAGCCTGTGTGAGATGGAAATCCAGAACCATACAGC 7282
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Qy   7283 CTATTGTGACAAGGTGCGCACTCCGCTTGAATTGCAGGTTGGGTGCTTGGTGGCAATGA 7342
Db   7260 CTATTGTGACAAGGTGCGCACTCCGCTTGAATTGCAGGTTGGGTGCTTGGTGGCAATGA 7319

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Qy   7403 CATTTGGTCTGGGGTGCCACTGACGAGGGCCACTCCGGCCCAAGCCCCCTGTGTGAGGCC 7462
Db   7380 CATCCTGGTCTGGGGTGCCACTGACTAGGGCCACCCGCCCAAACCACCTGTGTGAGGCC 7439

Qy   7463 GGTTGGGTCTCCTTGCTGGTGGCCCGACACCCGTATGTCACCAACCCGGACAATGT 7522
Db   7440 GGTAGGGTCTCTTTGTTGGTGGCCCACTACCACCAAGGTGACCAACCCGGACAATGT 7499

Qy   7523 TGGGGAAGAGTTGACAAGGTTACCTTCTGGCCCCTAGGGTTCATGACAAATTCCT 7582
Db   7500 GGGGAGGAGAGTGACAAGGTGACAAGGTGACCTTCTGGCCCGCGTCCATGACACAAGTTCCT 7559

Qy   7583 CGTGGACTCCATGAGAGCGCGCTAAGAGGGCCAGCCTCAAGCCTGCCTAAGCAGGTTACAC 7642
Db   7560 CGTGGACTCCATGAGAGCGCGCGCTAAGAGGGCCAGCCTCAAGCCTGCCTCAAGCATGGGTACAC 7619

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Db   7620 TTATGAGGAGGCAATAAGGACTGTAAGGCCCTACTACTGTCGACGGGATCTAAGGT 7679

Qy   7703 GTCGGTCAAGGACCTCGCCACCCGTGGGGAAGATGGCTGTCCATGGAAGCGGCTCCAGGA 7762
Db   7680 GTCGGTGAAGGACTTGGCCACCCGTGGGGAAGATGGCCGTTCATGACCGACTCCAGGA 7739

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Qy   8003 AAAGAAGACACCATGCGCCATCTGTGTGACGGACCGCCACATCTGCGACGCAGTAGCAATAACTGA 8062
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Qy   8183 GGGTGAGAGGTATTGTAGATGTTGTAGATCGTGGGCGTTTGACAACCAGTGCGAGCAACTGCTTGAC 8242
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Qy   8363 TTTGGGCAGGCCCCTGGCCAGGTGCCACTCCGCTGGAATTGCGAGGCCTTCGTGAGCCTTCGTGTATCGATCACT 8422
Db   8340 CCTGGGCAGGCCCCTGGCCAGGTTTACGGGTTTACGGTGTGCGAGCCGTGTCGTATCGATCATT 8399

Qy   8423 GGACACGGCCCCCTTCGCTCCACTTGGCTCCACTTGCGAGGCTCAGATGGGAAACGCCA 8482
Db   8400 GGACACGGCCCCCTTCGCTCCACTTGGCTCCACTTGCGAGGCTCAGATGGAAGCGCCA 8459

Qy   8483 TTTCTTCCTGACCACGGACTTTCCGGAGGCCCCCTCCTGCTCCTCTCTTA 8542
Db   8460 TTTCTTTCTGACCACGGACTTTCCGGAGGCCCCTCCTGCTCCTCTCCCTA 8519

Qy   8543 CCCAATGGCTTCGGCCCATCCGGTTACACCCGACAATGT 8602
Db   8520 CCCAATGGCTTCGGCCCATAGGTTTACATTCTCCTTTATCCCCATCCACACGGTG 8579

Qy   8603 GGTCATCATCCCTCACGTGCTTAGGGGTGTGGCACACCGTCTGATCC 8662
Db   8580 GGTCATCATCCTCACGTGCTGACGGCGGGGGCCCACACCGTCTGATCC 8639

Qy   8663 TGTGTGGTGCCAGGTACATGGTAATTACTACAAGTTTCCACTGGACAAACTGCCTAACAT 8722
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Qy   8783  AATGGAGGCCTGCCAAGTGCTGAGCGACCTCAAGCTCCCTGCCTAGCAGTCCACCGGAA  8842
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Qy   8843  GAAGGCCCGGGCATTGCGAACGCGTATGCTCCGGTCGCCGGTTGGGCTGCGAGTTGGCTAG  8902
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Qy   8903  GGGGTCGTTGTGGCGTCCAGGCCTGCGGCGTTCCCCCTCCGGAGATTGCTGCTGTATCCCGG  8962
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Qy   8963  GGGTTTCCCCCTTTCCCCCCCCTATATGGGGTGGTGTCATCAATTGGATTTCACAAGCCA  9022
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Qy   9023  GAGGAGTCGCTGGCGGTGGTTCTTAGCCCTGCTCATCGTAGCCCTTCCGGTG  9082
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Qy   9083  AACTAAATTCATCTGTTGCGGCAAGGTCCGTGACTGATCATCATCCGGAGGAGGTTCCCG  9142
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Qy   9143  CCCTCCCCGCCCAGGGGTCTCCCCCTGGGTAAAAAGGGCCCGGCCTTGGGAGGCATGG  9202
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Qy   9203  TGGTTACTAACCCCCTGGCAGGGTCAAAGCCTGATCGTGCTAATGCACTGCCACTTCGGT  9262
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Qy   9263  GGCGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGCTTGCTCGCAGAGCCCTCCCCG  9322
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Db   9240  GGCGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGGCTGCTCGCAGAGCCCTCCCCG  9299

Qy   9323  GATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCCGTAAGAGCTCG  9374
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RESULT 14
AF031829
LOCUS       AF031829                9351 bp ss-RNA     linear       VRL 22-DEC-1999
DEFINITION  Hepatitis G virus strain HGV-1539 polyprotein gene, complete cds.
ACCESSION   AF031829
VERSION     AF031829.1  GI:3004904
KEYWORDS    .
SOURCE      Hepatitis G virus.
  ORGANISM  Hepatitis G virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            GBV-C/HGV group.
REFERENCE   1  (bases 1 to 9351)
  AUTHORS   Bukh,J., Kim,J.P., Govindarajan,S., Apgar,C.L., Foung,S.K.,
            Wages,J. Jr., Yun,A.J., Shapiro,M., Emerson,S.U. and Purcell,R.H.
  TITLE     Experimental infection of chimpanzees with hepatitis G virus and
            genetic analysis of the virus
  JOURNAL   J. Infect. Dis. 177 (4), 855-862 (1998)
  MEDLINE   98194579
   PUBMED   9534956
REFERENCE   2  (bases 1 to 9351)
  AUTHORS   Bukh,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-OCT-1997) Hepatitis Viruses Section, LID, NIAID,
            National Institutes of Health, 7 Center Drive 0740, Building 7,
            Room 201, Bethesda, MD 20892-0740, USA
FEATURES             Location/Qualifiers
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ORIGIN
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us-09-828-498-1.rge

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Best Local Similarity 90.6%;   Pred. NO. 0;
Matches 8474;   Conservative  0;   Mismatches 877;   Indels 1;   Gaps 1;
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Qy     23 CCCCCCGGCACTGGGTGCAAGCCCCATAAACCGACGCGCTATCTAAGTAGACGCAATGAC     82
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Qy     83 TCGGCGCCGACTCGGCGACCGGCCAAAAGGTGTGGATGGGTGTGACAGGGTTGGTAGG    142
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Qy    143 TCGTAAATCCGGTCATCCTGGTAGCCACTATAGTGGGTCTTAAGAGAAGGTCAAGACT    202
          ||||||||||||||| | ||||| |||||||||| || |||| |||||| |||| ||
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Qy    203 CCTCTGTGCTGCGGAGACGCCGCACGGTGCTGCGCCTACCGGTGTGAA    262
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Qy    263 TAAGGGCCCGACGTCGGCTGCGTGCCTTAAACCGAGCCCGTCACCCACCTGGGCAAAACGAC    322
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Db    241 TAAGGGCCCGACGTCGGCTGCGTGTCTTAAACCGAGCCCGTCACCCACCTGGGCAAACGAC    300

Qy    323 GCCCACGTACGGTCGTCGCCCTTCAATGTCTCTCTTGACCAATAGGTTTATCCGGCG    382
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Qy    383 AGTTGACAAGGACCAGTGGGGCGCGGGGTTATGGGAAGGACCCCAAACCTGCCCTTC    442
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Qy    503 CCCAAGAATCCTTCGGGTGAGGGCGGTGGCATTTCTCTTTCTATACCATCATGGCAGT    562
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Qy    683 CCTGAAGGCGGATGCCTGTGGCCGGGTTGCACGGCCACCGCCGTTGCTGGCC    742
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 CCTGGAAGGTGGATGCCTGTGGCCGGGTCTCGCGCGTGTACAATGCGACCGATGCTGGCC    719

Qy    743 ACTGTATCAGGCGGGTTGGCTGTGCGGCCTGGCAAGTCCGCGGCCCAGCTCGTTGGGGA    802
          || |||||||||| || |||||| |||||||||||| ||||||||||||| |||||||
Db    720 ACTGTATCAGGCGGGTTCGCTGTGCGGCCTGGCAAGTCCGCGGCCCAACTGGTGGGGA    779

Qy    803 ACTGGGGAGCCGTACGGGCCCTGTGTACGGCCTTACGTAGCCGGATCCGGGTCT    862
          ||||||| ||||||||||||||||||||||||||||| |||||||||||||| ||
Db    780 GCTCGTGGCCACGGGCTCACGGGCCCTATCGGTCTCAGCCTACGTGGCGGGGTCCGGGCCT    839

Qy    863 GGGGCAGGTTTACTCGGGTTGGTGTTGCACGGTGGGCGCCGGGGTCTACCT    922
          |||||||||| |||||||||||||||||| |||||| |||||||||||||
Db    840 GGGTGAGGTATACTCGGGTGTCTGACAGTCGGTGGGGCGCCGGGTCTACCC    899

Qy    923 GATGCCCAACCTGAAGTGTGCAGTAGAAATCGACGTTAAGTGACGTTAAGTGGGGGAAGTTTTGGGAG    982
          | ||||||| |||||| ||||||||||| |||||||||||||||| ||||||||||||
Db    900 GGTGCCCAACCTGACGTGTCAGTGGGGGGTTCATGAACCCTGTGTCCGGGCGGGGTGGGAAGTGAGTTTTGGGAG    959

Qy    983 ATGGACTGAGCAGTTGGCCTCCAATTACTGGATTTTGGAATACCTTCGGAAAGTCCCATT    1042
          ||||||||||| ||||| |||||||||||||||| ||||||||||||| |||||||||
Db    960 ATGGACTGAACAGCTGGCCTCCAATTACTGGAATATCTCTGGAAGGTCCATT    1019
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Qy   1043 TGAATTTGGAGGAGGTGATGAGCCTGACCCCTCTGTTGGTTGGGTGGCCGCATTGCT    1102
          |||||||||||||||| |||||||||||||||||||||||||||||| ||| ||||
Db   1020 TGATTTCTGGAGGAGGTGTGATGAGCCTGACTCCCTTGTTGGTTTGCCTTGCTGCCCTGCT    1079

Qy   1103 TTTGCTGGAGCAACGGATTGTCATGGTTTCCTGCTGGTGACGATGGCGGGGATGTGCA    1162
          || || ||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1080 GCTGCTTGAGCAACGGCGTTGTCATGGTCTCGTGTGACGATGGCGGGGATGTGCGCA    1139

Qy   1163 AGGCGCCCCGCCTCCGTTTGGGGTCCCGGCCCCTTGGGGGTTGACTACGGGTGAAGTGGCAGTC    1222
          ||||||||||||||||||||||||||| ||||| |||||||||||||||||||||||
Db   1140 AGGCGCCCCGCCTCCGTCATGGGGTCTCGCATCGGGGTTGACTACGGGTTGACTTGGCAGTC    1199

Qy   1223 ATGCTCCTGCAGGGTCGGCGTAACGGCGTATTCCCACTGGGGAGAGGGTGTGGGATCCAGG    1282
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   1200 CTGCTCCTGCAGGGGTCGGCGTAACGGCGTATTCCGACCGGGGAGAAGGTGTGGGACCGTGG    1259

Qy   1283 GAATGTCACGCTCTTGTGTGACTGACGCCCCAAGCGCCCCTGGGTTTGGTGTCCCGGCCTTTTG    1342
          |||||||||||| | |||| ||| ||| ||||||| |||||||| |||||||||||||| |||
Db   1260 GAACGTCACACTCTTGTGCGACTGACGCGCCCCAACGGCCCCTGGGTGTGGCTCCCAGCTCTCTG    1319

Qy   1343 CCAGGCGGTTGGGTGGGGCGACCCCATCACCCATTGTGTGTCCGTAACGTGCGTGGGGTTCCGT    1402
          |||||||| ||||||||||||||||||| |||||||||||||| ||||||| |||||||||
Db   1320 CCAAGCAGTGGGCTGGGGTGATCCCATTACCCATTGGGGCCCACGGTCAAAATCGGTGGCC    1379

Qy   1403 CCTATCATGCCCCATATGTCTGACCGGCGTGTGATTCGAAGATCGATGTGGAGTTTGGTGCC    1462
          |||| |||||||| |||||||||||| |||||| |||||||||| ||||||||||| ||||
Db   1380 CCTTTCATGCCCCCAGTATGTCTGTTTGTTCGGTGTTCAGTCACTTGCGTTGCCGTGGGGTTCTGC    1439

Qy   1463 GTCTTGGTTTGCCTCACCGGCGTCGTGATTCGAAGATCGTGAAGATGTGGAGTTTGGTGCC    1522
          |||| ||||||||||| ||||| |||||||||| ||||||||||||||| |||||||||||
Db   1440 CTCCTGTTTGCCTCACCGTGGCCGTGACTCGAAGATCGTGAAGATGTGGAGTTTGGTGCC    1499

Qy   1523 GGTTGGATCTGCCAGCTGCACCATAGCGCGTCTCAGGGTCATCGGACGGACACGGTGGT    1582
          |||| |||||||||||||| ||||||||||||||| |||||||||||| |||||||
Db   1500 AGTTGGCTCTGCCACCTGCACCATAGCGCACTCGGGTCATCGGACGGTGGT    1559

Qy   1583 TGAGCTCTCCGAGTGGGAGTCCCGTGCGTAACGTGTATTCGGACCGTCGCGGCCTGCTTC    1642
          |||||||||||||| |||| || |||||| ||| |||||||||||||||| ||||||||
Db   1560 TGAGCTCTCCGAGTGGGGGATCCCGTGCGTGCGTGTATTCGGACCGTCGCGGCCTCCTC    1619

Qy   1643 ATGTGGCACCTGTGTGCGGGACTGCTGCCGGGCCGAAACCGGGTCGGTTAGATTCCCTTTCCA    1702
          || ||||| ||||| |||||||||||||| |||||||| |||| ||||| ||||| ||| ||
Db   1620 TTGCGGCACCTGTGAGGGGACTGTTGCCGGGCTGGGTCAGTCAGGTTTCCATTCCA    1679

Qy   1703 TCGGTGCGGCACGGGGCGGCCTCGGCTGACAAGGACACTTGGAAGCTGTGCCCTTCGTCAACAG    1762
          |||||| ||||||||||| |||||||||||| |||| | |||||||||||| |||||||||
Db   1680 TCGGTGCGCACGGGGCGGCCTCGGCTGACAAGGACACTTGGAAGCTGTGCCCTTCGTCAATAG    1739

Qy   1763 GACAACTCCCTTCACCATAAAGGGGCCCCTAGGCACGGAGAGGCAACCCGGTGCG    1822
          ||||||||||||| |||||||| ||||||||||||||||| |||||||||||||
Db   1740 GCCCGGCCCCTTAACAACTGTCTTAGGCACACAGAGGTGTCGAGGGTAACCCGGTGCG    1799

Qy   1823 GTCGCCCCCTGGGTTTTGGGTCGCGGGCTGGCAAGTCCTGGCGGATTCCTGCATTTGGT    1882
          |||||||||||| |||||||||||| ||||||||||||||| ||| |||||||| |||
Db   1800 GTCACCCCCTGGGGTTTTGGGGGGTGGCTCCTGGCGCGGGTTCGGAGACACCCTACATCTGGT    1859

Qy   1883 GAAATGTCCCACCACAGCCATAGAGCCTCCGACTGGAACGTTCGGGTTCTTCCCCGGAGT    1942
          |||||||||||||| ||||| |||||||||| ||||||||||| |||||| |||||||
Db   1860 GAAATGTCCCACCACCCCAGCCATTGAGCCTCCGCACCGGACGTTGGGTTCTTCCCCGGGAC    1919

Qy   1943 CCCGCCATTAACAACTGCATCGCGCTAGGCACGGAGAGTGTCTGAGGCATTGGCGGAGC    2002
          |||||||||||||||||| || |||||||| ||| |||||||||||| ||||||||||
Db   1920 GCCGCCCCTTAACAACTCCCTTAGGCACACAGAGGTGTCTGAGGCACTCGGTGTGGGGC    1979

Qy   2003 TGGGCTTTACGGGGGTTCTACGAGCCTCTGGTTCCGCAGGTTGATGGGACG    2062
          |||| || |||||| ||||||||| |||||||||||||| ||||||||||
Db   1980 TGGTCTCACGGGGGGTTCTATGAACCCTGTCGTTCGGCGCAGGTTCGGTGTGGGGCG    2039

Qy   2063 CCGAAATCCGGTTTGGCCTCCAATTACGGGTACGCCATGTGCGGGTACGGCGGGGTCAT    2122
          ||| ||||||||||| |||||||||| |||||||||||||||||||||||||||||
Db   2040 CCGCAATCCGGTTTGCCCGGGTTTGCATGGCTTCTCTGCGGGTTTGCGACCTGACCTGACGGGGTTTAT    2099

Qy   2123 ACACGTCCAGGGCACCTGCAGGAGGTGGATGCGGGGCAACTTCATCCCTCCTCCACGCTG    2182
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   2123
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Db  2100  ACATGTTCAGGGCACCTACAGGAGGTAGATGCTGGCAACTTCATCCCTCCTCCTCGTTG  2159
                ||| ||||  ||||       |||||||||||||||| ||||||| ||||||||||

Qy  2183  GTTGCTCTTGGATTTGTATTGTCCTGCTCTATCTGATGAAGCTGGCTGAGCACGGTT  2242
          ||||||||| ||||||  |||| ||||||||| || || |||||||||||||||||||
Db  2160  GTTGCTCTTGGACTTTGTTGTTGTCCTGTATACCTGGCTGAGCTGAGCACGGTT  2219

Qy  2243  GGTCCCGTTGATCTTGCTTGGGTGGTGGTGAACCAGTTGCCGGTTCTAGGACT  2302
          |||||||| |||||| | |||||| |||||||||||| || |||| ||| ||||
Db  2220  GGTCCCGCTAATCTTACTACTGCTGTGTGGTGGTGAACCAGTTAGCAGTCTAGGGCT  2279

Qy  2303  GCCGGCTGTGGACGGCTGGCGGTGAAGTTTTGCGGGCCCTGCCTTGTCATGTG  2362
          |||||||||||| |||||| | |||| ||||||||||||||||||| |||||||
Db  2280  GCCGGCGTGGGACGCCGCCCGTAGCTGGTGGGTGTTTGCGGGCCCTGCCTTGTCCTGTG  2339

Qy  2363  TTTGGGGCCTTCCCACTGTCGATGATGATACTAGTCTTAGCAAACCTGGTGTTGTACTTTCG  2422
          |||| ||||| || || |||    ||||||||| |  |||||||| ||||||||  |||||
Db  2340  CCTGGGCGTCCCCGGTAGTCAGTTAGCTGTGTCGTGTACTTTAG  2399

Qy  2423  GTGGATGGGCCCTCAGGCGCCTCATGTTCCTCGTGTTGTGGAAGCTCCTCGTGGGGACTTT  2482
           | |||||||||  ||  || ||||| | |||||| |||||| |||||||||||||||||
Db  2400  ATGGCTGGGACCCCCAACCCTGTGATGTTCCTTGTCTGTGGAAGCTCCGTGGGGAGCTTT  2459

Qy  2483  CCCGCTGGCACTTTTGATGGGATTTCGGGCGACCCCGGCGCCCACCTCTGTGCTGCTGGGC  2542
          |||||||||| || ||||||||| |||||||||||||  ||||||| ||||| |||||||
Db  2460  CCCGCTGGCTCTTCTGATGGGATTTCGGGCGACCCCGGCGCCCACCTCCGTGCTGCTGGGC  2519

Qy  2543  CGAGTTCTTGCTTCGATGTCACATTCGAGGTGGACACTTCGGTGTTGGGCTGGTGGTGGC  2602
          ||||||||||| ||| |||| ||||||||||||| ||||||||||||| |||||||||||
Db  2520  CGAGTTCTTGCTTCGATGTCACATTCGAGGTGGACACTTCGGTGTTGGGCTGGTGGTGGC  2579

Qy  2603  CAGCGTGGTGGCCATAGGACGCGTCCTGAGCTCAATGAGCGCAGGGGGGTGGAAGCA  2662
          |||| |||||||||||| | ||||| ||| |||| |||||||||||||||| |||||
Db  2580  CAGTGTGGTGGCTGGGCTAGACGCTCCTCGACTTCGGTGTCCGATGAGCGCAGGGGGGTGGAAGCA  2639

Qy  2663  CAAGGCCGTGATCTATAGGACGTGGTGTAAAGGGTACCAGGCTGTGCGCCAGAGGGGTGGT  2722
          |||| ||||||||||||||||||||| | |||| |||||||| ||| ||| ||||| |||
Db  2640  CAAAGCCCTGATCTATAGGACGTGGTGTAAGGGGTACCAGGCGTGCCAGAGAGTGGT  2699

Qy  2723  GCGACTGGCACGGGTGGTTGAGTGCTGTGATGGCGGCGTCCTGACCTTCGCGGTGCTTGGC  2782
          |   |||||||||||||||||||||||| |||||||||||||| ||||||| |||||||||
Db  2700  GAGGAGCCCCCTCGGGGAGGGGCCCCCACCAAAACCTTGACCTTCGGTGCTTGGC  2759

Qy  2783  CTCATACATCTGCCGATGCTGTGATGATGGTGGTGCCTTGGTGGTCCTCCTCTTCGG  2842
          || ||  ||||||||| ||   |||||| ||||| |||||| ||||||||||||||
Db  2760  CTCATACATCCGGCCGACGCCCTGATCATGGTGGTGCGCCTTGGTGTTACTCTTTGG  2819

Qy  2843  CCTGTTCGACGACTGGACTGGGCCCTGGAGAGCTCCTGGTCTCCCGGCCCTCGTTACG  2902
          |||||||||||||||||||||||| |||| ||||||||| |||| |||||||||||||
Db  2820  CCTGTTCGACGCCGTTGGACTGGGCTTTGGAGGATCTTGGTGTCCCGGCCCTCGTTACG  2879

Qy  2903  GCGACTGGCACGGGTGGTTGAGTGCTGTGATGGGCGAGAAGGCCACCACCATCCG  2962
          ||||||||||| ||||| | |||| ||||| ||||||||  ||||||||||||| |
Db  2880  CCGGTTGGCGCGCGGGAGGGGCCCCGGAGTGGATGGGCGAGGAGGCGCCACCAACCGGTTCG  2939

Qy  2963  ACTGGTCTTCCAAGATGTCGCAAGAGGGCGTTCTCAATGGGCTCTTTCTC  3022
          ||||| || |||| | ||||||| |||||| ||||||   ||||||||  ||
Db  2940  GCTGGTCTCCAAGATGTCGCCGGAGGGGCGCCTACTTGTTCGATCACATGGGCTCTTTTC  2999

Qy  3023  GCGCGTCTCAAGGAGGCTGTTGGAATGGCAAGACGCGGCCTTTGGACCCGCGCGGTCATTCAC  3082
          |||||||||||||||| || | |  ||||| ||  ||||| ||   |||||| ||||||||||
Db  3000  GCGCGTCTCAAGGAGGCTGCCCGGTGGGACGCGCCCTGGGAGTGGGGAACCCTGTCTTTCAC  3059

Qy  3083  TAGGACGGACTGTGCGCATCATCAGAGATGGCAAGGGCGCGGAGATGCCCGAGAAGCCGT  3142
          |||||||||||||||||| | |||||||| ||| |||||||||||||| ||||| |||||
Db  3060  TAGGACGGACTGTCGCATCATCATAGAGATGCGCGACCGGAGATGCCGAGAAGTCGT  3119

Qy  3143  CATGGGTTTACCCGTGGTAGCACGGCGTTCTCATCGGCGTCTTTCAGGA  3202
          ||||||||||||||||||||||||||||||||||||||| |||||||||
Db  3120  CATGGGCTTACCCGTGGTAGCCGGCGCGCCGCCGGTGATGAGTTCTTATCGGCGTTTTCAGGA  3179

Qy  3203  TGTGAATCATTTGCCTCCCGACTGCGTCATCCCGTCGGTGCGG  3262
          |||||||| ||| |||||||||| ||||| ||||||||||
Db  3180  TGTGAACCATCTGCCTCCCGGATTCGTTCCAACTGCGGCCAGTGTCATCCGGCGGTGCGG  3239
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Db  3180  TGTGAACCATCTGCCTCCCGGATTCGTTCCAACTGCGGCCAGTGTCATCCGGCGGTGCGG  3239
          |||||||| |||  ||||| ||  |||| ||||||||||| ||||||  |||||||||||

Qy  3263  AAAGGGCTTCCTCGGGGTCACGAAGGCAGCCTGACAGGTGATCCTGACTTACATCC  3322
          ||||| |||||| ||| |||||| |||||| |||||| ||| |||| |||||||||||
Db  3240  TAAGGGCTTCTGGAGTCACAAAGGCTGCCTTGACGGGTCGGGACCCTGACTTACATCC  3299

Qy  3323  AGGGAACGTCATGTGTTGGGACGGCTACGTCACGAGACATGGCACATGTCTGAATGG  3382
          |||| |||||||||||||||||||||||||| ||||||| |||||||||||||||||
Db  3300  AGGGAACGTCATGTGTTGGGACGGCTACGTCCGGGAGCATGGCAACATGGCCTAAACGG  3359

Qy  3383  CCTGCTGTTCACAACTTTCCATGGGCTTCATGGGCTTGTCATCGTGTCG  3442
          |||||||||||||| ||||||||||||||||||| |||| || ||||||
Db  3360  CCTGCTGTCACGACTTTCCATGGGCTTCCATGGGCTCGTTCCGAACCATCGCGACGCCCGGGGC  3419

Qy  3443  CCTTAATCCAGGTGGTGCTCAGCCAGTGATGACGTCACGGTGTACCCGTTCCAGATGG  3502
          ||||| ||||| |||||||||||||| |||| |||||| |||||| |||| || |||||
Db  3420  CCTTAATCCCAGGTGGTGCCCGGCCAGCGACGTCACGGTCTACCCGGTTATTAGATCCGA  3479

Qy  3503  GGCAACTTCGTTGCACGCCCTGCACTTGCCAGGCGGAGTCCTCGTTGGTTATTAGATCCGA  3562
           | |||||||||| | ||||| |||| || |  |||| ||||||||||||||| ||||||
Db  3480  AGCCACTTCGTTGCACGCCCTGCACTTGCCAGGCTGAGCTCCGTCATCAGGTCCGA  3539

Qy  3563  CGGGGCTTTGTGCCATGGCTTGAGCAAGGGGACAAGGTTGAGCTGGATGTGGCCATGGA  3622
          ||||||||| |||||| ||||| ||||||| ||||||||||| ||  ||||||||||||
Db  3540  CGGGGCCGCTATGTCATGGCTTGAGCAAGGGGACAAGGTGGAGCTAGAGTGGCCATGGA  3599

Qy  3623  GGTCTCTGACTTCCGTCGTTGTCTCCACTCTGGCGGCAGGGTTCACGTCGGTCTGGCTGGC  3682
          |||||||||||||||| |||||  |||||| ||| || ||||||| |||||||| ||||||
Db  3600  GGTCTCTGATTTCCGTCGTTGCTTCACCTGTCGGCAGGGTCCACCTGTCGGTTCACTAG  3659

Qy  3683  AAGAATGCTCGTCAGTGCTCCACTCTGGCGGCGGCGGTTACTCGCGGCGGCGATTCACTAG  3742
          | |||||| | ||  |||||||||||||||||||||| |||||||||||| ||||||||||
Db  3660  AGGAATGCTCGTCGTGTCGTGCTTCATTCCGGTGGCCAGGTGGCAGGTCCGGTTCACTAG  3719

Qy  3743  GCCGTGGACTCAAGTACCAACAGATGCCAAGACTACCACACAGAACCCCTCCGGTGCCGGC  3802
          |||| ||||| |||||||||||||| ||||||| |||||||| | ||||| |||| ||| |
Db  3720  GCCCTGGACCCAAGTACCAACAGATGCCAAGACTACCACACACCGGCGACCCCCGGTGCCGCAGC  3779

Qy  3803  AAAAGGAGTTTCAAGGAGGCCCCGTTGTTTATGCCTTATCGTACGGGCGGGGAAAGAGCACCCG  3862
          ||| ||||||||||||||||| ||| || || |||| ||||||||||||||||| ||||||||
Db  3780  AAAGGGAGTTTCAAGGAGGCTCCGTTCGTTTATGCCAACGGGGCGGGGAAGAGCACCCG  3839

Qy  3863  CGTACCGTTGGAGTACGGCCAACATGGGCCACAAGTCTTGATCTTGAACCCGTCGGTAGC  3922
          ||| ||| |||||||||||||||||| |||||||||| | |||  |||||| ||||| ||
Db  3840  CGTCCCCTTGGAGTACGGCCAACATGGGCCACAAAGTCTGATTTGAACCCCGGGTCGC  3899

Qy  3923  TACGGTGAGGGCCATGGGCCCATACACTGAGCCATGGAAACACCCCAGTATTA  3982
          || | | |||||| | ||||| |   |||||||| |||||||| ||||||||
Db  3900  TACTGTGCGGGCCATGGGCCCGTACATCGGTACATCGGAACAATCCAAGCATATA  3959

Qy  3983  CTGTGGCCATGACCACCACTGCTTTCACAAGGATCACTGCCCCCCTACGTATTCCAC  4042
          |||||||||||||| ||||||||||||| ||| || ||| |||| |||| |||| ||
Db  3960  CTGTGGGCCATGACCACCACTGCTTTTACAAGGATCACCCCTTTGACGTATTCAAC  4019

Qy  4043  TTACGGAAGGTTTTTGGCCAACCCTAGGCGGCTTTGACCACATGGGCTCTTTCTC  4102
           | | |||| ||  |||||||||| |||| |||| ||||| |||||| ||||| ||
Db  4020  CTATGGAGGTTCTTAGCCAACCCTAGCCGCTTTCGACGTGGTGGTGTCAGGGACT  4079

Qy  4103  TGACGAGTGCCCAGCATCATGACTCAACTGTGTTGTGTTGGGCATTGGGCATTCAGGGAGCT  4162
          ||||||||| |||| | ||||| ||||  |  |||||||||||| ||  ||||| |||||
Db  4080  TGACGAGTGCCCAGCATCATGACTCGTCAATTGACGACCAAACTGACGGATATTGGTGAGTT  4139

Qy  4163  GGCGGAGGATGTGGAGTGCAATTGGTGCGTCGCCGCCACTCCCCGGATCCCC  4222
          |||| |||||| ||  |||| |||  |  | ||||| |||||| ||||||
Db  4140  GGCGCCGGTGGATGTGGAGTCGCAACTTGCTCTACGCCACTGCTCTCCTGCCCGATCCCC  4199

Qy  4223  GATGACCCAGCCAGCACCCATCAATCATTGAGACAAAACTGACGTGGGAGATCCCTTCTA  4282
          |||||||| ||||||| |||| ||  |||| ||||| |||| ||||||||||||| ||||
Db  4200  GATGACCCCAGCCAGCACCCATCCATAATTGACGACCCAATCTGGTGGTGAGATCCCCTTCTA  4259

Qy  4283  TGGGCATGGCATACCTCTTGAGCGGATGCGGATGCGGAAGGCATCTCGTATTCTGCCACTC  4342
          |||||| ||| ||||| | ||| |||||||  | ||| ||||||| || |||||||
Db  4260  TGGGCATGGTATCCCCTCGAGCGGGATGCCGGCATCTCGTATTCTGCCATTC  4319
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Qy   4343 CAAGGCTGAGTGCGAGCGCCTGGCGGCGCAGTTTTCGGCTGGGGTAAATGCCATCGC 4402
           ||||||||||||||||||||||||||| ||| |||||||||||| ||||||||||||
Db   4320 TAAGGCTGCGAGCGCCTGGCTGGTCAGTTTTCCGCTGGGGGGTCAATGCCATCGC   4379

Qy   4403 CTATTACAGGGGAAAGACAGTTCTATCATCAAAGATGGAGACCTGGTTGGTGTGCTAC 4462
           ||||||||| ||||||||||||||||||||| ||||| | |||||||||||||||||
Db   4380 TTATTACAGGGGAAGGACAGTTCAATCATCAAGGACGCGGACTTAGTTGGTGTGCTAC 4439

Qy   4463 AGACGCACTATCCACTGGGAACTTCGATTCTGTTCACCGATTGTGGGTTAGT   4522
           ||||||||||| ||||||||||||| |||| |||||||||||||||||| ||
Db   4440 AGACGCACTATCCACTGGGTACAACTCGATTCTGTCACCGACTGTGGTGTTGGT   4499

Qy   4523 GGTGGGAGGAGGTCGTCGATGACCCTTGATCCCACCATTACCATCTCCCTGCGCACGGT 4582
           |||||||||||| |||| ||||| ||||| ||||| |||||||||||| |||||| |||
Db   4500 GGTGGGAGGAGGTCGTTGAGGTGACCCTTGACCCCTCCACCATTCCCTGCGGACAGT   4559

Qy   4583 GCCCGCGTCGGCTGAACTGTCGATGCAGCGGCGGGCGCAGGGTAGGGGCAGGTCTGG   4642
           ||||||| ||||||||||||||||||||| ||||||| |||||||||||||| |||
Db   4560 GCCCGCGTCGGCTGAATTGTCGATGCAGACGAGACCACGGGTAGGAGGCAGGTCCGG   4619

Qy   4643 CGCTACTACTACGCGGGGGTCGGCAAGGCCCCTGCTGGTGTCGTCAGTCCTGT   4702
           ||||||||||||||||||| |||| |||||||||||| |||||||||||| |||
Db   4620 GGCTACTACTACGGGGGGTTGGCAAAGCCCCCTGCTGGCTGTCGTCGGGTCCTGT   4679

Qy   4703 CTGGTCGGCGGTGGAAGCCGGTGACCTGGTACGGAATGGAACCTGACCTGACAGCAAA 4762
           ||||||||||| ||||| ||||||||| |||||||||||||| ||||||||||||
Db   4680 CTGGTCGGCGGTGGAGCCGGTGACCTGGTACGGAATGGAACCTGACCTGACAGCTAA 4739

Qy   4763 CCTACTGAGACTTTACGACACAGTGCCCTTACACCGGACCGCTCGCAGCTGACGTTGGGGA 4822
           |||||||||| |||||||||| ||||| |||| |||| |||||||||||||||||||||
Db   4740 CCTATTGAGACTTTCATGGCGGGGAAACTTTCATCAGACGCCGCTGACATTGGAGA   4799

Qy   4823 AGCCGCGGTGTCTTTTCGGGGCTTGCCCGTTGAGGATGCATCCCGGATGTTAGCTGGGC 4882
           ||||||| ||||||| || |||||||||| ||||||||||||||| |||||||||||
Db   4800 AGCCGCGGTGTCTTCCGTGCTTGCCCGTTGAGGATGCACCCCGATGTCAGCTGGGC   4859

Qy   4883 AAAAGTTCGGCGGCGTCAACTGGCCCTTCCTGGTGGGTGTTCAGCGGACCATGTGCCGGGA 4942
           |||||||||||||||||| ||||||||||| |||||||||||||||| |||||||||||||
Db   4860 AAAAGTGCGGCGGCGTCAACTGGCCCTTCTTGTGGGTGTTCAGCGGACCATGTGCCGGGA 4919

Qy   4943 AACACTGTCTCCCGGCCCATCGGATGACCCCAGTGGGCAGTGTCTGAAGGGGCCCGAATCC 5002
           ||||||| || ||||||||||||||||||||||||||||||||| |||||||||||||||
Db   4920 AACACTGTCTCCGGTCCATCGGATGACCCCAATGGGCAGTGTCTGAAGGGGCCCGAATCC 4979

Qy   5003 TGTCCCACTCCTGCTGAGGTGGGTTACAGAGTGGGATGCAATGATTTACCATCTAAAAGT 5062
           ||||| | ||||||||| |||||||| |||||||| ||||| ||||||||||| ||||| |
Db   4980 TGTCCCCGGTAGTGGGTGGTGGGATGTCAACGATTTGCCATCTAAGGTGGCCGGCCATCACAT   5039

Qy   5063 CGTGGACGACCTGGTCGTCCGTAGGCTGGCGGAGCTTGTCCGGACCATGCGGGG 5122
           ||||||||||||| ||||||||||| ||||||||| || ||| ||| |||||||||
Db   5040 AGTGGACGACCTGGTCCGAAGACTCGTGTCCGGGAAGGTTATGTCCGCTGCGATGCTGG 5099

Qy   5123 ACCCATCTTGATGGTGGGCCTCGTATTGCGGGGGGCCATGATCATACGCGGTCATCACACCGG 5182
           ||||||||||||||||||||||||||||||||| |||||||||| |||||||||||||||||
Db   5100 GCCGATCTTGATGGTGGGCCTTGCTATCGGATGATCTATGCGTCTTATGCGGTCTTTTACACCGG   5159

Qy   5183 GTCTCTCCGTGGTGGTTACAGACTGGGATGTGGAGAATGGTGTTGGCAGCCCCTTTATCGGCA 5242
           |||||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||
Db   5160 GTCCCCAGTAGTGGTGGTGACAGACTGGGATGTGGAGAATGGTGTTGGCATTGCTCTTTATCGGCA 5219

Qy   5243 TGGAGACCAGGCCACGCCGGTTGTCGGGGTTACCTCCCCGGTTGCGCAGGTCCCATCGGGG 5302
           ||||||||| | ||||||| |||||| |||| |||||| ||| |||||||| |||||||||
Db   5220 AGTGACCAGGCCACGCGGTTTGTCGGGGTACCCCCGGTGGCCAGGTACCCCGGGCCCAGGT   5279

Qy   5303 GGGAGAGTCTGCGGGATCATGACCCTGTCAGTTCAGTGGATGGGGACCAGTGCCGGGCCATCAAGGT 5362
           ||||||||||||| |||||| ||||||||||||| |||| |||||||||| ||||||||||||| ||
Db   5280 GGGAGAGTCCCGGCACCATCGGACGCGCCCAACACGTGACCAGAGATCGACAGTGCCAGCCATCAACCAGGT 5339

Qy   5363 GGGTTGCGATTGTCAGTTATGACCTGTCGATCGGGGAAGTGCTGTCCTTGGCCCAGGC 5422
           ||||||||||| |||||||||||||||||| |||||||||| || || ||||||||
Db   5340 GGACTGTGATTGGTCAGTTATGACCTGTCGATCGGAGAAGTTACTGTCCTTGGCTCAGGC   5399

Qy   5423 TAAGACGGCCGAGGCCTACCAGCTACCACCAAGTGGCTTGCTGCTGCTACACGGGGAC 5482
           ||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Db   5400 TAAGACGGCCGAGGCCTACCAGCGACCACCAAGTGGCTGGCTGCTGCTACACGGGGAC   5459

Qy   5483 GCGGGGCCGTCCCCACTGTTCAATTGTTGACAAGCTCTTCGCCGGGGGTGGGGGCCGGT 5542
           |||||||||||||||||||||| ||||||||||| |||||| |||| ||||||||||||
Db   5460 GCGGGCCGTCCCCACTGTTCAATTGTTGACAAGCTCTTCGCCGAGGGTGGGGCCGGCCGT   5519

Qy   5543 GGTAGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGGCGGCCTATGGGCTTCTAGGAG 5602
           ||| |||||||||||||| | ||||||| ||||||||| || ||||||| || ||||||
Db   5520 GGTGGGCCATTGCCACAGTGTAATAGCTGCGGCAGTGGCGGCGTGCTTACGGGGCTTCAAGGAG   5579

Qy   5603 CCCTCCATTGGCTGCTGCCGCTTCCTACCTACTAGGGGCGTCCATGGGGTTGGGCGTC 5662
           || | |||||||||| |||| |||| ||||| ||||||||||||||| |||||||||||
Db   5580 CCCGGCGTTGGCGGCGGCGAGCCGCTCCTACCTACTGATGGGGTTGGGCGTTGGGCAACGCTCA 5639

Qy   5663 AACCCGCTTAGCCTCCGCTCTCTACTAGGGCGCCGCTCTGGGACCCGGCTCTGGCACGCCTGT 5722
           || |||| |||| | ||||||| ||||||||| ||||||| |||||||| ||||||||| |||
Db   5640 GACGCGACTGGCGTCCGCTCCGCTCCTACTGGGCGTGCTGGCGTCCGCTCTGGGCCACTCCCCG 5699

Qy   5723 CGTGGGGTTAACCATGCGGGGCGCCCTCATTGGAAGTGCTAGCGTCCCTCCTCCCCTCCTGGT 5782
           |||| ||||||||||||||||||||| |||| || ||||||||||||| ||||||||||||||
Db   5700 CGTGGGTTTAACCATGGGGGGCGCCCTTCATGGGTGCGCAGCGGTTGGTGCCAGCGTATCCCCCTGGT 5759

Qy   5783 CACCATTTTACTGGGGGCCCGTCGGGGGGCGTGGGGGTCGGAGGGCGTCTAGCCTTGT 5842
           ||||| ||||||||| |||||||||||||||||||| |||||| ||| ||||||||||
Db   5760 CACCATCTTACTGGGGGCCGTCGGGGGGCGTGGGGGTCGGAGGGTTGGGCGAGCCTTGT   5819

Qy   5843 CTTCGACTTTATGCGGGAAACTATCATCAGAAGATCTGTGGTATGCCATCCCAGTGCT 5902
           || ||||||| ||| |||||||| | |||||| ||||||||||||| ||||||||||||
Db   5820 CTTCGACTTTCATGCGGGAAACTTCATCAGAAGATCTGTGGTATGCCATCCCAGTGCT 5879

Qy   5903 AACCAGTCCGGGGCAGGACTTGCGGGGGGACTTGGTGTTGGTTTGTTACTCAGCTAA 5962
           |||| |||| || |||||||||||||||||||| ||||||| |||||||||||||||
Db   5880 GACCAGCCCAGGGGCGGCCCAGGACTTGCGCGGGGACTTGGTGTTGGTTTGTTACTCAGCTAA   5939

Qy   5963 CAACTCTGGCACTACCACTTGGTTGAACCCTCGTCGACTACATTGCCAAGGTCCTCATG 6022
           ||||||||||||||||||||| ||||||||| ||||||||||| ||||||||||||||
Db   5940 CAACTCTGGCACTACCACTTGGTTGAACCGTCTGTCGACCACCAGTGTCCAAGGTCTTCATG   5999

Qy   6023 CATCCCTGACACAGTTACTTTCAGCAGCCGCCGATTACTGTGACAAGGTCTCAGCTGTTGCTCCG 6082
           |||||||||||||||||||| || ||||||||||||||||| | ||||||||| ||||||||||
Db   6000 CATCCCTGACACAGTTACTTTTCAACAGCTGACTACTGCCACTACAGGTCTCGCCCGTGTTCTCCG 6059

Qy   6083 ACGCTTGAGCCTCACTGCACCGTGGTTGCCCGTTCAACAGGGAGGCCTAAGGTTGGATGA 6142
           || ||||||||||||| ||||||| |||| ||||| |||||||||||||| ||||| |||
Db   6060 TCGCCTGAGCCTCACTAGAAACGGTTGGTCGCCCCTGTCAACAGGGAGGAGCCCAAAGTTGGATGA 6119

Qy   6143 GGTTCAGGTGGGGTACGTCTGGGACTTGTGTGGGAGTCATGCGCATGGT 6202
           ||||||||||| |||||||||||||||||||||||||||||||||| |||
Db   6120 GGTTCAGGTGGATACGTCTGGGATCTGTGTGGGAGTCATGCGCAGTACGCATGGT   6179

Qy   6203 GATGGCCAGACTTCGGGCGCCTCGTCCCCCGGTGTGTCATTACCCTTATGGCACTCGGCGGGA 6262
           ||||||||||| ||| |||||| ||||| |||||| |||||||||| |||||||||||||||
Db   6180 CATGGCCAGACTTAGGGCCCTCGTCCGCCGCTGTGGTGTCATTTATGGCACTGCGGGGA 6239

Qy   6263 GGGGTGGTCCGGGAGAATGGTGTTGTTGGACACGTCGTTGCTTGTTGTTTGGGTTG 6322
           |||||||||||||||||||||||||||||| |||||| ||||||||| ||||||||
Db   6240 GGGGTGGTCCGGGAGAATGGTGTTGTTAGATGGCATGTTGAGAGCCGCTGCTTGTTGTTTGGGTTG 6299

Qy   6323 CGTGATCACCGGTGATGTTTGAATGGCAACTCCAGTTACTCTACCAAGCT 6382
           |||||||||||||| |||||||||||| |||||||| ||||||| |||||
Db   6300 CGTGATCACAGGCGACGCGTGGGAACATGGGACAGTGTCAAATGGCAACTCCAGTTACTTACTCTACCAAGCT 6359

Qy   6383 GTGCAGGCATTATTGGATGGGACAGTCCCTTGTGAACATGCTGGCGAGACGTC 6442
           ||| ||||||| | ||||| |||||| | |||||||||| ||||||||| || |
Db   6360 GTGCCGGCACTATTGGACGCTAATGGACAGTGTTCCAGTGAACTGTGGTTACGTGGGCTGAAACATC 6419

Qy   6443 GCCTTTGCTCGCCTCAGACACCCCGAGGTGGTACCATTCGGACACTCGGGTGGGCTGA 6502
           ||| | ||| ||| ||||||||| ||||||||||||| || ||||| ||||||||| |
Db   6420 GCCCCTCCTGGCCTCCGCACACCCCAAAGGTCGTACCTTTTGGACGTCTCGGCTGGCTCAGGTGA 6479

Qy   6503 GGTGGTGGTGACCCGTACCCCACCACGTTGTGATGCAGGCGAACATCCGCTACCAGTGCTGCGG 6562

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Db   6480  GGTGTGGTTGCACCTACCCGTGTTGCTGCTGGATCGATCAGGAGGACTTCCGCCCTACAAGTTGCTCG  6539
Qy   6563  CCAGCAAATCCTGTCGGCTATTACGTCGAGCCCTATTACGTCGACGGCCATGGCATACCGGCTCTC   6622
Db   6540  CCAGCAAATCCTATCCATTGGCTGCTGTAGCTGAGCCCTACTATGTTGACGGCCATCCCGGCTCTC   6599
Qy   6623  ATGGCAACGGCGACCGCGAGCGCCTGCCATGGTCTATGGCCCTGGCAAAGTGTCACCAT          6682
Db   6600  GTGGCGACGGCGACCGCCGTGCGCGCCGTGCCGCCGTCATGGCCCCGACAAAGTGTTACCAT       6659
Qy   6683  TGACGGGGAACGCGTACACCCTTCCGCCATCAACTGCGGCTTAGGAATGTGGCGCCCTCTGA       6742
Db   6660  TGACGGGGAACGCGTACACCCTTGGCGCTTGCCGCCACCAGTTGCGGCTTAGGAATGTGGCGCCCTCTGA  6719
Qy   6743  GGTGTCATCCGAGGTGTCCATTGACCATTGGGACGGAGACTCAGAACTGACTGA              6802
Db   6720  GGTTTCATCCGAGGTATCCATTCCAGCTGCCACGGAGACTGAGAACTGACTGA               6779
Qy   6803  GGCCGACCTGCCGCCGGCGACCTTCAGCTATCGAGAATGTGCGAGAATTCT                 6862
Db   6780  GGCCGATTTGCCGCCGGCGACCTTCAGCTATTGAGAATGTGCGAGAATTCT                 6839
Qy   6863  TGAACCTCACATAGATGTCATCATGAGAGTTGCAGTGACCACCCTCTCTTGTGTGGAGTAC       6922
Db   6840  TGAGCCACCACATTGATGTCATCATGGAGGACTGTAGTACACCCTCTCTTGTGTGGTAGTAG      6899
Qy   6923  CCGAGAGATGCCTGTGTGGGAGAAGACATACCCCACTCCATCCGCAGCACTTATCTC           6982
Db   6900  CCGAGAGATGCCTGTGTGGGAGAAGACGTCCCCCACTCCATCCAGCACTTATCTCC            6959
Qy   6983  GGTTACTGAGAGCAGCCCAGATGATGAAGAAGACCCCGTCGGTGTCTTCCTCGCAGGAGGATAC    7042
Db   6960  GGTTACTGAGAGCAGCTCAGATGATGAAGAAGAGCCCGTCGGTCTCCTCTCGCAGGAGGATAC     7019
Qy   7043  CCCGTCTTCGACTCATTCGAGGTCATCGCAAGCCGCGAGACGCCGAAGGCCGAGGGGGAAAAG     7102
Db   7020  CCCGTCTCTGACTCATTCGAGGTCATCGCAAGCCGCGAGACAGCCGAAGGGGAGGACAA         7079
Qy   7103  CGTCTTCAACGTGGCCTCTTTCCGTACTAAAAGCCTTGTTTCCACAGAGCGGATGCCACAAG      7162
Db   7080  CGTCTTCAACGTGGCCTCTTTCCGTACTAAAAGCCTTATTTCCACAGAGTGATGCCCACTAG      7139
Qy   7163  AAAGCTTACCGTTAAGAATGTCATGCGTGTGTTGAGAAGAGCGTAACACGCTTCTCTTTCATT     7222
Db   7140  GAAGCTTACTGTCGAAGAATGTCATGCGTGTTGAGAAGAGCGTCACGCGCTTCTCTTTTCATT     7199
Qy   7223  GGGATTGACGGTCGCTGACGTGGCAAGCCTGTGTGAGATGGAAATCCAGAACCATACAGC        7282
Db   7200  GGGGTTGACGGTTCCGGGGTTGCCGACGTGGCTAGCCTGTGTGAGATGGAAATCCAGAACCATACAGC 7259
Qy   7283  CTATTGTGACAAGGTGCGCACTCCGCTTGGTGTGGGCGACACCACCAAGGTGTATGGGGCAATGT   7342
Db   7260  CTATTGTGACAAGGTGCGCACTCCGACGCCGACCACCTACCAAGGTGTACGTGACCACCGCGAATGA  7319
Qy   7343  ACTTACCTTTGAATGTGACAAGTTACCTTCTGGCGTTGCCTTCATGACAAATTCCT            7402
Db   7320  ACTTACCTTTGAATGTGACAAGTTGACCTTCTGGCTTCTGCGGTCCATGGGTCCATCAACAGTTCCT 7379
Qy   7403  CATTGTGGTCTGGGGTTGCCACTGCCACTCCGGCCAAGCCCCTGTGGTGAGGCC              7462
Db   7380  CATCTGGTCGTCCGGGGTTGCCGACTAGGGGCCACCACCAAACACCTGTGGTGAGGCC          7439
Qy   7463  GGTTGGCTCCTTGCCTGTGGGCCGACACCACCAAGGTGTATGCACCAACCCGGACAATGT        7522
Db   7440  GGTAGGCGTCTTTGTTGGTGGCCGACAACTACCAAGGTGTACGTGACCACCGCGAATGA         7499
Qy   7523  TGGGAGAAGAGTTGACAAGGTTACCTTCTGGCGTTGCCTTCATGACAAATTCCT              7582
Db   7500  GGGGAGGAGAGTGGACAAGGTGACCTTCTGCGCGCCGCCGCCTCCTGGGTCCATCAACAAGTTCCT  7559
Qy   7583  CGTGGACTCCATAGAGCAGGGCCGCCTAAGCAGGCTGCCTCAAGCCTGCCATGGGTTACAC       7642

Db         CGTGGATTCAATCGACGGGCCGAGGAGGGCTCGCTCAAGCCTGCCATGGTTACAC             7619
Qy   7643  TTATGAGGGAGCAATAAGGACTGTAAGGACTTCCGCATGGCTGGGATCTAAGGT              7702
Db   7620  TTATGAGGGAGCAATAAGGACTGTAAGGCCATGGGCTGGGATCTTAAGGT                  7679
Qy   7703  GTCGGTCAAGGACCTCGCCACCCGTGCGGGGAGATGGCTGTCATGACCGGCTCCAGGA          7762
Db   7680  GTCGGTGAAGGACTTGGCCGCGTTCATGACCGGCTCCAGGA                           7739
Qy   7763  GATACTTGAAGGAGGCACGCCAGTCCCCTTTACTCTTACTGTGAAAAAGGAAGTGTTCTTCAA     7822
Db   7740  GATACTTGAAGGACGCCAGTCCCCTTTACCCTTACTGTGAAAAAGGAGGTGTTCTTCAA         7799
Qy   7823  AGACCGAAAGAAGAAGAGAAGGAAGGCCCCCGCCTCATTGTGTTCCCCCCCTGACTTCCGGAT     7882
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Qy   7883  AGCTGAAAAGCTTATTCTGGGAGACCCTGACGGGTAGCCACGGGCTGTTGGGGGGGC           7942
Db   7860  AGCTGAAAAGCTCATCCTGGGGGACCCTGGGGCAGCCAAAGCGTGTTGGGGGGGC             7919
Qy   7943  CTACGCCTTCCAGTACACCCCAAATCAGCCAGGAATTAGGGAGGATGCTCAAACTGTGGGAATC    8002
Db   7920  TTACGCCTTCCAGTACACCCCAAACCAGCGGGTTAAGGAGATGCTCAAACTATGGGGAGTC       7979
Qy   8003  AAAGAGACACCATGCGCCCATCTGTTGGACGGCCACATGCTTCGACAGTAGCATAACTGA        8062
Db   7980  TAAGAAAACACCTTGCGGCATCTGCGGTGGATGCCACAGTGCTTCGCAGTAGTATTACTGA       8039
Qy   8063  AGAGGACGTGGCGCTTGGAGACAGAGCTTTATGCCCTGGCTTCAGACCATCCAGAATGGGT       8122
Db   8040  AGAGGACGTGGCTTTGGAGACAGCGCCTATACGCCCTGGCTGAGTCGAGCAGTGGGT           8099
Qy   8123  GCGTGCCCTGGGAAATACTATGCCTCTGCGCACAATGGTAACCCCGAGGGGGTGCCAGT         8182
Db   8100  GCGAGCGCTCGGGAAATACTATGCCTCCGGGCACCGCAGTGTCACCCGGAAGGGGTGCCCGT      8159
Qy   8183  GGGTGAGAGGTATTGTAGATCCTCAGGGGTCTTGACCACCAGTGCGAGCAACTGCTTGAC        8242
Db   8160  TGGTGAGAGGTATTGTAGATCCTCGGGCGTTTTGCAACCAGTGCGAGCAACTGCTTGAC         8219
Qy   8243  TTGCTATATCAAGGTGAAAGCCGCCGCTGTGAGAGGGTGGGCTGAAAAATGTCTCCGCTCCT      8302
Db   8220  TTGCTACATCAAGGTGAAAGCCGCCGCTGTGAGAGGGTGGGCTGAAAAATGTCTCACTCATT      8279
Qy   8303  CATCGCTGGGCGATGACTGTTTGATCATATGCCTGTGTGCCGATCCTGCCAGT              8362
Db   8280  CATAGCCGGGCGATGACTGTTTGATCATATGCCACCCGAGTGCGGGTCGAGCGAGCGC          8339
Qy   8363  TTTGGGCCAGAGCCCCTGCGAGCTACGCGGCATCCTCCTATCATGCACT                  8422
Db   8340  CCTGGCCAGAGCCCCTGCGGCGTACGGGTATGCGTCGCGAGCGTGTCGTATCATT             8399
Qy   8423  GGACACGGCCCCCTTCTGCTCCACTTGGCTAGCTGAGTGCAGATGGGAAACGCCA            8482
Db   8400  GGACATCATCCCCTTCTGCGTCTCCACTTGGCTCCGGGTTCGGGTGCAATGGGAAGCGCCA      8459
Qy   8483  TTTCTTCCTGACCACGGACTTTCGGAGCGCCATGTGAGCGAGTACAGTGA                8542
Db   8460  TTTCTTTCTGACCACGGACTTTCGGAGACCGCCGTGCTGCTCCGAGCGAGTATAGTGA         8519
Qy   8543  CCCAATGGCTTCGGCGAGCCCATCGGTTACATCCTCCTATCACACGGTG                 8602
Db   8520  CCCAATGGCTTCGGCATAGTTACATTCTCCTTTATCCCTGGCATCCACACGGTG            8579
Qy   8603  GGTCATCATCCCCACGTGCTCACCTTTAGGGGGTTGGGTTGGCACACCGTCTGATCC         8662
Db   8580  GGTCATCATCCCCACGTGCTGACGTGCCGACGTGCGTCCGGGGTGGCCACACCGTCTGATCC     8639
Qy   8663  TGTGTGGTGCCAGGTACATGTGGTCAGTTAATTACTACAAGTTGCCTAACAT              8722
Db   8640  GGTATGGTGTCAGGTACATGTCAGTTAATTACTACAAGTTTCCACTGACAAACTGCCTAACAT    8699
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Qy    8723  CATCGTTGCCCTCCACGGACCACCAGCAGCGTTGAGGGTTACCGCAGACACAACTAAGACAAA  8782
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Db    8700  CATCGTTGCCCTCCACGGACCACCAGCAGCGTTGAGGGTTACCGCAGACACAACCAAAACAAA  8759

Qy    8783  AATGGAGGCTGGCAGGTGCTGAGCGACCTCAAGCTCCCTGGCCTAGCAGTCCACCGGA  8842
            ||||||||| |||| ||  ||||||| ||  |||||||||||||||||||| |
Db    8760  AATGGAGGCCGGCAAGTGTCTTAAGCGACCTCAAGCTCCCTGGCCAGTCCACCCGCAA  8819

Qy    8843  GAAGGCCCGGGCAATTGCGAACGCGTATGCTCCGTGCCCGGTTGGGCTGAGTTGGCTAG  8902
            |||||||| ||| ||| ||| ||||||||||  ||||||||||| |||||||||||||
Db    8820  GAAGGCCCGCGAGCACTGCGCAGACACGCATCCGTGCCCTGGGCCTGGGCTGAGTTGGCTAG  8879

Qy    8903  GGGCTGTTGTGCGGTCCAGGGCTTCCGCGCTTCCCCTCCCCGGAGATTGTTGGTATCCCGG  8962
            |||||||||||||||||||||||||||| |||||| ||||||| |||||||||||||||
Db    8880  GGGCCGTGTTGTGGCCATCCAGGGCTCACGGCCCTCCCCTCCCCGAGATTGCTGGTATCCCGGG  8939

Qy    8963  GGGTTTCCCCCTTTCCCCCCTATATGGGGGTGGTTCATCAATTGGATTTCACAAGCCA  9022
            ||||||||||||||| ||||||||| |||| |||||||||||||||||||| ||||||
Db    8940  GGGTTTCCCCCTTTCCCCCCTACATGGGGGTGGTTCATCAATTGGATTTTACAAGCCA  8999

Qy    9023  GAGGAGTCGCTGGCGGTGTGTTGGGGTTCTTAGCCGTCATCCGTAGCCCGTTCGGGTG  9082
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Db    9000  GAGGAGTCGCTGGCGGTGTGTTGGGGTTCTTAGCCGTCATCCGTAGCCCGTTCTCTCGGGTG  9059

Qy    9083  AACTAAATTCATCTGTTGCGGCAAGGTCCGGTGACTGATCATCACTGGAGGAGTTCCCG  9142
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9060  AACTAAATTCATCTGTTGCGGCAAGGTCCGGTGACTGATCATCACTGGAGGAGTTCCCG  9119

Qy    9143  CCCTCCCCGCCCCAGGGGTCTCCCCGCTGGGTAAAAAAGGGCCCGGCCTTGGGAGGCATGG  9202
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9120  CCCTCCCCGCCCCAGGGGTCTCCCCGCTGGGTAAAAAAGGGCCCGGCCTTGGGAGGCATGG  9179

Qy    9203  TGGTTACTAAACCCCTGGCAGGGTCAAAGCCTGATGGTGCTAATGCACTGCCACTTCGGT  9262
            |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    9180  TGGTTACTAAACCCCTGGCAGGGTCAAAGCCTGATGGTGTGCTAATGCACTGCCACTACGGT  9239

Qy    9263  GGGGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGCGTGCTCGCAGAGCCCTCCCCG  9322
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9240  GGGGGGTCGCTACCTTATAGCGTAATCCGTGACTACGGCGTGCTCGCAGAGCCCCTCCCCG  9299

Qy    9323  GATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCCGGTAAGGAGCTCG  9374
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 15
AR026878
LOCUS       AR026878                9327 bp    DNA        linear        PAT 29-SEP-1999
DEFINITION  Sequence 234 from patent US 5856134.
ACCESSION   AR026878
VERSION     AR026878.1  GI:5937718
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 9327)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie., Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5856134-A 234 05-JAN-1999;
FEATURES             Location/Qualifiers
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BASE COUNT     1682 a   2532 c   2984 g   2129 t
ORIGIN
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Query Match    83.9%;  Score 7885.6;  DB 6;  Length 9327;
Best Local Similarity   90.4%;  Pred. No. 0;
Matches 8433;  Conservative 0;  Mismatches 894;  Indels 1;  Gaps 1;
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Qy      40  GCAAGCCCCATAAACCGACGCCTATCTAAGTAGACGCAATGACTCGGCCGCCGACTCGGCG  99
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Db       1  GCAAGCCCCAGAAACCGACGCCTATCTAAGTAGACGCAATGACTCGGCCGCCGACTCGGCG  60
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Qy  1180  TTTTGGGGTCCCGCCCCTTTGACTACGGGTTGAAGTGGCAGTCATCGTCCTCGCAGGGCTA  1239
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Db  1140  TTTTGGGGTCGCACGCCCCTTTGACTACGGGTTGACTTGGCAGACGTTCTCTGTTGCAGGCCCA  1199

Qy  1240  ACGGGTTCGCGTCGTATTCCCACTGGGGAGAGGGTGTGGACGAGGTGTGGGACCGCTCTTGT  1299
          ||||||  || ||||||||||||||||| ||||  ||||||||||  |||||
Db  1200  ACGGGTTCGCGTTTTCGACTGGGGAGAAGTGTGGGACCGTTACGGTTCAGT  1259

Qy  1300  GTGACTGCCCCAACGGCCCCTGGGTTTGGGTCCCGGCCCTTTGCCAGGCGGTTGGGGTGGG  1359
          |||||||||||||| ||  ||||||||| | |||| ||||||| ||||||||||
Db  1260  GTGACTGCCCCTAACGGCCCCTGGGTGTGGTTGCCAGCCTTTTGCCAAGCAATCGGCTGGG  1319

Qy  1360  GCGACCCCATCACCCATTGGAGACCACGGACAAAACCAGTGGCCCCTATCATGCCCCCAAT  1419
          ||||||||||||||| ||||||||||| |||| |||||||||||| ||||||||| |||| |
Db  1320  GTGACCCCATCATTATTGGAGACCACGGACAAAATCAGTGGCCCCTTTCATGCCCCCAGT  1379

Qy  1420  ATGTCTATGGGTCTGTGTCCGTAACGTGCGTGTGGGTTCCGTGTCTTGGTTTGCCTCGA  1479
          ||||| |||||||||||||  | |||||||||||||||||||| ||||| |||| |||||
Db  1380  ATGTCTATGGGTCTGCTGCTACAGTACTGCCGTGTGGGGTCCTGTCTTCGCTGTATGCCTCCA  1439

Qy  1480  CCGGGCCGTCGTGATTCGAAGATCGATGTGTGGAGTTGGTGCCGGTTGGTGATCGCCAGCT  1539
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Db  1440  CCAGTGTCGCGGACTCGAAGATAGTGTTGGAGTTTAGTGCCAGTTGGCTCTGCCACCT  1499

Qy  1540  GCACCATAGCCGCTCTAGGGTGTCATCGGATCCGACACGTGCTCTCCGAGTGGG  1599
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Qy  1600  GAGTCCGTGCGTAACGTGTATTCTGGACCGTCGCTCGTTCATGTGCACCTGTGTGC  1659
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Db  1560  GAATCCGTGCGTGACGTGTGTTCTGGACCGTGCGCTCGTTCATCGGCGCCACCTGTGTGA  1619

Qy  1660  GGGACTGCTGCCCGAAACCCGGTCGGTTAGATTCCCTTTCCATCGTGCGGCACGGGGC  1719
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Db  1620  GGGACTGCTGCCCGAGACCCGGTCGGTTAGGTTCCATTCCATCCGTGCGGCGTGGGGC  1679

Qy  1720  CTCGGCTGACAAAGGACTTGGAAGCTGTGCCCTTCGTCAACAGGACAACTCCTTCACCA  1779
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Db  1680  CTCGGCTGACAAAGGACTTGGAAGCTGTGCCCTTCGTTCAATAGGACAACAACTCCCTTCACCA  1739

Qy  1780  TAAGGGCCGTCAGGCACGGAGAGGCAACCGGTGCGGTCGCGCCGTGTGTTTTG  1839
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Db  1740  TTAGGGGCCGTCAGGCACGGAGAGGCAACCGGTGCGGTCGCGCCGTGGGGGGG  1799

Qy  1840  GGTCCTACCACATGACCAAGATCCCGGATTCCCTGCCATTGGTGAAATGTCCACCACCAG  1899
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Db  1800  GGTCCTACGCCATGACCAAGATCCCGCGAATCCCTACACATCTGGTGAGTGTCCACCACCAG  1859

Qy  1900  CCATAGAGCCTCCGACTTGGAAGCGTTCGGGTTCTTCCCCGAGTCCCGCCATTAACAAACT  1959
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Db  1860  CCATCGAGCCTCCCCACCCGGACGCGCCTCTTCGGGTTCTTCGGGACCGCCTCTCAACAACT  1919

Qy  1960  GCATGCCGCTAGGCACGGAAGTGTCTGAGCCATTGGCGGCGAGCTGGGCTTACGGGGGGGT  2019
          |||| || ||||||| |||| |||| |  || |||||||||||||| |||||||| |||||
Db  1920  GCATGTCGCTAGGCACGGAAGTGTCCGAGCCATTGGCGGCGCACTTGGGGGCTGCCTCACGGGGGGGT  1979

Qy  2020  TCTACCAGCCTCTGGTTCGCGAGGTTCGCGAGCTGTCGCAGGTCGAAAATCCGGTTGCC  2079
          | ||||||||||| | ||||| ||||||||||||||||| |||||||||| |||||||||
Db  1980  TCTATCAACCCCTCGGTGCGCGAGGCTCGCGAGCTGTCGCAGGTCCGAAAATCCGGTTTGTC  2039

Qy  2080  CGGGGTTACGGCAATGGCTGTCCCTGTAGACCTGACGGGTTCATACAGTCCAGGGCCACC  2139
          ||||||| ||| ||||| ||||||| |||| |||||||||||||| |||||||||||||
Db  2040  CGGGGTTTGCATGGCTCTCTTCGGGGCCAGGCCTGACGGGTTTATACAGTCCAGGGTCACT  2099

Qy  2140  TGCAGGAGGTTGGATGCGGGCAACTTCATCCCTCCACCGCTGGTTGCTCTTGGGGATTTTTG  2199
          ||||||||| ||||||| || |||||| | ||||||||||| ||||| |||||||| |||
Db  2100  TGCAGGAGGTGGATGCGGGCAACTTCATCCCTCCACCGCTGGTTGCTCTTGGGACTTTG  2159

Qy  2200  TATTTGTCCGTCTATCTGATGAAGCTGATGAGCGTTCCCGTTGCCTTGTCCCGTTGATCTTGC  2259
          ||||| || |||| ||||| ||||| |||||||||||| ||||| |||||||| ||||||||
Db  2160  TATTTGTCCGTTTATACCTGATGAAGCTGATGAGCGTTCGGGATCCGTTGGTCCCGCTGATCTTGC  2219

Qy  2260  TTCTGCTGTGTGGGTGGGGTGAACCAGTGGCGGTTGCGCGGTTGCGGCGGGTGGACGCTG  2319
          |||||||||||||| ||||| ||||| ||| |||| |||| ||||  |||||||||||||
Db  2220  TGCTGCTATGGTGGTGGGTGAAGTTTTGCGGGGTGACCAGTGGCGCCTAGGGCTGGCAGTCCTAGGGC  2279

Qy  2320  CCGTGGCGGGTGAAGTTTTGCGGGGCCGCTGGGGCCGTTCCTCATGGTGTTCGGGGCTGGT  2379
          |||||||||||||||  |  | || ||  | || |||||| || ||||||||||||||| |
Db  2280  CCGTGGCAGGTGAGGTGCTTCGGGGCCGTTCGGGACTGTCTCCGGGGACTCTGGGGACTCG  2339

Qy  2380  TCAGTATGATACTAGGTCTAGCAAACCTGGTGTTGTACTTTCGGTGATGGGCCCTCAGC  2439
          ||||| ||| |  || ||||| |||||| || || || || || ||||||| || ||||
Db  2340  TCAGTATGATATTGGGTTGGCAAACCTGGTGTGCTGTACTTTAGATGTTGGGACCCCAAC  2399

Qy  2440  GCCTCATGTTCCTCGTGTTGTGAAGCTCGCTCGGCGGGAGCTTTCCCGCTGGCACTTTTGA  2499
          || |||||||||||| |||| |||||| | || ||||||||| |||| |||||| ||||||
Db  2400  GCCTGATGTTCCTCGTGTTGTGAAGCTTGCTCGGGCGGGAGCTTCCCGCTGGCCCTCTGA  2459

Qy  2500  TGGGGATTTCGGCGACCCGGCGCACCTCGTGCTCTCGGGGCCGAGTTCTGCTCTCGGATG  2559
          |||| |||||||||||||||| |||||||| |||| |||||||||||| ||||||||||||
Db  2460  TGGGGATTTCGGCGACCCGGCGCACCTCGTGCTCTCGGGGCCGAGTTCGCTTCTCGGATG  2519

Qy  2560  TCACATTCGAGGTGGACACTTCGGTGTTGGGGTGGTGCCAGCGTGGTTGGCTTGGG  2619
          ||| |||||| ||||| |||||| | || ||| ||||| ||||| || |||||||
Db  2520  CTACATTCGAGGTGGACACTTCGGTGTTGGGGTGGTGCCAATGTGGTAGCTTGGG  2579

Qy  2620  CCATAGGCGTCCTCGAGCTCAATGAGCCGCAGGGGGTGGAAGCACAAGGCCGTGATCTATA  2679
          |||||||| || ||||||| || |||||||| ||||||| |||||||| ||||||||||||
Db  2580  CCATTGCGCTCGAGCTCGATGAGCCGCAGGGGGTGAGCGCCAAAAGCCGTTGATCTATA  2639

Qy  2680  GGACGTGGTGTAAAGGGTACCAGGCTGTGCGCGGACGGTGTTGCGGAGCCCCCTCGGGG  2739
          |||||||| ||||||| |||||| |||| |||||||| ||||| |||||||||||||||
Db  2640  GGACGTGGTGTAAGGGGTACCAGGCAATCCGTCAAAGGGTTGAGGAGCCCCCTCGGGG  2699

Qy  2740  AGGGGCGTCCTACCAGCTTCTGACGTTTCGCGTGTGCTTGGCCTCATACATCTGGCCCGG  2799
          ||||| |||| |||||||| |||| | || ||||||||||| || ||||||| ||||||
Db  2700  AGGGGCCGGCCTGCCAAACCCCTACCTTGCCTTGTGCTGCTTGGCCTCCATCATCTGGCCCAG  2759

Qy  2800  ATGCTGTGATGATGGTGGGTGGTGCTCCTCGGCCGGCTGTTCGACGGTGGCGGCCACTGG  2859
          ||||||||||||||| || ||||| ||||||| ||||| || || || |||||||||| ||
Db  2760  ATGCTGTGATGATGGTGGGTGGTGCTTGGCCTGGTGGTTGTTTGGCCGTGCTGTTGCACGGGTTGG  2819

Qy  2860  ACTGGGCCCTGGAGGAGCTCCGTTCGGTGGCGGTGGCACGGGTGG  2919
          | ||||||||||| ||| | |||||||||| || | |||||||||
Db  2820  ATTGGGCCTTGGAGGAGATCTTGAACCTCGTGTCGTGTTTGGCTCGTGGTGG  2879

Qy  2920  TTGAGTGCTGTTGGCGGCGGCTCATCCGACTCGTCTCCAAGATGT  2979
          |||||| ||||||||||| |||||| |||| |||||||||||||||
Db  2880  TTGAGTGCTGTTGGCGGTGGCTTCATCCGCCTCGTCTCCAAGATGT  2939

Qy  2980  GCGCAAGAGGGGCCTACCTGTTTGACCACATGGGCTCTTCTCGCCGGCGTGTCAAGGAGC  3039
          || | |||||||||| ||||| | |||| ||||||||||||| ||||| ||||||||||||
Db  2940  GTGCGAGAGGGGCCTGCCTGTTTGGTCGTCATATGGGCTCATTTCGCCGTGCTGTCAAGGAGC  2999

Qy  3040  GCTTGTTGGAATGGCACGGACGGCCCCTTGTCATTCACTAGGACGGACTGTCCCA  3099
          |||| |||||||||| |||| ||| | |||| |||| ||||||||||||| |||
Db  3000  GCCTGTTGGAATGGCACGGACGGCTCTTGTCATTCACTAGGACGGACTGTCGCA  3059

Qy  3100  TCATCAGAGATGCCGCGAGGACCCCGTCCTGCGGACAGTGCGTCATCGGTGG  3159
          |||| |  ||||| || |||||||||| | |||||| ||||||||| ||||||
Db  3060  TCATACGGGATGCGCGGAGGACTTTGTCCTGCGGATCGGAATGCGGCAATCGGTGG  3119

Qy  3160  TAGCACGGCGGTCGATGAGGTTCTGATCGCCGGCTCTTCAGGAGGTGAATCATTTGCCTC  3219
          |||  ||| ||| ||| |||||||||||| ||||||||| ||||| ||||||||| |||||
Db  3120  TTGCGCCGCCGTTGTGATGAGGTTCTGATCGGGCCTCATTTCGGCGTGCTGCTGAATCATTTGCCTC  3179

Qy  3220  CCGGGTTGTTCCCGACTGTCATCCGTCGCGGAAAGGGCTTCCTGGGGG  3279
          ||||||| ||| |||| |  |||| |||||||||||||||| ||||||
Db  3180  CCGGGTTGTTCCCGAGACGTGTCATCCGACGGTGCGGAAAGGGCTTGTGGGGG  3239

Qy  3280  TCACGAAGGCAGCCTTGACAGGTAGGATCCTGACTTACATCCAGGAACGTCATGTGT  3339
          |||| |||||| | ||||| ||||||| | |||||||||||||| |||| |||||||
Db  3240  TCACAAAGGCGTCCCTTGACAGTCGGGATCCTGACTTACATCCAGGAACGTCATGGTGT  3299

Qy  3340  TGGGGACGACGTACGTCACGAAGCAGCAATGTCTGGCTTGCGGGACTGTCGTGGACGCTG  3399
          ||||||||||| |||||||||| ||||||||||||||||| || ||  |||||||||||
```

Db   3300 TGGGGACGGCTACGTCCGCGAACATGGGAACATGCTTGAACGGCCTGCTGTTCACGGACCT 3359

Qy   3400 TCCATGGGGCTTCATCCCGAACCATCGCCACGCCCGGGGGCCCTTAATCCCAGGTGGT 3459
          |||||||||| ||||||||||||||| | ||||| ||||||| ||||||||| ||| |||
Db   3360 TCCATGGGGCTTCATCCCGAACCATCGCCACACCCGTGGGGCCCTTAATCCCAGATGGT 3419

Qy   3460 GGTCAGCCAGTGATGAGTCACGGTACCCGGTTCCAGATGGGCAACTTCGTTGACGC 3519
          |||||||||| ||||||||||||| ||| |||||||||| ||||||| ||||||
Db   3420 GGTCAGCCAGTGATGATGTCACGGTATCCACTCCCGATGGGGCTACTTCGTTAACGC 3479

Qy   3520 CCTGCACTTGCCAGGCGGAGTCCTGTTTATTAGATCCGACGGGGCTTTGTGCCATG 3579
          |||||||||||||||| | |||||||| ||||||||||||||||||
Db   3480 CTTGTACTTGCCAGGCTGAGTCCTGTCATCAGATCCCGACGGGCCCTATGCCATG 3539

Qy   3580 GCTTGAGCAAGGGGACCAAGGTTGAGCTGGATGGCCATGGAGGTTCTCTGACTTCCGTG 3639
          ||||||||||||||||||| |||||||||| |||||||||| ||||||||| ||||||
Db   3540 GCTTGAGCAAGGGGACAAGGTGGAGCTGGATGTGGCCATGGAGGTTCCCTGATTTCCGTG 3599

Qy   3640 GTTCGTCTGGTTCACCCGTCCTTTGCGACAAAGGGCACGCAGTAAGAGATGCTCGTGTCAG 3699
          | |||||||||||||||||| || ||||||||||||||||||||| |||||||||
Db   3600 GCTCGTCTGGCTCACCCGTCCTATGTGACGAGGGGCACGCAGTAGGAATGCTCGTGTCTG 3659

Qy   3700 TGCTCCACTCTGGCGGACGGGTTACTGCGGCCGATTCACTAGGCCGTGGACTCAAGTAC 3759
          ||||| |||||||| || ||||||||| || |||||||| ||||||||| |||||
Db   3660 TGCTTCACTCCCGTGGTAGGGTCACCCGGCACGGTTCACTAGGCCGTGGACCCAAGTGC 3719

Qy   3760 CAACAGATGCCAAGACTACCACGAGAACCCCCTCCCGGTGCGCGCAAAAGGAGTTTCAAGG 3819
          |||||||||||| | ||| || || ||||||||||| |||||||||||||| |||||
Db   3720 CAACAGATGCCAAAAACCACTGAACCCCCTCCCGGTGCCGGCCAAAGGAGTTTCAAAG 3779

Qy   3820 AGGCCCCGTTGTTATCCTACGGGGCGGGAAAGAGCACCCGGTACCCGTTGGAGTACG 3879
          ||||||||||||||||| ||| || |||||||| |||||||| |||||||||
Db   3780 AGGCCCCGTTGTTATGCCTACGGGAGCGGGAAAGAGCACTCGGTACCCGTTGGAGTACG 3839

Qy   3880 GCAACATGGGCCACAAGGTCTTGATCTTGAACCCGTCGGAGTAGCTACCGTGAGGGCCATGG 3939
          ||||||||||||||||||| ||| |||||||||||| | |||||||| |||||||||||||
Db   3840 GCAACATGGGCCACAAGGTCTTAGTCTTGAACCCCTCCAGCTGCCACTGTGCGGGCCATGG 3899

Qy   3940 GCCCATACATGGAGCGGCTGGCGGGAAACACCCCAGTATTTACTGTGGCCATGACACCA 3999
          ||| || ||||| ||||||||| |||||| || | ||||| ||||| |||||||
Db   3900 GCCGGTACATGGAGCGGCTGGCGGGTAAACATCCAAGTATATACTGTGGGCATGATACAA 3959

Qy   4000 CTGCTTTCACAAGGATCACTGACTCGCCCCTTACGTATTCCACTTACGGAAGGTTTTTGG 4059
          ||||||| ||||||||||||||| ||||| | |||||| | || |||| ||||||||||||
Db   3960 CTGCTTTCACAAGGATCACTGACTCCCCCGTGCGTATTCAACCTATGGGAGGTTTTTGG 4019

Qy   4060 CCAACCCTAGGCAGGTCTGAGGCGTGTCGGTCATTGTGACGAGTGCCACAGTC 4119
          ||||||||||| ||||||||||| | | ||| ||||| |||||| ||||||||
Db   4020 CCAACCCTAGGCAGGTCTGAGGCGTTTCGGTCATTGTGATGAGTGCCACAGTT 4079

Qy   4120 ATGACTCAACTGTGTTGTTGGCATTGGGCGTGTCAGGGAGCTGGCGAGGATGTGGAG 4179
          |||||||||||||| || ||||||||||||||| ||||||||||| |||||||||
Db   4080 ATGACTCAACCGTGCTTAGGCATTGGGAGGGTTCGGGAGCTGGCGGTGCCGGAG 4139

Qy   4180 TGCAATTGGTGCTCTACGCCACTGCCACCCCTCCCAGCACTGACCCAGCACCCAT 4239
          ||||||||| | | |||| ||||| || || |||||||| |||||||||||||| |
Db   4140 TGCAACTAGTGCTCTACACCACCGTGCCCGGATCCCGGATCCCATGCACCAGCACCCTT 4199

Qy   4240 CAATCATTGAGACAAAACTGGGAGAGAGATCCCTTCTATCTCGTATTGTTCCACCTGCATACCTC 4299
          | |||||||||||||||||||||||||| |||||| ||||| |||||||||||| |||||||| |
Db   4200 CCATAATTGAGACAAAATTGGACGTGGGCGAGAATTCCCTTTATGGCACGGAATACCCCC 4259

Qy   4300 TTGAGGCGGATGCGACCGGAAGGCATCTCGTATTCTCCACCTCCAAGGCTGAGTGCCGAGC 4359
          | |||||||||||||||||||| ||||| ||||| || ||||||| |||||||||| ||||
Db   4260 TCGAGCCGGATGCGAACCGGAAGGTTCCTTGTGTCCATTGCCATTCTAAGGCTGAGTCCGAGC 4319

Qy   4360 GCCTGGCGCGGGCCAGTTTCGGCTAGGGGTAAATGCCATCGCCTATTACAGGGGAAAG 4419
          ||||| ||| | |||| |||| ||||||| ||||||||| ||||||| |||| ||||
Db   4320 GCCTTGGCCAGTTCCTCCCGGAGGTCAATGCCATTGCCTATTATAGGGGTAAAG 4379

Qy   4420 ACAGTTCTATCATCAAAGATGGAGACACGCACTCGCTGCTACAGACGCACTATCCACTG 4479
          |||||||||||||||||| ||||| |||||||||||||||||| || |||||||||
Db   4380 ACAGTTCTATCATCAAGGATGGGGGGACCTGGTGGTGCTGCTACAGACGCGCTTTCCACTG 4439

Qy   4480 GGTACACTGGGAACTTCGATTCTGTCACCGATTGTGGGTTAGTGTGTGAGGAGGTCGTCG 4539
          |||||||||||||| | |||||||||| || || |||| ||||||||||||||||||||
Db   4440 GGTACACTGGAAATTCGACTCCGTGCCACCGTGGATTAGTGTGTGGAGGAGGTCGTTG 4499

Qy   4540 AGGTGACCCTTGATCCCACCATTACCATTACCAATTCCTGCCACGTCCGCGTCGGCTGAAC 4599
          ||||||||||| ||| ||||| ||||||| ||||| | |||||||||||||||||| ||||
Db   4500 AGGTGACCCTGGATCCTACCATTCCTGCCACAGTGCCTGCTGCCGTCCGCTCGGCTGAAC 4559

Qy   4600 TGTCGATGCAGCGGCGGAGGACGCACGGGTAGGGCGGCTTGGGCGGCTCTGGGCGTGGCCATG 4659
          |||||||||||| |||| | |||| |||| || || | |||||||||||||||| |||||||
Db   4560 TGTCGATGCAGCGGGACGAGGACGCACGGGTAGGGCGGCTGGGCGGCTCTGGGCGTGGCCATG 4619

Qy   4660 GGGTCGGCAAGGCCCCTGTCGTGGTGGTGCGGCCCTGTCCTGGTCGGCGGTGGAAG 4719
          ||| |||||||||||| ||| |||||| ||||| ||||||||| |||||| ||||||
Db   4620 GGGTGGGCAAAGCCCCCTGCGGGTGTGGTGCGGCCCTGTCCTGGTCGGCGGTGGAAG 4679

Qy   4720 CCGGTGTGACCTGGTACGGATGGAATGGAACCTGACCTGACGACTTACTTACG 4779
          || ||||||| |||| || |||| |||||||||||||| |||| |||| |||
Db   4680 CTGGAGTGACCTGGTACGGATGGAATGGAACCTGACCTGACTTTGACAGCTAACCTACTTACG 4739

Qy   4780 ACAACTGCCCTTACACCGCAGCCGTGCGCAGCTGACATTGGGAAGCCGCGGCGTGTCTTTT 4839
          | |||||||||||||| | |||| | |||| | ||| ||||||||| ||| |||| | |
Db   4740 ACGACTGCCCTTACACCGCAGCCGTGATATCGGCTGATATCGGAGAAGCGCCGCGGTGTCTTTCT 4799

Qy   4840 CGGGGCTTGCCCCGTTGACGATGCATCCCGATGTGTTAGCTGGCAAAAGTTCGGCGGCGTCA 4899
          || ||||| ||||||| | |||| |||| |||| |||| ||||| |||||| ||||||||
Db   4800 CTGGGCTGCGCCCATTGAGGATGCCCGATGTGTTCAGCTGGCAAAAGTTCGGCGGCGTCA 4859

Qy   4900 ACTTGACCCTTCCTGTTGTCGGGTGGGCCATCGCGGGACCATGTGCCCGTCTCTCCGGCC 4959
          | |||| || | |||||||||||||||||| |||||||| |||||||||| |||||||
Db   4860 CTGAGTGACCTCTTGTGGGTGTTCAGCGGACCATGTGTCGGACCATGTGTCTCTCCGGCC 4919

Qy   4960 CATCGGATGACCCCCAGTGGGCAGGTCTGAAGGGCCGAATCCTGTCCCACTCCTGCTGA 5019
          |||||||||||||||| |||||||||||| ||||| |||| |||| ||||||||||||||
Db   4920 CATCGGATGACCCCCAAATGGGCAGGTCTGCAAATCCTGTCCCAAATCCTGTCCCACTCCTGCTGA 4979

Qy   5020 GGTGGGGCAATGATTTACCATCTAAAGTGCCCGGCCATCACACGTGGACGACCTGGTCC 5079
          |||||||||||||||||||||||||||| |||||||| || |||||||| ||||||||||
Db   4980 GGTGGGGCAATGATTTACCATCTAAAGTGCCGGCCACCATAGTGGACGACCTGGTCC 5039

Qy   5080 GTAGGCTCGGGGTGGCGGAGGGTTACGTCCGGTCGGACCATCTTGATGGTGTG 5139
          | | ||||| |||||| ||||| ||| |||||| ||||||| ||| |||||||
Db   5040 GGAGACTCGGTGTGCGGAGGGTTACGGCCCGGTCGGACATCTTGATGATCG 5099

Qy   5140 GCCTCGCTATTGCGGGGGCATGATCTATCGCGGGTCTCTCGTGGTGGTTA 5199
          |||| |||||| |||| ||| |||||| ||||| || | ||||||| |||
Db   5100 GTCTCAGCTATCGCGGTGGAATGATCTACACCGGTCGTACACCGGGTCGTGGTGA 5159

Qy   5200 CAGACTGGGATGTGAAAGGGGGTGGCGCATGGAGACCAGGCCACGC 5259
          ||||||||||||||||||||||||| ||||||||| |||| |||||||||
Db   5160 CAGACTGGGATGTGAAGGGGGTGGCGCATGGAGACCAGGCCACGC 5219

Qy   5260 CCCAGCCGTGTGCAGGTCCCCCGGTTCCCGGTAGACCATCGCGGCCCAT 5319
          |||||||||| | ||||| || |||||||| || ||||||||||| ||||
Db   5220 CTCAGCCGTGGTGTCAGGTTCCTCCGGTTGAGCCATCGGCGTGAATCAGCACCAT 5279

Qy   5320 CGGATGCCAACACAGTGACACGTGCGGCGGCGGCCATCCAGGTGGATTGCGATTGGTCAG 5379
          |||||| |||| ||| |||||||| | |||||| ||||| |||||| || ||||||||
Db   5280 CGGATGCCAAGACAGTGACGACGTGCTGCGGCGGCCATCCAGGTGGACTGACTGGACTA 5339

Qy   5380 TCATGACCCTGTCGATCGGGAAGTGCTTGGCCTTCCTTGGCCTTGAGTGCCGAGGCCT 5439
          |||||||||| |||| ||||||||||| || ||||||||| ||||||||||||||||
Db   5340 TCATGACTCTGTCGATCGGAGAAGAGTGTTGTCCTTGGCTCTCACGGGGGACGGCCGAGGCCT 5399

Qy   5440 ACGCAGCTACCACCAAGTGCTTGTGGCTGCTACACGGGCCGTCCCCACTG 5499
          | ||| ||| |||||||| || ||| || || || |||||||||||||||
Db   5400 ACACAGCAGCCACCAAGTGCTGCGGCTGCTATACGGGCCGTCCCCACTG 5459

Qy   5500 TTTCAATTGTTGACAAGCTCTTCGCGTACAGACGCACTATCCACTG 5559
          | |||||||||||||||||||||| || ||||| |||||| |||||
Db   5460 TATCCATTGTTGACAAGCTCTTCGCGGTGTGTGGGGCCATTGCCACA 5519

Left column:

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Qy  5560  GTGTAATAGCTGCGGCAGTGGCGGCCTATGGGGCTTCTTAGGAGCCCTCCATTGGCTGCTG  5619
          ||  |||||||||  ||||||||||||||  || |||| ||  |||||  ||||  | |  |
Db  5520  ACGTGATTGCTGCGGCGGGTGGCGGCCGTTCAAAGAGCCCGCGTTGGCAGCCG  5579

Qy  5620  CCGCTTCCTACCTGATGGGGTTGGCGTCGAGGCAACGCGCAAACCCGCTTAGCCTCCG  5679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5580  CGGCTTCCTACCTGATGGGGTTGGCGCAACGCTCAGACGCGTCTCGGCGCATCTG  5639

Qy  5680  CTCTCCTACTAGGGGCCGCTGGGACCGCGTCTGGGCACGCGTCGTGGGGTTAACCATGG  5739
          ||| ||||||||||||||||||||||| |||||||  ||||||||||| |  |||||||
Db  5700  CCCTCCTATTGGGGGCTGCTGGAACCGCGTCCTGTCGTGGGCACTGTCGTGGCACCATGG  5759

Qy  5740  CGGGGCCGTTCATGGGAAGTGCTACCGTCTCGCCTCCCCCTCCTTGGTCACCATTTACTGGGG  5799
          ||||| |  ||||||||||  ||||||||||||| ||  ||| |||||||||||||||||||||
Db  5700  CAGGTGCGTTCATGGGGGCCGCAGGTCTCCCCTGGTCTCCCCTGGTCACCATTTATTGGGG  5759

Qy  5800  CCGTGGGGGCTGGGAGGGCCGTGGTGAATGCGGCTAGCCTTGTCTTCGACTTTATGGCGG  5859
          ||| |||||||||||||||||||||| || ||||||||||||||||||||||||||||||
Db  5820  CCGTGGAGGTTGGGAGGGCTGTGGTGTTTGCAACCGCCAGTGTCTTTGACTCTTCATGGCGG  5879

Qy  5860  GGAAACTATCATCAGAAGATCTGTGGTATGCCATCCCAGTGCTAACCAGTCCGGGGGCAG  5919
          |||||| |||||||||||||| |||||| ||||||||||| | || |||||||||||||
Db  5820  GGAAACTTTCATCAGAAGATCTGTGGTATGCCATCCCGGTACTCCCAGTCCGGGGGCGCG  5879

Qy  5920  GACTTGCGGGGATCCCCTCGGGTTGTTGTACTCAGCTAACAACTCTGGCACTACCA  5979
          ||| || |||||| |||||||||||||||||||||||||||||||||||| ||||||
Db  5880  GCCTTGCGGGGTCGTCTCGGGTTTGTATTCAGCTAACAACTCTGGCACTACCA  5939

Qy  5980  CTTGGTTGAACCGTCGTCGTGCTACTACTTGCCAAGGTCCTCATCGCATCCCTGACAGTTACT  6039
          ||||||||||||||||||||||| ||||||||||||||| | |||||||||||||||||||||
Db  5940  CTTGGTTGAACCGTCGTCGTGCTGCTACCGTCTCATGTATCCCGGACAGTTACT  5999

Qy  6040  TTCAGCAGGCCGATTACTGTGACAAGGTCTCAGCTGTCGCTCCGACGCTTGAGCCTTCACTC  6099
          |||||||||||||| ||| ||||| || |||||||||||||||| |||| ||||||||||||
Db  6000  TTCAGCAAGTTGACTATTGCGACAAGGTCTCAGCCGTGCTCCGCGCGTGCTCCCAGGCCTCACCC  6059

Qy  6100  GCACCGTGGTTGCCCTGGTCAACAGGAGCCTAAGGTGATGAGGTTCAGGTGGGTACG  6159
          ||||||||||| |||  ||||||||||||||||||||||||||||||||||||||||
Db  6060  GCACAGTGGTTGCCCTGGTCAACAGGAGCCTAAGGTGATGAGGTGTACAGGTGGGTATG  6119

Qy  6160  TCTGGGACTTGTGGAGTGGATCATGCGTCAAGTGCGCATGTGATGGCCAGAGTTCGGG  6219
          || |||||||||| |||| |||||||||||||||||| |||| |||||||||| ||||
Db  6120  TCTGGGACCGTGTGGGAGTGGATCATGCGGTCATGTTCATGCGGTCATGGGCACTGTCAGG  6179

Qy  6220  CCCTCGCCCGTGTGTCATTACCCTTATGGCGTATGGGCTATGGGCACTGCGGAGGGGTGGTCCGGGAGAAT  6279
          ||| ||||||||||||| |||||| || ||||||||||| |||||||||| |||||||  ||||
Db  6180  CCCTCGCCCGTGTCATTACCCTTGTGGCGTATGGGCTATGGGCACTGCGGAGGGGTGGTCCGGGGAAT  6239

Qy  6280  GGTTGTTGGACGGCCATGTTGAGAGTCGTTGTCTTGTGGTTGCCGTGAGGTGGTGTACACCGTGATG  6339
          ||||||||||||| |||||| || || ||| |||| |||||||||| ||||||||||||||||||
Db  6240  GGTTGCTTGGACCGTCATGTTGAGAGTCGCCTGCTCCGATCACTGGTGACG  6299

Qy  6340  TTTGAAATGGCAACTCAAAGATCCAGTTACTCTACCAAGCTGTCAGGCATTATTGGA  6399
          |||| ||||||||||||||||  ||| ||| ||||||||||||| ||| |||||||||
Db  6360  CCCACGTTCTTTCTGGCGTCTCAGGGGTCGTGGTGATGCAGTCCATAGAGC  6419

Qy  6400  TGGGACAGTGCCCTGTGAACATGTCTATGGGCGTATGCGAGACGCTGCGCCTCGCCTTGCTGCCTCCAG  6459
          |||| |||||| || |||||||||||  |  |||| |  |||||||||  ||||| |||||||||||
Db  6360  TGGGGACACACTGTGTCCCTGTCTGACGTAAACGTGAAACGTGCTCGCTCCTGCCTCCG  6419

Qy  6460  ACACCCCGAAGGTGTACCAGTTCGGACGTCTGAGGTGGTGTTCAGGTGTGACCCCTA  6519
          |||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db  6420  ACACCCCGAAGGTGTTCCGCTGGCGTCTGAGGTGGTGGTTGGTGACCACTA  6479

Qy  6520  CCCACGTTGTGATCAGGCGGAACATCCGCCTACAAACTGCCTCGACGCATCCTGTCG  6579
          ||| ||||| |||  ||  ||||||||||||| || ||||||||||||||||||
Db  6480  CCCACGTTGTAATCAGGAGAACTTCCGGTAATCCTATCGG  6539

Qy  6580  CTGCTGTTGCTGAGCCTTATTACGTCGACGGCCATACCGTGTCTCATGGGACGGCGGCGC  6639
          ||||||||  | || |||| |||| |||| |||||  ||||||||||||| |||||||||
Db  6540  CTGCTGTTGTGAGCCTCACCGTGTCTCATGGGACGGCGGACGCTC  6599

Qy  6640  GAGCGGCCTGCCATGGTCATGGCCCATGGTGCCGGGCAAAGTGTCACCATTGACCAGGCTACA  6699
          |||||||||||||||||||| |||  |||||||||||||||||||||||||||||||||||||
Db  6699
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Right column:

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Db  6600  GTGCGCCCGGCCCATGGTCTATGGCGGCTTGCTGGCCCTGGGGCAAAGTGTTACCATTGACGGGGGCTG  6659

Qy  6700  CCCTTCCGCATCAACTGCGGCTTAGGAATGTGGCGCCCCTGAGGTGTCATCCGAGGTGT  6759
          || ||  ||||||||||||||  || |||| |||||||| ||||||||||||||||||||
Db  6660  CCCTGCCTCATCAACTGAGGCTCAGGAATGTGGCGCCCCTGAGGTTTCATCCGAGGTGT  6719

Qy  6760  CCATTGACATTGGGACGGCAGGACTGAGACTCAGAACTGACTGACCGGCTGGTCATGA  6819
          ||||||||  |||||||||| ||||||||| | |||||||  ||||||||||||||||
Db  6720  CCATTGACATTGGGACGGACTGGAGACTGACTGACCGATCTGCCGCCGG  6779

Qy  6820  CGGCTGCGAGCCCTTCAGGCTATCGCAGAATGCTGCGAGAATTCTGAACCTCACATAGATG  6879
          ||||||||  | ||||  ||  ||||||||||||  ||||||||||||||| |||||| |||
Db  6780  CGGCTGCTGTCTCCAAGCGATCGAGGAGCAATTCTTGAACCGCCACCATTGATG  6839

Qy  6880  TCATCATGGAAGATTCAGTACACCCTCTTTGTGGGAGTACGCCGAGATGCCTGTGT  6939
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  6840  CCATCATGGGAGGACTGCAGTCGTCAGTACACCCTCTTGTGGTGAGATGCCTGTAT  6899

Qy  6940  GGGGAGAAGACATACCCCGCACTCATCGCCAGCACTTACTCGGTTACTGAGCAGCC  6999
          |||||||||||||||||||| ||||||||||||||||||||||||||| ||||||||
Db  6900  GGGGAGAAGACATCCCGTACTCGCCAGCACTTACTCGGTTACTGAGCAGCT  6959

Qy  7000  CAGATGAGAGACCCCGTCTTCCTCGCAGGAGATACCCCGTC  7059
          |||||||||||||||| ||||  |||||||||||||||||||
Db  6960  CAGATGAGAGACCCCGTCTCCTCGCAGGAGATACCCCGTC  7019

Qy  7060  TCGAGGTCATCCAAGAGTCGTGGATGAATCCAGAGAAATGGAAATCAACGTCTTCAACGTCTGCTC  7119
          | ||||||||||||||| ||||| ||||| |||||||||||||||||||||||||||||||||||
Db  7020  TCGAGGTCATCCAAGAGTCGTGGAGATGTGGATGGAAATCCAGAGAACCAGAGCGTCTTCAACGTCTGGCTC  7079

Qy  7120  TTTCCGTACTAAAAGCCTTGTTTCCACAGAGCGATGCCAGAAGAAGCTTACCCGTTAAGA  7179
          |||||||||| ||||||||||||||||||||||||||||||| ||||||||||||| ||||
Db  7080  TTTCCGTATTTAGAAGCCTCATTCCACAGAGCGACGACCGACCAGGAGAAGCTTACCCGTTCAAGA  7139

Qy  7180  TGTCATGCGTGTTGAGAAGAGCGTAACACGTTGCTTCTTCATTGGATTGACGGTCGCTG  7239
          || |||||||||| |||| |||||||||||||  || ||  || |||||||||||||||
Db  7140  TGTCGTGCTTCCGTTGAAAAGAGCGTCACGCGCCGCTTTTTCTCATTGGGGTTGACGGTGGCTG  7199

Qy  7240  ACGTGCCAAGCCGTGTGAGATGAAATCAGAGAATCCATACAGCCTATTGTGACAAGGTGC  7299
          | | |||||||||||||| ||| || ||||||| | |||||||||  ||||||||||||||
Db  7200  ATGTTGCTAGCCGTGTGAGATGAAATCCAGAGAACCATACAGCCTAATGTGACAAGGTGC  7259

Qy  7300  GCACTCCGCTTGAATTGCAGGTTGGGTGCTTGGTGGTCGTGGGCAATGAACTTACCTTTGAATGTG  7359
          ||||| ||||||||||||||||||| ||||  |||||||||| ||||||||||||||||||||||
Db  7260  GCACTCCGCTTGAATTGCAGGTTGGGTGCTTGGTGGTCGTGGGCAATGAACTTACCTTTGAATGTG  7319

Qy  7360  ACAAGTGTAGGCAAGAGACCTTGCTGCTCCTCTCTTACATTTGGCTGTGGGGGTGTG  7419
          ||||||||||||||||| ||||||||||| ||  || |||| |||||||| ||||||
Db  7320  ACAAGTGTAGGCAAGGCAGAAACCTTGGCCTCCTCCTTTACACTTGGGTTCTGGGAGTGC  7379

Qy  7420  CACTGACGAGGGCCACTCCGGTTGCTCCTTCTTGGAGCCGGTTGCCTCCTGG  7479
          |||  |||||||||||||||||| |||||||||||||||||| |||| ||||
Db  7380  CGCTGACTAGGGCCACCGCACGCCCGTCCCGTCCCGTGGTGAGGCCGGTTGGCTCTTATTAG  7439

Qy  7480  TGGCCGACACCACCCAAGGTGTATGTCACCAACCCGGACAATGTTGGGAGAAGAGTTGACA  7539
          ||||||||| ||||||||||| ||||||||||  ||| ||||||||||||| |||||||||
Db  7440  TGGCCGACACTACTAAGGTGTATGTTACCAATCCAGACAATGTGGGACGGAGGGTGGACA  7499

Qy  7540  AGGTTACCTTCTGGGCTGCCCCTGGGTGTGGTCCCATAGAGC  7599
          |||  || ||||||||| |||| || ||||||| ||||||||
Db  7500  AGGTGACCTTCTGGGCGTCCTCCTAGGGTTCATGATAAGTACCTGTCTATTGAGC  7559

Qy  7600  GCGGTAAGAGGGGCAGCTCAAGCGCTTACACTTATGAGGAGGCAATAA  7659
          ||||| |||||||||||| ||||||  ||||||||| |||||||||||
Db  7560  GCGGCTAAGAGGGGCCGCTCAAGCGCCTGCTCTAAGCATGGGTTACACTTATGAGGAAGCAATAA  7619

Qy  7660  GGACTGTAAGGCCACATGGCTGGGATCCTAAGGTGTCGGTCAAGGACCTCG  7719
          |||||| |||||||||| | || ||||| |||||||||| ||||||| |||
Db  7620  GGACTGTAAGGCCACATGGCTGGGATCCTAAGGTGTCGGTTAAGGACTTAG  7679

Qy  7720  CCACCCCTGCGGGGAAGATGCTGTCCAGGATGCTTCCATTGACGGGCAAAGTGTCACCATTGACGGGGAACCGCTACA  7779
          ||||||||  || |||||| |||  ||||  |||||||||||||||||||||||||||| |||||||||||  |||||
Db  7720  -
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Db  7680  CCACCCCGCGGGGAAGAATGCCGTCCATGACCGGCTCCAGGAGATACTTGAAGGGACTC  7739

Qy  7780  CAGTCCCCTTTACTCTTACTGTGAAAAAGGAAGTGTTCTTCAAAGACCGAAGGAAGAGA  7839
          | ||||||||||||||||||||||||||||||  ||||||||||||||| |||| ||
Db  7740  CGGTCCCCTTTACTCTTACTGTGAAAAAGGAGGTGTTCTTCAAAGACCGGAGGAGGAGG  7799

Qy  7840  AGGCCCCCGCCGCTCATTGTGTTCCCCCCTGACTTCCGGATAGCTGAAAAGCTTATTC   7899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db  7800  AGGCCCCCGCCGCTCATTGTGTTCCCCCCTGACTTCCGGATAGCTGAAAAGCTCATCT   7859

Qy  7900  TGGGAGACCCTGGACGGGTAGCCAAGCGGTGTTGGGGGGGCCTACGCCTTCCAGTACA   7959
          ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db  7860  TGGGAGACCCGGACCGGGTAGCCAAGCGGTGTTGGGGGGGCCTACGCCTTCCAGTACA   7919

Qy  7960  CCCCAAATCAGCGAATTAGGAGATGCTCAAACTGTGGGAATCAAAGAAGCACCATGCG   8019
          ||||||||||||||  ||||||||||||||||  ||||||||||| ||||  || ||||
Db  7920  CCCCAAATCAGCGAGTTAAGGAGATGCTCAAGCTATGGGAGTCTAAGAAGCACCCCTTGCG 7979

Qy  8020  CCATCTGTGTGGACGCGCCACATGCTTCGACAGTAGCATAAACTGAAGAGGACGTGGCGCTGG 8079
          ||||||||||||| |||||||||| |||||||||||||| |||||||||||||||| ||||
Db  7980  CCATCTGTGTGGACGCCACCTGCTTGACAGTAGCATAAACTGAAGAGGACGTGGCTTTGG  8039

Qy  8080  AGACAGAGCTTTATGCCCTGGCTTCAGACCATCCAGAATGGGTGCGTGCCCTGCCCTGGGAAAT 8139
          ||||||||||||||  ||  |||||||||||  |||||||||||  ||||||||||||||||
Db  8040  AGACAGAGCTGTACGCTCGGCCTCTGACCATCCAGAATGGGTGCGGGCACTTGGGAAAT  8099

Qy  8140  ACTATGCCTCTGCCACAATGGTAACCCCGAGGGGGTGCCAGTGGGTGGAGAGGTATTGTA  8199
          ||||||||||||||| |||| ||||||||||||| ||||||| |||||||||||||| ||
Db  8100  ACTATGCCTCAGGCACCATGGTCACCCCGAGGGGGTGCCAGTGGGTGAGAGGTATTGCA  8159

Qy  8200  GATCCCAGGGGTCTTCGACCACCAGTGCGAGCAACTGCTTGACTTGCTATATCAAGGTGA  8259
          |||||||||||| || ||  |||||||||||||||||||||||| |||| |||||||||
Db  8160  GATCCTCGGGGTGTCCTGACTACGGGCGCGAGCAACTGCTTGACCTTGACCTACATCAAGGTGA 8219

Qy  8260  AAGCCCCTGTGAGAGGTGGGCTGAAAAATGTCTCGCTCCTCATCGCTGCCGATGACT   8319
          ||||||||||||||||||||||||||||||||| | |||||||||| || ||||||||
Db  8220  AAGCCGGCTGTGAGAGGTGGGCTGAAGATGCTCTCTCTTCTCCATAGCCGCGGATGACT   8279

Qy  8320  GTTTGATCATATGCGAACGGCCGTGTGCGATCCTAGCGACGCCTTTGGGCAGAGCCCCTGG  8379
          |  || |||||| | |||||||||||||||| |  | |||||||||||||||||||||||
Db  8280  GCTTGATCATATGTGACGGGCCAGTGTCGCACCCCAAGCGACGCCTTTGGGCAGAGCCCCTAG 8339

Qy  8380  CGAGCTACGGGTACGCATGCCGAGCCTTCGTATCATGCATCACTGGACACGGCGCCCCTTCT 8439
          ||||| ||||||| | ||  ||||||||| | |||||||| |||||||||||||||||||
Db  8340  CGAGCTATGGGTACGCAGGCGGAGCCCTCATATCATGCATCACCTTGGACACGGCGCCCCTTCT 8399

Qy  8440  GCTCCACTTGGCTAGCTGAGTGCAATGCAGATGCAGATGGGAAACGCCATTTCTTCCTGACCACGG 8499
          ||||||| ||||| |||||||||||| || |||| |||||||| || ||| |||| |||||||||
Db  8400  GCTCCACTTGGCTTGCTGAGTCAATGCAGATCGAGATGGGAAGCCGCCATTTTCTTCCTGACCACGG 8459

Qy  8500  ACTTTCGGAGGCCCCTTCGCCATGTCGCTCGCCATGTCGCAGGTACAGTGACCCAATGGCCTTCGGCCA 8559
          ||||  |||||||||||||||||| | ||||||||  | |||| ||| ||||  ||||||||||||
Db  8460  ACTTCCGGAGGCCCCTTCGCTGCTCGCCATGTCGCGTGAGTAGTGACCCGATGGCCTTCGGCCGA 8519

Qy  8560  TCGGTTACATCCTCCTATACCCTGGCATCCTATCACACGGTGGGTCATCATCCCTCACG  8619
          |||||||||| || ||  |  |||||||  |||||||||||||||| |||||||||||||
Db  8520  TCGGTTACATCCTCCTTATCCTTGGCACCCCATCACACGGTGGGTCATCATCCCTCATG  8579

Qy  8620  TGCTCACCTGCGCGTTTAGGGTGGTTGGTGGCACCACCGTCTGATCCTGTGTGGTGCCAGTTAC 8679
          |||||||||||| || ||||| |||||||||||||||| || |  |||| |||||||||||||
Db  8580  TGCTAACGTGCGCCATTCAGGGGTGGAGGCGGCACACCGTCGATCCTGTGATCCGGTGCCAGTTAC 8639

Qy  8680  ATGGTAATTACTACAAGTTCCACTGGACAAAACTGCCTAACATCATCGTTCCCTCACG  8739
          ||||| ||| |||||||||||||||||||||| |||||||| |||||||||||||||||
Db  8640  ATGGTAACTACTACAAGTTCCACTGGACAAAACTGCCTAACATCATCGTGCCCCTCACG  8699

Qy  8740  GACCAGCAGCGTTGAGGGTTACCGCACAGACAACTAAGACAAAAATGGAGGCTGGCCAAGG 8799
          ||||||||||||||||||||||||||| ||||||| |||| ||||  ||||| |  |||||
Db  8700  GACCAGCAGCGTTGAGGGTTACCGCACACACAACTAAGATGGAGGCTGGTTAAGG  8759

Qy  8800  TGCTGAGCGACCTCAAGCTCCCTGCCTAGCAGTCCACCGGAAGAAGGCCGGGGCATTGC  8859
          ||||||||||||||||||||  || ||||||||||||||||||||||| ||||||||||
Db  8760  TTCTGAGCGACCTCAAGCTCCCTGGCTAGCAGTCCACCGGAAAGAGAGGCCGGGGCGTTGC  8819
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Db  8860  GAACCGCGTATGCTCCGGTCGCGCGCGGTTGGGCTGAGCTGTGTTGGGCGTC  8919
          ||| ||  ||||| |||||||| |||| ||||| ||||  ||||||||||||||
Db  8820  GAACACGCCATGCTGCGGTCGCGCGCGGTTGGGCTGAGCTTGCTTGTTGTGGCATC  8879

Qy  8920  CAGGCCTGCGGCTTCCCCCTCCGGAGATTGCTGCGGTATCCCGGGGGGTTCCCCCTTTCCC  8979
          ||||||||||||||||||||||  ||| ||||| ||||||||| ||||||||| |  ||||
Db  8880  CAGGCCTACGGCTTCCCCCTGACGGATTGCTGCGGTATCCCGGGGGGTTCCCTCTCCCC  8939

Qy  8980  CCCCCTATATGGGGTGGTTCATCAATTGGATTCAACAAGCCAGAGAGTCGCTGGCGGT  9039
          ||||||||||||||| |  ||||| ||||||| | ||||||||||||||||| ||||||
Db  8940  CCCCCTATATGGGGTTTACAAGCCAGAGAGTCGCTGGCGGT  8999

Qy  9040  GGTTGGGGTTCTTAGCCCTGCTCATCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTT  9099
          ||||| |||| | || ||||||| |||||||||| |||||||| ||||||||||||||||
Db  9000  GGTTGGGGTTCTTAGCCCTCGTAGCCCTCTTCGGGTGAACTAAATTCATCTGTT  9059

Qy  9100  GCGGCAAGGTCCGTGACTGACTAATGGCATGGTTCCCGCCCCTCCCCGCCCCAGGG  9159
          ||| ||||| ||| ||||||||| | || |||||||||||||||||||||||||||
Db  9060  GCGGCGAGGTCTGTGACTGACTAATGTCTCACCGGAGGTTCCCGCCCCTCCCCGCCCCAGGG  9119

Qy  9160  GTCTCCCCGCTGGGTAAAAAGGGCCCGGCCTTGGGAGGCATGGTTGTTACTAACCCCCTG  9219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9120  GTCTCCCCGCTGGGTAAAAAGGGCCCGGCCTTGGGAGGCATGGTTGTTACTAACCCCCTG  9179

Qy  9220  GCAGGGTCAAAGCCTGATGGTGTCTAATGCACTGCCACTTCGGTGCGGGTCGCTACCTTA  9279
          |||||||  ||||| | |||||||||||||| |||||| |||||||||||||||||||||
Db  9180  GCAGGGTTAAAGCCTGATGTGTCTAATGCACTGCCACTTCGGTGCGGGTCGCTACCTTA  9239

Qy  9280  TAGCGTAATCCGTGACTACGGGCTGCTCCGAGCCCCTCCCCGAGCCCCCGATGGGCCACAGTGCAC 9339
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  9240  TAGCGTAATCCGTGACTACGGGCTGCTCCGAGCCCCTCCCCGAGCCCCCGATGGGCCACAGTGCAC 9299

Qy  9340  TGTGATCGAAGGGGTGCACCCCGGTAA  9367
          || |||||||||||||| |||||||||
Db  9300  TGAGATCTGAAGGGGTGCACCCCGGGAA  9327
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Search completed: October  9, 2002, 03:22:01
Job time : 10951 secs
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